

98	565.2	38.1	582.5	BP209837	BP209837	171	393.6	26.5	505.7	CM332972
99	564.6	38.0	921.4	BP547056	BP547056	172	393.4	26.5	491.6	CD552555
100	563.4	37.9	620.1	BM016283	BM016283	173	391.8	26.4	514.6	AI105051
101	554.8	37.4	558.5	BP338657	BP338657	174	391.8	26.3	503.2	BE048740
102	553.8	37.3	557.4	BP1063664	IL3-UT01.1	175	390.6	26.3	833.3	BI690860
103	551.4	37.1	581.5	BP314951	BP314951	176	389.8	26.2	712.4	BI413660
104	547.8	36.9	564.5	BP276942	BP276942	177	388.4	26.2	502.1	AA771125
105	546.4	36.8	574.4	BP981070	602310292	178	382.4	25.8	696.2	BE782251
106	545.2	36.7	581.5	BP276312	BP276312	179	381.4	25.7	593.5	BP307809
107	545	36.7	582.5	BP201409	BP201409	180	381.4	25.7	724.5	EX669268
108	541.2	36.4	582.5	BP200472	BP200472	181	380	25.6	486.6	CD555983
109	536.4	36.1	538.7	CN389163	CN389163	182	380	25.6	489.6	CD563086
110	531.8	35.8	535.4	BI828549	603078437	183	378.6	25.5	483.4	BE061538
111	531.6	35.8	572.7	CR769410	DMZP463A	184	378.6	25.4	448.1	AI991455
112	530.8	35.7	859.4	BP169273	603385477	185	376.6	25.4	745.6	CA317425
113	527.4	35.5	583.5	BP210065	BP210065	186	376.6	25.3	509.7	H38402
114	526.4	35.4	762.4	BI759941	603044370	187	374.6	25.2	765.6	CA9292190
115	521.4	35.1	762.5	BP455530	BP455530	188	370	24.9	1181.4	BE971521
116	519.8	35.0	886.4	BI522778	603175862	189	369.2	24.9	450.5	BQ290404
117	516.4	34.8	519.4	BM712632	UT-E-EO-	190	368	24.8	582.5	BP256865
118	515.8	34.7	786.5	BM712632	EX390052	191	368	24.8	366.2	BE048014
119	512	34.5	582.5	BP360443	BP360443	192	364	24.5	929.4	BI765290
120	511	34.4	582.5	BP310036	BP310036	193	362.8	24.4	925.4	BI835577
121	506.4	34.1	508.2	BP593274	7058H08.X	194	357.4	24.1	399.1	AI923506
122	502.6	33.8	789.4	BI838884	603087255	195	357	24.0	358.1	AI1202519
123	501.4	33.8	505.7	CN389161	170005338	196	357	24.0	358.1	AI1202519
124	501	33.7	501.4	BM797230	K-EST0080	197	357	24.0	856.4	BI769105
125	490.8	33.1	494.7	CN389162	170004276	198	353	23.8	354.1	AI650570
126	479	32.3	674.2	BP528522	602043502	199	349	23.5	602.5	BE194456
127	472.4	31.8	528.1	AA205873	AA205873	200	348	23.4	437.7	H48181
128	457.2	30.8	579.4	BM015437	603641625	201	346.8	23.4	447.1	AA016714
129	451.6	30.4	641.5	BQ234450	BQ234450	202	346.2	23.3	474.4	BI103185
130	450.2	30.3	477.1	AI012717	AD45d12.9	203	345.8	23.3	474.4	BI103185
131	449.2	30.2	581.5	BP348656	BP348656	204	344.2	23.2	451.5	EX330868
132	448.8	30.2	452.1	AA743902	CB05B02.8	205	338.8	22.8	461.2	BE793478
133	443.6	29.9	577.5	BQ233938	BQ233938	206	338	22.8	338.7	CN389158
134	443	29.8	572.4	BQ233938	BQ233938	207	337	22.7	337.7	AM194588
135	441	29.7	547.1	BI523405	BI523405	208	336.6	22.7	767.6	AM194588
136	441	29.7	547.1	BQ233937	qf39h07.9	209	335.2	22.6	581.5	BP362329
137	438.2	29.5	457.1	AI826065	wk28b06.x	210	334.4	22.5	387.7	W76917
138	437.4	29.5	2427.3	AK045539	Mus muscu	211	334.4	22.5	489.9	BE396181
139	435.8	29.3	828.7	CP952132	CP952132	212	330.6	22.3	495.2	AM952422
140	435.8	29.3	931.5	B0516181	UT-M-HLO-	213	327.2	22.0	519.1	AI790943
141	428.6	28.9	2910.3	AK028955	Mus muscu	214	322.2	21.7	355.4	BF954537
142	428.6	28.8	882.6	CA977847	AGENCYCOURT	215	322	21.7	353.1	AA328405
143	427.2	28.8	763.5	B0558976	B0558976	216	322	21.7	583.5	BP308011
144	425.6	28.7	875.6	CA462133	AGENCYCOURT	217	321.8	21.7	645.2	AM961113
145	424.4	28.6	426.1	AI244708	q192b09.x	218	321.4	21.6	478.1	AA592448
146	421.4	28.4	844.6	CA481096	AGENCYCOURT	219	321	21.6	330.7	CN389164
147	421.2	28.4	864.6	CA494764	AGENCYCOURT	220	318	21.4	327.2	AM087794
148	420	28.3	574.6	CB575856	AGENCYCOURT	221	307	20.7	442.2	BB847205
149	419.4	28.2	547.5	BP339377	BP339377	222	305.8	20.6	582.4	BI337628
150	419.2	28.2	744.7	CB595984	AGENCYCOURT	223	301.8	20.3	675.6	CH955311
151	417.8	28.1	649.6	BY737042	BY737042	224	301.4	20.1	470.7	H41594
152	417.8	28.1	653.2	BB643983	BB643983	225	299	20.1	379.2	BP089310
153	417.8	28.1	596.2	BB611100	BB611100	226	298.2	20.1	424.1	AA815577
154	417.8	28.1	744.5	BQ746584	UT-M-ERO-	227	297	20.0	409.2	BB850462
155	417.8	28.1	807.6	CA468685	AGENCYCOURT	228	294	19.8	484.4	CV029091
156	417.8	28.1	849.7	CK789647	AGENCYCOURT	229	293	19.7	493.9	AY414945
157	417.2	28.1	686.7	CF168746	B0804A09-	230	291.6	19.6	437.2	AM204234
158	417.2	28.1	689.7	CF168755	B0804A02-	231	291	19.6	293.9	AY414946
159	415.8	28.0	588.5	BQ257760	NISC_Kp05	232	289.6	19.5	322.1	AI470870
160	415.8	28.0	591.4	BQ808095	H3058G01-	233	287.2	19.3	355.6	BI793102
161	412.4	27.8	708.2	BE279745	601157722	234	285.2	19.2	307.1	AA233558
162	410.8	27.7	594.6	CB545546	AMGNNUC:N	235	280.8	18.9	327.1	AA206055
163	409.4	27.6	505.2	BF723284	maB30B06.	236	280.8	18.9	931.5	BQ708775
164	409	27.5	608.2	BB613347	BB613347	237	277.4	18.7	280.2	BE928022
165	405.8	27.3	526.6	CB719919	AMGNNUC:N	238	277.2	18.7	459.1	AA656581
166	404.8	27.3	780.5	BU708166	UT-M-FCO-	239	277.2	18.7	582.5	BP274760
167	404.6	27.2	517.6	CD561266	B0427G08-	240	275.8	18.6	477.2	AM319231
168	403.2	27.2	527.7	H41343	YmB1f08.r1	241	274.8	18.5	583.5	BP361943
169	400.4	27.0	513.3	N28515	YK37a01.r1	242	272	18.3	335.6	BP782047
170	395.2	26.6	722.2	BE890311	601431764	243	271.8	18.3	634.6	CB271068

244	271.8	18.3	640	4	B1390073	B1390073 ppp1c.pk0	317	228.6	15.4	442	4	B1875973	B1875973 f165903.y
245	271.8	18.3	672	5	B0277862	B0277862 603577269	318	228.2	15.4	619	4	B1876510	B1876510 f185c09.y
246	270.6	18.2	669	4	B1103099	B1103099 602889328	319	224.8	15.1	516	7	C0799071	C0799071 AGENCOURT
247	270.2	18.2	542	4	BG709745	BG709745 pgl1n.pk0	320	224	15.1	265	1	A1527943	A1527943 u138a12.y
248	270.2	18.2	667	5	B0280025	B0280025 603599847	321	222.8	15.0	928	4	B1090937	B1090937 602859175
249	270	18.2	378	2	BB847268	BB847268 BB847268	322	218.2	14.7	771	7	CV111128	CV111128 AGENCOURT
250	268.8	18.1	313	1	A1527941	A1527941 u138a10.y	323	216.8	14.6	433	3	H49932	H49932 y025a02.r1
251	267.8	18.0	839	5	B0107229	B0107229 603110585	324	213.4	14.4	710	2	BF937885	BF937885 fme69h08.y
252	267.6	18.0	511	1	AA821445	AA821445 v625f01.r	325	210.4	14.2	685	9	CC519350	CC519350 CH240.366
253	267.2	18.0	365	5	BY230544	BY230544 BY230544	326	210.2	14.2	302	2	BB565259	BB565259 BB565259
254	266.2	17.9	395	5	BY025499	BY025499 BY025499	327	209	14.1	727	6	CB593062	CB593062 AGENCOURT
255	265.4	17.9	363	5	BY036259	BY036259 BY036259	328	209	14.1	860	6	CD253668	CD253668 AGENCOURT
256	263.2	17.7	1217	2	BB535866	BB535866 601060567	329	209	14.1	881	7	CF591853	CF591853 AGENCOURT
257	263.2	17.7	383	5	BY023280	BY023280 BY023280	330	209	14.1	892	6	CB198304	CB198304 AGENCOURT
258	262	17.6	375	1	AA110032	AA110032 mp10b11.r	331	207.4	14.0	653	7	CN084451	CN084451 EC2BBA24A
259	260.8	17.6	704	7	CO505714	CO505714 GGEZEB102	332	207.4	14.0	756	7	CN075936	CN075936 EC2BBA11A
260	260	17.5	456	1	AA657100	AA657100 vs23e12.r	333	207.4	14.0	927	7	CK441905	CK441905 CR441905
261	259.2	17.5	391	5	BY126248	BY126248 BY126248	334	207	13.9	797	7	CK363543	CK363543 AGENCOURT
262	258.8	17.4	377	5	BY025812	BY025812 BY025812	335	206.6	13.9	764	7	CF271342	CF271342 AGENCOURT
263	257.8	17.4	293	9	AY414947	AY414947 Mus. musicu	336	206.6	13.9	942	7	CK803918	CK803918 AGENCOURT
264	257.8	17.4	691	5	B0302599	B0302599 603737887	337	205.8	13.9	909	7	CO801966	CO801966 AGENCOURT
265	256.8	17.3	356	5	BY235679	BY235679 BY235679	338	205.2	13.8	264	2	BB864814	BB864814 BB864814
266	255.8	17.2	285	1	AA339850	AA339850 EST14971	339	205	13.8	832	7	CK797080	CK797080 AGENCOURT
267	254.2	17.1	680	5	BU454572	BU454572 603767910	340	201.8	13.6	929	7	CN325880	CN325880 AGENCOURT
268	251	16.9	379	5	B0029649	B0029649 UI-H-DT0-	341	197	13.3	737	7	CO581559	CO581559 ILLUMIGEN
269	248	16.7	360	1	A1358973	A1358973 qy19f08.x	342	196.2	13.2	803	2	BF106155	BF106155 AGENCOURT
270	245	16.5	718	7	CV118715	CV118715 AGENCOURT	343	196	13.2	410	1	A1263238	A1263238 q236h07.x
271	245	16.5	772	7	CF347849	CF347849 AGENCOURT	344	195.6	13.2	388	6	CB84427	CB84427 C08427 Carp
272	244.2	16.4	354	5	BY232554	BY232554 BY232554	345	195.2	13.1	760	7	CN057491	CN057491 Salamande
273	243.8	16.4	302	6	BY783751	BY783751 BY783751	346	193.8	13.1	554	1	AJ709348	AJ709348 AJ709348
274	243.4	16.4	670	7	CV490080	CV490080 AGENCOURT	347	193.8	13.1	558	2	BB856263	BB856263 7E91e02.x
275	243.4	16.4	708	7	CN512587	CN512587 AGENCOURT	348	193.8	13.1	647	1	AV715206	AV715206 AGENCOURT
276	243.4	16.4	784	7	CP998223	CP998223 AGENCOURT	349	192.8	13.0	638	4	BG435747	BG435747 602506851
277	243.4	16.4	790	7	CK017959	CK017959 AGENCOURT	350	192.8	13.0	647	6	CD521600	CD521600 AGENCOURT
278	243.4	16.4	844	7	CK363113	CK363113 AGENCOURT	351	192.6	13.0	819	6	CD521694	CD521694 AGENCOURT
279	242.4	16.4	853	7	CN176901	CN176901 AGENCOURT	352	192.2	12.9	519	1	AA482171	AA482171 aa53d12.r
280	242.4	16.3	583	5	BP349530	BP349530 BP349530	353	192.2	12.9	535	4	BF439336	BF439336 UI-E-COI-
281	241.8	16.3	566	4	BI876477	BI876477 f172h06.y	354	192.2	12.9	549	2	BF438657	BF438657 nab89e05.
282	241.8	16.3	567	4	BI875861	BI875861 f164a09.y	355	192.2	12.9	560	5	BU198346	BU198346 DCBGMF07
283	241.8	16.3	575	1	A1722021	A1722021 f618d09.y	356	192.2	12.9	574	6	CA307834	CA307834 UI-H-FPTI-
284	241.8	16.3	579	2	BF157393	BF157393 f149g06.y	357	192.2	12.9	604	2	AM951219	AM951219 EST363289
285	241.8	16.3	602	4	BM315713	BM315713 f6w4c03.y	358	192.2	12.9	647	7	CK004698	CK004698 AGENCOURT
286	241.8	16.3	622	2	AM343367	AM343367 f176f12.y	359	192.2	12.9	649	5	BU929744	BU929744 AGENCOURT
287	241.8	16.3	637	2	AM343018	AM343018 f172c03.y	360	192.2	12.9	653	1	AV735265	AV735265 AV735265
288	241.8	16.3	655	5	BM889951	BM889951 f6y3c06.y	361	192.2	12.9	660	6	CD522794	CD522794 AGENCOURT
289	241.8	16.3	680	4	BM777661	BM777661 f6y3f09.y	362	192.2	12.9	676	1	AV733822	AV733822 AGENCOURT
290	241.8	16.3	733	4	BI888826	BI888826 ZP637-2-0	363	192.2	12.9	692	5	BU929850	BU929850 AGENCOURT
291	241.8	16.3	747	7	CV490839	CV490839 AGENCOURT	364	192.2	12.9	705	1	AV714777	AV714777 AGENCOURT
292	241.8	16.3	791	7	CV120378	CV120378 AGENCOURT	365	192.2	12.9	710	1	AV714667	AV714667 AGENCOURT
293	241.8	16.3	819	7	CN020307	CN020307 AGENCOURT	366	192.2	12.9	736	1	AV714455	AV714455 AGENCOURT
294	241.8	16.3	841	7	CO814959	CO814959 AGENCOURT	367	191.8	12.9	642	1	AV715253	AV715253 AGENCOURT
295	241.8	16.3	855	7	CN024858	CN024858 AGENCOURT	368	191.4	12.9	732	2	BF527057	BF527057 602039969
296	241.8	16.3	882	7	CO925434	CO925434 AGENCOURT	369	191.2	12.9	566	1	A1147216	A1147216 qab89c10.x
297	241.8	16.3	918	7	CN832815	CN832815 AGENCOURT	370	190.6	12.8	556	5	BU198397	BU198397 DCBBA12
298	241.4	16.3	541	5	B0285026	B0285026 faa17e08.	371	190.6	12.8	598	5	BU199056	BU199056 DCBVC09
299	241.4	16.3	597	4	BM775975	BM775975 f6y19d07.y	372	190.6	12.8	633	6	CD521795	CD521795 AGENCOURT
300	241.2	16.2	791	7	CN021410	CN021410 AGENCOURT	373	190.6	12.8	639	1	AV717067	AV717067 AGENCOURT
301	241	16.2	936	7	CN179527	CN179527 AGENCOURT	374	190.6	12.8	659	1	AV717298	AV717298 AGENCOURT
302	240.4	16.2	551	2	AM174473	AM174473 f143f04.y	375	190.6	12.8	665	1	AV715034	AV715034 AGENCOURT
303	240.2	16.2	554	2	AM422967	AM422967 f166f01.y	376	190.6	12.8	697	1	AV717754	AV717754 AGENCOURT
304	240.2	16.2	612	2	AM134031	AM134031 f114f08.y	377	190.6	12.8	698	7	CN094476	CN094476 EC2BBA3DC
305	240.2	16.2	647	7	BM776472	BM776472 f6y25h12.y	378	190.6	12.8	700	6	CD614977	CD614977 AGENCOURT
306	238.2	16.0	742	7	CV119794	CV119794 AGENCOURT	379	190.6	12.8	710	1	AV713498	AV713498 AGENCOURT
307	236.4	15.9	448	1	AA206236	AA206236 zq54c06.r	380	190.2	12.8	534	1	AV716954	AV716954 AGENCOURT
308	235.8	15.9	859	7	CO916637	CO916637 AGENCOURT	381	190.2	12.8	709	1	AV707768	AV707768 a635c03.x
309	235	15.8	590	1	A0176996	A0176996 AU176996	382	189.4	12.8	547	1	AV716847	AV716847 AGENCOURT
310	234.4	15.8	417	5	BG061227	BG061227 BY061227	383	189.4	12.8	534	1	A1707931	A1707931 a634f01.x
311	234.4	15.7	323	4	BG062669	BG062669 L0956807-	384	189.4	12.8	558	6	CB053926	CB053926 NISC_gm01
312	233.6	15.7	709	5	BX082727	BX082727 BX082727	385	189.4	12.8	596	6	CB053925	CB053925 NISC_gm01
313	233.2	15.7	727	5	B0042180	B0042180 UI-M-E00-	386	189.4	12.8	598	6	CD521003	CD521003 AGENCOURT
314	231.4	15.6	685	5	B0279023	B0279023 603601345	387	189.4	12.8	603	1	AV715633	AV715633 AGENCOURT
315	231.2	15.6	494	4	BG062759	BG062759 L0957E03-	388	189.4	12.8	648	1	AV714479	AV714479 AGENCOURT
316	229.6	15.5	527	4	BG738554	BG738554 f6p0a07.y	389	189.4	12.8	654	1	AV715129	AV715129 AGENCOURT

390	189.4	12.8	721	1	AV716806	AV716806	AV716806	463	177.2	11.9	401	2	BF039286
391	189	12.7	584	1	AV713748	AV713748	AV713748	464	177	11.9	613	1	AV735626
392	189	12.7	590	1	AV715528	AV715528	AV715528	465	176.8	11.9	457	4	BI244719
393	189	12.7	706	1	AV716279	AV716279	AV716279	466	175.6	11.8	557	1	AA854452
394	189	12.7	707	1	AV716933	AV716933	AV716933	467	173.4	11.7	474	5	BO037559
395	188.4	12.7	419	9	AV421431	Homo sapi	AV421431	468	173.4	11.7	594	5	BO198503
396	188.4	12.7	588	5	BU198551	DCBWA04	CE271352	469	173.2	11.7	580	5	BP331936
397	188.2	12.7	759	7	BI555766	AV714543	AV714543	470	172.6	11.6	672	7	CN834368
398	188	12.7	528	4	BI555766	AV714543	AV714543	471	171.6	11.6	619	5	BU199128
399	188	12.7	731	1	AV714543	AV714543	AV714543	472	170.8	11.5	386	1	AA372010
400	187.8	12.6	935	5	BU198757	DCBWA04	CE271352	473	170.8	11.5	529	1	AA372010
401	187.6	12.6	886	6	CB97534	BE855886	7906A08.x	474	170.6	11.5	531	4	BM366826
402	187.4	12.6	558	2	BE855886	7906A08.x	AA256092	475	170.6	11.5	627	5	BM366826
403	187.4	12.6	648	1	AA256092	AA256092	AA256092	476	170.6	11.5	631	5	BM366826
404	186.6	12.6	501	1	AA256092	AA256092	AA256092	477	170.6	11.5	631	5	BM366826
405	186.4	12.6	451	1	AA256092	AA256092	AA256092	478	168.2	11.4	376	4	BO711587
406	186	12.5	186	1	AA731304	AV713104	AV713104	479	168.2	11.3	881	7	CN978034
407	185.8	12.5	186	1	AA731304	AV713104	AV713104	480	167.4	11.3	546	5	BP112693
408	185.8	12.5	438	1	AA731304	AV713104	AV713104	481	166	11.2	499	5	BP112693
409	185.8	12.5	437	1	AA731304	AV713104	AV713104	482	165.8	11.2	719	6	CA465342
410	185.6	12.5	1020	6	CA529800	CA529800	CA529800	483	165	11.1	492	1	AI133670
411	185.2	12.5	600	6	CA529800	CA529800	CA529800	484	164.6	11.1	547	6	CB489425
412	185.2	12.5	735	1	AV046029	AV046029	AV046029	485	164.6	11.1	547	6	CB489425
413	185.2	12.5	874	3	AK006562	AK006562	AK006562	486	163.8	11.0	528	4	BI290741
414	185.2	12.5	875	3	AK006562	AK006562	AK006562	487	163.8	11.0	389	5	BY088751
415	184.8	12.4	395	2	BF921332	MR2-NT013	AA951231	488	163.6	10.9	823	2	BF07413
416	184.8	12.4	469	2	BF921332	MR2-NT013	AA951231	489	163.6	10.9	823	2	BF07413
417	184.6	12.4	467	4	BM432904	LOE7RE3.a	BM432904	490	160.8	10.8	795	7	CO805806
418	184.2	12.4	467	4	BM432904	LOE7RE3.a	BM432904	491	160.6	10.8	543	7	N32605
419	184.2	12.4	482	5	BU198959	DCBWA04	CE271352	492	159.8	10.7	769	7	CE271352
420	184.2	12.4	524	1	AV662884	AV662884	AV662884	493	159	10.7	884	3	CR270419
421	184.2	12.4	544	2	AA652741	AA652741	AA652741	494	158.6	10.7	780	3	CR270419
422	184.2	12.4	559	7	CO880878	CO880878	CO880878	495	157.6	10.6	1288	3	CR270419
423	184.2	12.4	590	7	CO880878	CO880878	CO880878	496	157.6	10.6	1288	3	CR270419
424	184.2	12.4	595	7	CO880878	CO880878	CO880878	497	157	10.6	421	1	AA045718
425	184.2	12.4	669	7	CO880878	CO880878	CO880878	498	156.4	10.5	803	7	CO549829
426	183.6	12.4	765	4	BI685258	BI685258	BI685258	499	155.4	10.5	931	7	CR441906
427	183.6	12.4	772	6	CB601178	CB601178	CB601178	500	154.6	10.4	440	1	AA045718
428	183.6	12.4	772	6	CB601178	CB601178	CB601178	501	154.6	10.4	440	1	AA045718
429	183.4	12.4	220	1	AA754746	AA754746	AA754746	502	154	10.4	649	7	CO679014
430	182.8	12.3	563	1	AA754746	AA754746	AA754746	503	153.6	10.3	487	1	AA946905
431	182.8	12.3	720	1	AA754746	AA754746	AA754746	504	153.2	10.3	566	1	AI566824
432	182.6	12.3	918	6	CB997566	CB997566	CB997566	505	152.8	10.3	207	5	BO369020
433	182.6	12.3	546	1	AV712111	AV712111	AV712111	506	152.4	10.3	207	5	BO369020
434	182.6	12.3	632	7	CK770649	958848.MA	CB529249	507	152.4	10.3	207	5	BO369020
435	182.6	12.3	713	6	CB529249	UI-H-FPT-2	BM632874	508	151	10.2	1119	6	CD522672
436	182.2	12.3	492	4	BM632874	BM632874	BM632874	509	150.8	10.2	187	2	AW743164
437	182.2	12.3	495	4	BM632874	BM632874	BM632874	510	150.6	10.2	538	4	BI325080
438	182.2	12.3	527	4	BM632874	BM632874	BM632874	511	150.6	10.2	470	1	AI147271
439	182.2	12.3	531	4	BM632874	BM632874	BM632874	512	150.2	10.1	612	7	CV027982
440	182	12.3	647	4	BI278279	UI-R-CY0-	BI278279	513	149.6	10.1	413	4	BM287376
441	181.6	12.2	461	1	AV734963	AV734963	AV734963	514	149.6	10.1	468	1	AI088997
442	181.6	12.2	835	5	BU963161	AGENCOURT	AV714476	515	148.4	10.0	480	4	BM672323
443	181.4	12.2	594	1	AV714476	AV714476	AV714476	516	147.8	10.0	480	4	BM672323
444	181.2	12.2	565	2	BF940967	huf62c06.x	BF940967	517	147.8	10.0	480	4	BM672323
445	181	12.2	454	2	BF940967	huf62c06.x	BF940967	518	147	9.9	451	1	AI338162
446	181	12.2	476	4	BM636075	BM636075	BM636075	519	146.6	9.9	485	1	AI338162
447	181	12.2	630	6	CB480047	CB480047	CB480047	520	146.6	9.9	485	1	AI338162
448	180.4	12.1	633	6	CB480047	CB480047	CB480047	521	145.6	9.8	470	1	AI057299
449	180.4	12.1	419	9	AY421433	Mus muscu	AY421433	522	145.4	9.8	444	1	AI052165
450	180	12.1	439	1	AA878897	AA878897	AA878897	523	145.4	9.8	444	1	AI052165
451	180	12.1	446	1	AV734741	AV734741	AV734741	524	144.8	9.8	450	1	AI094373
452	179.6	12.1	996	6	BY706281	BY706281	BY706281	525	144.4	9.7	377	5	BY444739
453	179.6	12.1	785	5	BU962218	AGENCOURT	AV715059	526	144.4	9.7	513	1	AV756012
454	178.6	12.0	640	1	AV715059	AV715059	AV715059	527	143.6	9.7	726	7	CN441830
455	178.6	12.0	753	6	CB591949	AGENCOURT	AM028268	528	143.6	9.7	726	7	CN441830
456	178.4	12.0	520	2	BF472539	UI-M-BH3-	AA923155	529	143	9.6	208	7	CO693581
457	178.4	12.0	560	2	BF472539	UI-M-BH3-	AA923155	530	143	9.6	208	7	CO693581
458	177.8	12.0	563	7	CN984526	CN984526	CN984526	531	142.4	9.6	338	5	BO708258
459	177.6	12.0	655	7	CN984526	CN984526	CN984526	532	142	9.6	338	5	BO708258
460	177.6	12.0	787	7	CN984526	CN984526	CN984526	533	141.4	9.5	449	1	AI083862
461	177.6	12.0	531	1	AI423895	AI423895	AI423895	534	140.6	9.5	418	5	BY277446
462	177.4	11.9	531	1	AI423895	AI423895	AI423895	535	140.6	9.5	418	5	BY277446

[illegible]

C 682	90.6	6.1	1029	4	BF677777	602287670	755	70.6	4.8	747	7	CK363896
C 683	90.2	6.1	223	1	AA742490	mx20906.8	756	70.6	4.8	765	7	CY073847
C 684	90	6.1	407	1	AI111729	qo92908.x	757	70.6	4.8	869	7	COS56098
C 685	89.4	6.0	345	1	AI335182	qo85f12.x	758	69.4	4.7	725	4	BI597567
C 686	89.2	6.0	423	2	AW153547	AI153547.f12zh11.y	759	69.4	4.7	740	7	CV102637
C 687	89	6.0	408	1	AI648598	tz56h07.x	760	69.2	4.7	172	7	R28847
C 688	89	6.0	472	6	CG598998	OST265164	761	69.2	4.7	312	7	CN028954
C 689	89	6.0	477	9	CD333918	StPn536	762	69.2	4.7	645	1	AUI39545
C 690	88.8	6.0	318	7	CN555613	tae14g09.	763	69	4.6	163	1	AA216197
C 691	87.6	5.9	329	2	AW794442	RC6-UM001	764	69	4.6	583	5	BP195948
C 692	87	5.9	288	2	BB566814	BB566814	765	69	4.6	654	5	BP147700
C 693	86.6	5.8	303	1	AA046284	zk77d05.x	766	69	4.6	673	7	CN788776
C 694	86.6	5.8	531	7	CK988762	BqHC-10.8	767	69	4.6	863	1	AI545843
C 695	86.6	5.8	565	7	CF675310	tae99a01.	768	68.8	4.6	444	4	BG688875
C 696	86	5.8	329	2	AW794640	RC6-UM001	769	68.8	4.6	447	6	CI69651
C 697	86	5.8	374	1	AI763751	UI-R-Y0-a	770	68.8	4.6	548	4	BI598284
C 698	85.6	5.8	416	7	CN770263	tae46g911.	771	68.8	4.6	583	5	BP211992
C 699	85.6	5.8	495	7	CN555282	tae14g09.	772	68.8	4.6	586	2	BE299401
C 700	85.6	5.8	938	5	BX355822	BX355822	773	68.8	4.6	607	2	AW411072
C 701	85.4	5.8	362	2	BF190380	236897.MA	774	68.8	4.6	629	2	AW410900
C 702	85.2	5.7	686	9	CC541655	CH240.422	775	68.8	4.6	641	4	BG826674
C 703	85	5.7	498	2	AN838647	RC5-LT005	776	68.8	4.6	671	2	BE264542
C 704	84.6	5.7	848	2	BF529223	602041673	777	68.8	4.6	693	4	BM718744
C 705	84.4	5.7	569	1	AV714854	AV714854	778	68.8	4.6	737	2	BE298457
C 706	84	5.7	932	5	BU717102	AGENCOURT	779	68.8	4.6	884	1	AI551444
C 707	83	5.6	336	2	BF602955	268335.MA	780	68.8	4.6	894	5	BUB49635
C 708	83	5.6	457	2	BF651777	274644.MA	781	68.8	4.6	910	6	CA487350
C 709	82.6	5.5	520	7	CK989616	BqHC-19.5	782	68.8	4.6	916	5	BO681872
C 710	82.4	5.5	466	5	BX669266	BX669266	783	68.8	4.6	917	1	AI544055
C 711	81.4	5.5	363	1	AA492947	AV167C08.x	784	68.8	4.6	922	5	BO929825
C 712	80.6	5.4	245	1	AA380326	AA380326	785	68.8	4.6	941	5	BX453804
C 713	80.6	5.4	337	2	AW214766	up01f07.y	786	68.8	4.6	985	5	BX399814
C 714	80.4	5.4	310	1	AA491303	aa53d12.8	787	68.8	4.6	1004	1	AI546572
C 715	80.2	5.4	447	4	BM255927	518155.MA	788	68.8	4.6	1005	1	AI548946
C 716	78.6	5.3	1694	4	BG336860	602404528	789	68.8	4.6	1012	5	BO722957
C 717	77.2	5.2	329	6	CB508938	sga1tc028	790	68.8	4.6	1021	5	BX417423
C 718	76.8	5.2	458	7	T79402	y4f5a05.81	791	68.8	4.6	1058	4	BG037157
C 719	76.6	5.2	643	1	AI645493	vt90f10.x	792	68.8	4.6	1061	4	BM560630
C 720	76.6	5.2	632	7	CN082452	EC2BBA21A	793	68.8	4.6	1064	5	BM923206
C 721	76.4	5.1	832	7	CK188508	EST777823	794	68.8	4.6	1074	1	AI551936
C 722	75.8	5.1	408	7	CN267263	170004708	795	68.8	4.6	1076	2	BF203295
C 723	75.8	5.1	417	7	W67363	z4d0c11.81	796	68.8	4.6	1083	1	AI545414
C 724	75.4	5.1	546	4	BI708855	fp93c11.y	797	68.8	4.6	1114	2	BE793016
C 725	75.4	5.1	581	4	BI845516	fb98c04.y	798	68.8	4.6	1179	5	BM924255
C 726	75.4	5.1	672	4	BJ003659	BJ003659	799	68.8	4.6	1188	5	BM925699
C 727	75.4	5.1	673	2	AW280732	fi45a09.y	800	68.8	4.6	1544	3	AP176923
C 728	75.4	5.1	699	4	BI891222	ZF637-3-0	801	68.8	4.6	1778	3	CR624361
C 729	75.4	5.1	782	7	CN506945	AGENCOURT	802	68.8	4.6	1831	3	CR599516
C 730	75.4	5.1	833	7	CK016721	AGENCOURT	803	68.8	4.6	1833	3	CR597707
C 731	75.4	5.1	861	7	CO914049	AGENCOURT	804	68.8	4.6	1834	3	CR603402
C 732	75.4	5.1	876	7	CK395467	AGENCOURT	805	68.8	4.6	1894	3	CR620373
C 733	75.4	5.1	906	7	CN023023	AGENCOURT	806	68.8	4.6	1998	3	BC035476
C 734	75.2	5.1	540	6	CD604091	R2151A3EO	807	68.8	4.6	2227	3	CR599551
C 735	75.2	5.1	563	4	BI706206	Iq02901.y	808	68.6	4.6	695	4	BG829306
C 736	74.2	5.0	329	2	AW009539	W8B4B02.x	809	68.6	4.6	1097	5	BX397591
C 737	74.2	5.0	557	7	CK890315	SGP150543	810	68.4	4.6	784	7	CN502422
C 738	74	5.0	328	2	AW794441	RC6-UM001	811	68	4.6	546	6	CB517420
C 739	74	5.0	631	4	BM781995	K-BST0058	812	67.8	4.6	225	6	BI038199
C 740	73.8	5.0	482	7	CK989768	BqHC-22.4	813	67.8	4.6	868	6	CD519669
C 741	73.8	5.0	569	4	BI845563	fb99d12.y	814	67.2	4.5	461	3	CN50949M
C 742	73.8	5.0	584	4	BI845474	fb97d05.y	815	67.2	4.5	638	4	BG707999
C 743	73.8	5.0	837	7	CN832603	AGENCOURT	816	67.2	4.5	744	4	BG702116
C 744	73.4	4.9	325	7	T69387	YC37h11.f1	817	67.2	4.5	773	6	CB988040
C 745	72.8	4.9	391	2	BF156959	fl59a11.y	818	67.2	4.5	884	5	BX427985
C 746	72.6	4.9	479	2	BB862177	UI-M-BHO-	819	67.2	4.5	921	4	BI600392
C 747	72.6	4.9	590	3	CN509AOK	Single.re	820	67.2	4.5	938	4	BG394370
C 748	72.6	4.9	1240	6	BI867753	CD429-D07	821	67	4.5	477	1	AA797956
C 749	72.4	4.9	752	4	BI669979	fb63c06.y	822	66.8	4.5	666	4	BI553529
C 750	71.4	4.8	752	4	BI669979	603294491	823	66.8	4.5	550	4	BO898800
C 751	71.2	4.8	1037	1	AI533084	AI533084	824	66.6	4.5	182	7	NS4755
C 752	70.6	4.8	572	6	CB615310	AMGNNTC:N	825	66.4	4.5	545	6	CD730522
C 753	70.6	4.8	700	7	AG092733	Pan.ctogl	826	66.4	4.5	571	4	BP710682
C 754	70.6	4.8	742	7	CK367504	AGENCOURT	827	66.4	4.5	585	5	BP257027

CK363896	AGENCOURT
CY073847	AGENCOURT
COS56098	AGENCOURT
BI597567	603243702
CV102637	AGENCOURT
R28847	F1-BD 22 we
CN028954	UMC-pb1iv
AUI39545	AUI39545
AA216197	hp0871.8e
BP195948	BP195948
BP147700	BP147700
CN788776	AI23144.B
AI545843	AL545843
BG688875	336669.BA
CI69651	CI69651
BI598284	603245465
BP211992	BP211992
BE299401	601118703
AA410900	fh10b12.x
AM410900	fh09a11.x
BG826674	602750807
BE264542	601192302
BM718744	UI-E-B01-
BE298457	601119260
AI551444	AL551444
BUB49635	AGENCOURT
CA487350	AGENCOURT
BO681872	AGENCOURT
AI544055	AL544055
BO929825	AGENCOURT
BX453804	BX453804
BX399814	BX399814
AI546572	AL546572
AI548946	AL548946
BO722957	AGENCOURT
BO3037157	602288169
BM560630	AGENCOURT
BM923206	AGENCOURT
AI551936	AL551936
BI203295	601866085
AI545414	AL545414
BE793016	601585424
BM924255	AGENCOURT
BM925699	AGENCOURT
AP176923	AGENCOURT
CR624361	full-1eng
CR599516	full-1eng
CR597707	full-1eng
CR603402	full-1eng
CR620373	full-1eng
BC035476	Homo.sapi
CR599551	full-1eng
BG829306	602753016
BX397591	BX397591
CN502422	AGENCOURT
CB517420	sga1ixb50
BI038199	113-NT028
CD519669	AGENCOURT
BX041606	Single.re
BG707999	602671320
BG702116	602684018
CB988040	AGENCOURT
BX427985	BX427985
BI600392	603246430
BG394370	602456582
AA797956	ub60a05.x
BI553529	603197521
BO898800	HOA22-1-F
NS4755	yz16h12.f1
CD730522	4038907.1
BP710682	pg1.in.pk0
BP257027	BP257027

828	66.4	4.5	646	4	B1392555	B1392555 pppin.pk0	901	64.4	4.3	869	6	CA987481	CA987481 AGENCOURT
829	66.4	4.5	804	7	CN219157	CN219157 WLA001H08	902	64.4	4.3	901	5	BUR99794	BUR99794 AGENCOURT
830	66.4	4.5	848	4	B1460146	B1460146 603201729	903	64.4	4.3	913	6	CA792351	CA792351 AGENCOURT
831	66.4	4.5	853	5	BUI107470	BUI107470 603112686	904	64.4	4.3	916	6	CA788575	CA788575 AGENCOURT
832	66.4	4.5	861	1	AL544229	AL544229 AL544229	905	64.4	4.3	926	6	CA984841	CA984841 AGENCOURT
833	66.4	4.5	871	1	AL540364	AL540364 AL540364	906	64.4	4.3	992	6	CA983119	CA983119 AGENCOURT
834	66.4	4.5	1490	3	CR611215	CR611215 full - leng	907	64.2	4.3	308	7	T30350	T30350 EST15261 Hu
835	66.4	4.5	1529	3	CR616869	CR616869 full - leng	908	64.2	4.3	446	5	BX486916	BX486916 DKF2686A
836	66.4	4.5	1836	3	CR627385	CR627385 Homo sapi	909	64.2	4.3	505	4	BM490756	BM490756 K-BST0070
837	66.2	4.5	321	2	BR093306	BR093306 PM1-TN012	910	64.2	4.3	526	4	BM484390	BM484390 K-BST0121
838	66.2	4.5	1049	2	BR257579	BR257579 PM1-TN012	911	64.2	4.3	537	2	AM410192	AM410192 H05B08.x
839	66.2	4.5	1049	2	BR205499	BR205499 601867894	912	64.2	4.3	549	2	BM179552	BM179552 UT-B-EJ1-
840	65.8	4.4	427	7	CK883885	CK883885 SGPI67833	913	64.2	4.3	556	2	AM673424	AM673424 ba54h03.y
841	65.8	4.4	503	1	AI605719	AI605719 mac2e12.y	914	64.2	4.3	562	2	BM021900	BM021900 le73e03.y
842	65.8	4.4	632	7	CK620135	CK620135 mk32e08.y	915	64.2	4.3	582	6	CD657109	CD657109 fe19b02.y
843	65.8	4.4	647	6	BY707612	BY707612 BY707612	916	64.2	4.3	585	5	BX357454	BX357454 BX357454
844	65.8	4.4	673	2	BB649238	BB649238 BB649238	917	64.2	4.3	586	4	BM023210	BM023210 le81b07.x
845	65.8	4.4	678	2	BB649239	BB649239 BB649239	918	64.2	4.3	586	4	BM023312	BM023312 le82g05.x
846	65.8	4.4	688	6	BY753713	BY753713 BY753713	919	64.2	4.3	595	1	AL776367	AL776367 AL776367
847	65.8	4.4	744	6	BY736698	BY736698 BY736698	920	64.2	4.3	603	6	CB528447	CB528447 UT-H-FT2-
848	65.8	4.4	770	4	BT656335	BT656335 603282642	921	64.2	4.3	609	6	CD365628	CD365628 UT-H-FT2-
849	65.8	4.4	858	2	BP138444	BP138444 601782596	922	64.2	4.3	614	6	CA431118	CA431118 UT-H-FT1-
850	65.8	4.4	864	7	CF617205	CF617205 AGENCOURT	923	64.2	4.3	620	5	BQ575162	BQ575162 UT-H-EJ1-
851	65.8	4.4	882	4	BF584891	BF584891 602098764	924	64.2	4.3	625	4	BM742136	BM742136 K-BST0014
852	65.8	4.4	891	2	BF584891	BF584891 602098764	925	64.2	4.3	651	4	BI829555	BI829555 603080387
853	65.8	4.4	926	5	BQ925890	BQ925890 AGENCOURT	926	64.2	4.3	657	1	AL882958	AL882958 AL882958
854	65.8	4.4	930	5	BQ947300	BQ947300 AGENCOURT	927	64.2	4.3	668	4	BI085428	BI085428 602869915
855	65.8	4.4	943	5	BQ897301	BQ897301 AGENCOURT	928	64.2	4.3	701	6	CD366973	CD366973 UT-H-FT2-
856	65.8	4.4	947	5	CF585383	CF585383 AGENCOURT	929	64.2	4.3	706	4	BM682862	BM682862 UT-B-EJ1-
857	65.8	4.4	1032	5	BQ686354	BQ686354 AGENCOURT	930	64.2	4.3	732	5	BX462778	BX462778 BX462778
858	65.8	4.4	2049	3	AK007560	AK007560 Mus muscu	931	64.2	4.3	739	5	BI460106	BI460106 603201672
859	65.8	4.4	2123	3	AK011219	AK011219 Mus muscu	932	64.2	4.3	752	5	BUI65459	BUI65459 UT-H-FG0-
860	65.8	4.4	2382	5	AK048475	AK048475 Mus muscu	933	64.2	4.3	758	5	BX341939	BX341939 BX341939
861	65.6	4.4	351	5	BX357453	BX357453 BX357453	934	64.2	4.3	760	6	CB240768	CB240768 UT-CF-FN0
862	65.6	4.4	635	6	CA332916	CA332916 hab18a10.	935	64.2	4.3	795	4	BI753983	BI753983 603027415
863	65.6	4.4	635	7	CK598261	CK598261 AGENCOURT	936	64.2	4.3	813	7	CF222019	CF222019 AGENCOURT
864	65.6	4.4	688	4	BJ738800	BJ738800 BJ738800	937	64.2	4.3	823	4	BG748791	BG748791 602706127
865	65.6	4.4	690	6	CB8420	CB8420 CB8420 CA1P	938	64.2	4.3	838	5	BX362459	BX362459 BX362459
866	65.6	4.4	746	7	CK474032	CK474032 AGENCOURT	939	64.2	4.3	867	7	BE331131	BE331131 601278305
867	65.6	4.4	752	7	CK482038	CK482038 AGENCOURT	940	64.2	4.3	870	7	CF593217	CF593217 AGENCOURT
868	65.6	4.4	755	7	CK469333	CK469333 AGENCOURT	941	64.2	4.3	870	7	CR424943	CR424943 CR424943
869	65.6	4.4	757	7	CV107376	CV107376 AGENCOURT	942	64.2	4.3	871	5	BI148475	BI148475 AGENCOURT
870	65.6	4.4	760	7	CK474093	CK474093 AGENCOURT	943	64.2	4.3	878	7	CR435674	CR435674 CR435674
871	65.6	4.4	801	7	CK602945	CK602945 AGENCOURT	944	64.2	4.3	885	5	BUI55199	BUI55199 AGENCOURT
872	65.6	4.4	817	7	CK470702	CK470702 AGENCOURT	945	64.2	4.3	889	7	BQ881044	BQ881044 AGENCOURT
873	65.6	4.4	819	7	CK602625	CK602625 AGENCOURT	946	64.2	4.3	897	7	CF377547	CF377547 AGENCOURT
874	65.6	4.4	827	7	CK597533	CK597533 AGENCOURT	947	64.2	4.3	923	5	BUI45649	BUI45649 AGENCOURT
875	65.6	4.4	836	7	CK652925	CK652925 AGENCOURT	948	64.2	4.3	932	5	BX712713	BX712713 BX712713
876	65.6	4.4	1005	5	BQ678462	BQ678462 AGENCOURT	949	64.2	4.3	940	5	BQ941943	BQ941943 AGENCOURT
877	65.4	4.4	479	2	BR286638	BR286638 EST451229	950	64.2	4.3	942	5	BQ219478	BQ219478 AGENCOURT
878	65.4	4.4	599	7	CK835564	CK835564 4059961.B	951	64.2	4.3	983	5	EX401762	EX401762 BX401762
879	65.4	4.4	960	5	BQ844837	BQ844837 AGENCOURT	952	64.2	4.3	1012	5	BQ71614	BQ71614 AGENCOURT
880	65	4.4	271	2	AM128286	AM128286 fe37d03.x	953	64.2	4.3	1016	5	BX421204	BX421204 BX421204
881	65	4.4	649	4	BG706326	BG706326 602669643	954	64.2	4.3	1021	5	BQ934215	BQ934215 AGENCOURT
882	65	4.4	1217	7	BM909152	BM909152 AGENCOURT	955	64.2	4.3	1039	5	BX362886	BX362886 BX362886
883	65	4.4	1217	7	T69310	T69310 y437h11.B1	956	64.2	4.3	1046	5	BX396406	BX396406 BX396406
884	64.6	4.4	506	2	BE514790	BE514790 601316718	957	64.2	4.3	1055	5	EX363513	EX363513 BX363513
885	64.4	4.3	433	4	BI349433	BI349433 dae62e08.	958	64.2	4.3	1062	5	BQ056222	BQ056222 AGENCOURT
886	64.4	4.3	444	4	BQ072850	BQ072850 BQ072850	959	64.2	4.3	1136	4	BM544927	BM544927 AGENCOURT
887	64.4	4.3	514	5	BX925677	BX925677 BX925677	960	64.2	4.3	1151	1	AL534927	AL534927 AL534927
888	64.4	4.3	544	4	BQ069518	BQ069518 BQ069518	961	64.2	4.3	1300	5	BM919262	BM919262 AGENCOURT
889	64.4	4.3	549	4	BQ039077	BQ039077 BQ039077	962	64.2	4.3	2210	1	CR616014	CR616014 full - leng
890	64.4	4.3	573	4	BQ059508	BQ059508 BQ059508	963	64.2	4.3	238	1	AA718055	AA718055 vt90f10.r
891	64.4	4.3	574	4	BI477519	BI477519 da143b04.	964	64.2	4.3	389	1	AL837900	AL837900 AL837900
892	64.4	4.3	577	4	BQ072660	BQ072660 BQ072660	965	64.2	4.3	604	5	BUR05770	BUR05770 haa22a10.
893	64.4	4.3	592	5	BQ383510	BQ383510 N1SC mm01	966	64.2	4.3	609	6	CA589719	CA589719 haa37f02.
894	64.4	4.3	592	5	CK654220	CK654220 AGENCOURT	967	64.2	4.3	611	5	BUR06039	BUR06039 haa52a03.
895	64.4	4.3	731	7	CK804649	CK804649 AGENCOURT	968	64.2	4.3	652	6	CA589027	CA589027 haa52h05.
896	64.4	4.3	755	7	CF287392	CF287392 AGENCOURT	969	64.2	4.3	659	5	BUR07595	BUR07595 haa62h01.
897	64.4	4.3	784	7	CF286348	CF286348 AGENCOURT	970	64.2	4.3	673	5	BX889152	BX889152 BX889152
898	64.4	4.3	790	7	CF270916	CF270916 AGENCOURT	971	64.2	4.3	674	5	BUR07896	BUR07896 haa18h08.
899	64.4	4.3	855	6	CA971881	CA971881 AGENCOURT	972	64.2	4.3	818	6	CA846215	CA846215 haa11a06.
900	64.4	4.3	866	6	CA985745	CA985745 AGENCOURT	973	64.2	4.3	880	5	BQ951778	BQ951778 AGENCOURT

974	64	4.3	1729	3	AK045911	AK045911	Mus muscu	1047	61.4	4.1	856	2	BF309230	BF309230	601890171
975	64	4.3	1805	3	AK016491	AK016491	Mus muscu	1048	61	4.1	856	2	BF309230	BF309230	601890171
976	63.8	4.3	460	7	CK608216	CK608216	ITN B06 I	1049	61	4.1	856	7	TI2612	TI2612	CHR90132 Ch
977	63.8	4.3	591	7	CK307425	CK307425	SB02043B1	1050	61	4.1	584	2	B1115218	B1115218	602861671
978	63.8	4.3	649	2	AM321637	AM321637	U036611.Y	1051	61	4.1	570	2	AM664179	AM664179	h105e10.x
979	63.6	4.3	400	7	AM321637	AM321637	U036611.Y	1052	61	4.1	652	5	BX371495	BX371495	BX371495
980	63.6	4.3	422	5	BU315594	BU315594	603854882	1053	61	4.1	1017	5	BO886792	BO886792	AGENCOURT
981	63.6	4.3	512	2	CN223477	CN223477	RJA094C04	1054	61	4.1	1026	5	BO936435	BO936435	AGENCOURT
982	63.6	4.3	550	5	BP213919	BP213919	BM490118	1055	60.8	4.1	514	4	BM151565	BM151565	TCBAP1E04
983	63.6	4.3	556	4	BI392159	BI392159	PDP2n.pX0	1056	60.6	4.1	442	7	CN959409	CN959409	6909.1001
984	63.6	4.3	616	4	BU231422	BU231422	603800637	1057	60.6	4.1	567	7	CF723843	CF723843	UT-M-G20
985	63.6	4.3	636	4	BG488856	BG488856	602534848	1058	60.6	4.1	645	4	BM044488	BM044488	603622007
986	63.6	4.3	651	7	CN222639	CN222639	WLA042C04	1059	60.6	4.1	671	4	BM044488	BM044488	603622007
987	63.6	4.3	727	5	BU211470	BU211470	604152150	1060	60.6	4.1	806	4	BG775636	BG775636	602650573
988	63.6	4.3	766	5	BU368992	BU368992	603598513	1061	60.6	4.1	947	5	CN455679	CN455679	UT-M-HP0-
989	63.6	4.3	775	5	BU255007	BU255007	603747266	1062	60.6	4.1	825	7	BO958968	BO958968	AGENCOURT
990	63.6	4.3	776	5	BU255007	BU255007	603747266	1063	60.4	4.1	331	7	CR522276	CR522276	CR522276
991	63.6	4.3	781	7	CN221062	CN221062	WLA029G03	1064	60.4	4.1	505	2	BE259279	BE259279	CR522276
992	63.6	4.3	809	5	BU132109	BU132109	603117794	1065	60.4	4.1	693	7	CN094528	CN094528	601106373
993	63.6	4.3	827	5	CN236257	CN236257	WLA110D09	1066	60.4	4.1	858	1	AI533024	AI533024	SID04693.5
994	63.6	4.3	886	7	CO635663	CO635663	CON119272	1067	60.4	4.1	1134	5	BM921410	BM921410	AGENCOURT
995	63.6	4.3	886	7	BU327241	BU327241	603492036	1068	60.2	4.1	664	6	BY724416	BY724416	BY724416
996	63.6	4.3	894	5	BU433641	BU433641	603221461	1069	60.2	4.1	824	5	BM921410	BM921410	AGENCOURT
997	63.6	4.3	895	5	BB643629	BB643629	BX359251	1070	60	4.0	412	2	AM961315	AM961315	AM961315
998	63.4	4.3	695	2	BE643629	BE643629	BX359251	1071	60	4.0	929	5	BM122713	BM122713	AM961315
999	63.4	4.3	671	7	CR415574	CR415574	CR573735	1072	59.8	4.0	523	2	AM012274	AM012274	AM012274
1000	63.2	4.3	671	7	CR415574	CR415574	CR573735	1073	59.8	4.0	554	2	BB611133	BB611133	BB611133
1001	63.2	4.3	699	7	CR415574	CR415574	CR573735	1074	59.8	4.0	698	4	BG708540	BG708540	602670438
1002	63.2	4.3	699	7	CR415574	CR415574	CR573735	1075	59.6	4.0	504	9	CG517489	CG517489	OST77927
1003	63.2	4.3	963	7	CF590100	CF590100	AGENCOURT	1076	59.4	4.0	946	5	BO959396	BO959396	AGENCOURT
1004	63	4.2	598	1	AA544785	AA544785	AGENCOURT	1077	59.4	4.0	611	4	BG270782	BG270782	UT-M-BH0-
1005	63	4.2	598	1	AA544785	AA544785	AGENCOURT	1078	59.4	4.0	666	4	BI548144	BI548144	1899603.Y
1006	63	4.2	165	2	BE636449	BE636449	601334785	1079	59.2	4.0	375	7	CO196389	CO196389	603189484
1007	62.8	4.2	625	2	BE887503	BE887503	601508152	1080	59.2	4.0	356	2	AM841732	AM841732	603003383
1008	62.6	4.2	585	4	BI966097	BI966097	ie73e03.X	1081	59.2	4.0	773	5	BU16139	BU16139	RC3-CN001
1009	62.6	4.2	601	5	BO520975	BO520975	NISC_n108	1082	59.2	4.0	290	4	BG062118	BG062118	LO957E03-
1010	62.6	4.2	638	1	AL848424	AL848424	AL867994	1083	58.8	4.0	340	2	BF702856	BF702856	mab51b10.
1011	62.6	4.2	651	1	AL867994	AL867994	CR577323	1084	58.8	4.0	340	2	BF702856	BF702856	mab51b10.
1012	62.6	4.2	659	7	CR577323	CR577323	AGENCOURT	1085	58.8	4.0	340	2	BF702856	BF702856	mab51b10.
1013	62.6	4.2	758	7	CF149892	CF149892	AGENCOURT	1086	58.8	4.0	340	2	BF702856	BF702856	mab51b10.
1014	62.6	4.2	787	5	BK723292	BK723292	AGENCOURT	1087	58.8	4.0	374	2	AI854880	AI854880	UT-M-BH0-
1015	62.6	4.2	847	7	CR419046	CR419046	CR419046	1088	58.8	4.0	409	2	BM751438	BM751438	UT-M-BH0-
1016	62.6	4.2	865	7	CR433581	CR433581	CR433581	1089	58.8	4.0	430	4	BG062057	BG062057	UT-M-BH0-
1017	62.6	4.2	869	7	CR433581	CR433581	CR433581	1090	58.8	4.0	437	1	AA794516	AA794516	LO956B07-
1018	62.6	4.2	915	5	BO224847	BO224847	AGENCOURT	1091	58.8	4.0	480	4	BM751438	BM751438	UT-M-BH0-
1019	62.6	4.2	983	5	BO224847	BO224847	AGENCOURT	1092	58.8	4.0	480	4	BM751438	BM751438	UT-M-BH0-
1020	62.6	4.2	538	5	BU367925	BU367925	AGENCOURT	1093	58.8	4.0	539	4	BG067837	BG067837	H3058G01-
1021	62.4	4.2	566	7	CF104721	CF104721	ma314H08.	1094	58.8	4.0	589	1	AA276201	AA276201	VC40601.X
1022	62.4	4.2	566	7	CF104721	CF104721	ma314H08.	1095	58.8	4.0	651	7	CF751563	CF751563	UT-M-HK0-
1023	62.4	4.2	575	7	BI477647	BI477647	da144H11.	1096	58.8	4.0	659	1	AV133913	AV133913	AV133913
1024	62.4	4.2	588	4	BO399256	BO399256	NISC mp02	1097	58.8	4.0	666	5	BM651957	BM651957	UT-M-EH0-
1025	62.4	4.2	614	5	CV074265	CV074265	AGENCOURT	1098	58.8	4.0	729	6	CA751143	CA751143	UT-M-FD0-
1026	62.4	4.2	616	7	BO74265	BO74265	AGENCOURT	1099	58.8	4.0	769	6	CB601978	CB601978	AGENCOURT
1027	62.4	4.2	642	4	BJ057809	BJ057809	AGENCOURT	1100	58.8	4.0	837	6	CB321187	CB321187	AGENCOURT
1028	62.4	4.2	691	5	BX849635	BX849635	AGENCOURT	1101	58.6	3.9	1165	4	BM462345	BM462345	AGENCOURT
1029	62.4	4.2	724	7	CN832945	CN832945	AGENCOURT	1102	58.4	3.9	592	4	BG896911	BG896911	H0A59-1-A
1030	62.4	4.2	796	7	CV074535	CV074535	AGENCOURT	1103	58.4	3.9	637	2	BF309494	BF309494	AGENCOURT
1031	62.4	4.2	829	7	BU274575	BU274575	AGENCOURT	1104	58.4	3.9	668	5	BX860019	BX860019	AGENCOURT
1032	62.4	4.2	850	5	BU274575	BU274575	AGENCOURT	1105	58.4	3.9	753	5	BX860019	BX860019	AGENCOURT
1033	62.4	4.2	865	5	BU274575	BU274575	AGENCOURT	1106	58.4	3.9	784	5	BX860019	BX860019	AGENCOURT
1034	62.4	4.2	871	6	CH558697	CH558697	AGENCOURT	1107	58.4	3.9	784	5	BX860019	BX860019	AGENCOURT
1035	62.2	4.2	762	5	BX878989	BX878989	AGENCOURT	1108	58.4	3.9	796	5	BX860019	BX860019	AGENCOURT
1036	62	4.2	612	7	CN084450	CN084450	EC2BBA24A	1109	58.4	3.9	803	5	BX860019	BX860019	AGENCOURT
1037	62	4.2	1328	7	AL843094	AL843094	AGENCOURT	1110	58.2	3.9	943	4	BG306330	BG306330	AGENCOURT
1038	61.8	4.2	417	1	BM805414	BM805414	AGENCOURT	1111	58.2	3.9	487	4	BM792003	BM792003	AGENCOURT
1039	61.6	4.1	612	7	CN084258	CN084258	EC2BBA23D	1112	58.2	3.9	517	4	BI349547	BI349547	dag38a03.
1040	61.6	4.1	618	7	CN084258	CN084258	EC2BBA23D	1113	58.2	3.9	780	4	BG775584	BG775584	602650513
1041	61.6	4.1	889	5	BU147032	BU147032	603135411	1114	58.2	3.9	810	6	CD752612	CD752612	AGENCOURT
1042	61.4	4.1	614	2	CB215777	CB215777	NISC mp09	1115	58.2	3.9	856	4	BI647230	BI647230	603279477
1043	61.4	4.1	732	2	BF304475	BF304475	601887835	1116	58	3.9	307	2	BF093126	BF093126	PML-TN012
1044	61.4	4.1	803	4	BF671128	BF671128	602282670	1117	58	3.9	498	7	R26367	R26367	YH40a05.81
1045	61.4	4.1	820	4	BI667411	BI667411	603292201	1118	57.8	3.9	727	7	CN389160	CN389160	170005599
1046	61.4	4.1	854	5	BU900811	BU900811	AGENCOURT	1119	57.8	3.9	638	4	BG700206	BG700206	602679827

1120	57.8	3.9	689	5	BO572309	UI-M-PD0-	C1193	52.2	3.5	313	1	AA919092
1121	57.8	3.9	1026	5	BUS02727	AGENCYCOURT	C1194	52.2	3.5	347	2	AA188838
1122	57.6	3.9	4572	1	AV736028	AV736028	1195	52	3.5	455	5	BY059640
1123	57.2	3.9	346	1	AT644492	ml80e10.x	1196	52	3.5	672	5	BO100286
1124	57.2	3.9	392	2	BB837430	BB837430	1197	52	3.5	881	4	BB699656
1125	57.2	3.9	408	1	AA755465	AA755465	1198	51.8	3.5	428	2	BB509232
1126	57.2	3.9	412	5	BY377835	BY377835	1199	51.8	3.5	730	4	BT1756029
1127	57.2	3.9	455	2	BB834887	BB834887	1200	51.8	3.5	1342	5	BM0505941
1128	57.2	3.9	467	2	BB829666	BB829666	1201	51.4	3.5	538	7	CF366674
1129	57.2	3.9	512	2	BB952054	UI-M-CD0-	1202	51.2	3.4	447	5	BK520763
1130	57.2	3.9	549	1	AA583494	AA583494	1203	51.2	3.4	508	1	AU261278
1131	57.2	3.9	555	1	AI570209	AI570209	1204	51	3.4	455	6	CB741222
1132	57.2	3.9	933	5	BUS43148	BU543148	1205	51	3.4	580	4	CB741222
1133	57.2	3.9	931	5	BO928218	BO928218	1206	50.8	3.4	263	1	AI300099
1134	57	3.8	435	6	CB8366	CB8366	1207	50.8	3.4	316	2	BB501029
1135	57	3.8	708	6	CB836603	CB836603	1208	50.8	3.4	429	4	BT841846
1136	56.8	3.8	573	4	BF310120	BF310120	1209	50.8	3.4	474	6	CB729237
1137	56.8	3.8	696	4	BI546531	BI546531	1210	50.8	3.4	503	4	BT846300
1138	56.8	3.8	908	5	BU179913	BU179913	1211	50.8	3.4	570	4	BT845458
1139	56.4	3.8	327	1	AI849272	AI849272	1212	50.8	3.4	701	7	CK172514
1140	56.4	3.8	517	7	CK137373	CK137373	1213	50.8	3.4	701	7	CK172515
1141	56.2	3.8	390	5	BY380023	BY380023	1214	50.8	3.4	711	6	CD492738
1142	56.2	3.8	1091	5	CL648805	CL648805	1215	50.8	3.4	1101	9	CNS0178P
1143	56	3.8	441	5	BO221449	BO221449	1216	50.8	3.4	1174	5	BO671970
1144	56	3.8	930	5	BO940582	BO940582	1217	50.6	3.4	246	2	BF896928
1145	55.8	3.8	561	9	AV039984	AV039984	1218	50.6	3.4	401	2	AM188794
1146	55.8	3.8	561	9	CE603961	CE603961	1219	50.6	3.4	653	5	BM436126
1147	55.6	3.7	275	1	AI118784	AI118784	1220	50.6	3.4	704	5	BM436127
1148	55.6	3.7	348	5	AY412711	AY412711	1221	50.6	3.4	764	5	BU258414
1149	55.6	3.7	366	5	BY415990	BY415990	1222	50.6	3.4	765	5	BM429595
1150	55.6	3.7	385	4	BM852501	BM852501	1223	50.6	3.4	1051	5	BX464372
1151	55.6	3.7	415	9	AY412710	AY412710	1224	50.4	3.4	514	2	AM337550
1152	55.6	3.7	591	2	AMS00528	AMS00528	1225	50.4	3.4	601	5	BM341587
1153	55.6	3.7	700	2	BE296236	BE296236	1226	50.4	3.4	675	5	BM248558
1154	55.6	3.7	839	4	BI820066	BI820066	1227	50.4	3.4	686	5	BM056869
1155	55.6	3.7	931	6	CD359314	CD359314	1228	50.4	3.4	687	5	BM250225
1156	55.6	3.7	932	6	BE735129	BE735129	1229	50.4	3.4	699	5	BM047661
1157	55.6	3.7	1154	5	BO054990	BO054990	1230	50.4	3.4	707	5	BM478438
1158	55.6	3.7	1275	6	CB7647	CB7647	1231	50.4	3.4	712	5	BM041956
1159	55.4	3.7	427	6	CB7647	CB7647	1232	50.4	3.4	806	5	BU301036
1160	55.2	3.7	725	7	CO378095	CO378095	1233	50.2	3.4	308	1	AV040523
1161	54.6	3.7	659	4	BG705925	BG705925	1234	50.2	3.4	325	7	CO966620
1162	54.6	3.7	763	4	BE377559	BE377559	1235	50.2	3.4	444	2	AM087991
1163	54.4	3.7	759	8	AO743175	AO743175	1236	50.2	3.4	491	7	CF157964
1164	54.4	3.7	781	7	CN756232	CN756232	1237	50.2	3.4	574	5	BA422742
1165	54.4	3.7	950	8	AO743172	AO743172	1238	50.2	3.4	707	1	AU081289
1166	54.4	3.7	986	5	BM909681	BM909681	1239	50	3.4	281	1	AV082140
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1168	54.2	3.6	426	4	BG745652	BG745652	1241	50	3.4	819	4	BI647605
1169	54.2	3.6	531	4	BG745918	BG745918	1242	49.8	3.4	590	4	BI455815
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1171	54	3.6	465	2	BB830143	BB830143	1244	49.8	3.4	793	7	CN053475
1172	54	3.6	632	7	BU055145	BU055145	1245	49.8	3.4	999	5	BO918433
1173	53.8	3.6	281	7	FI9347	FI9347	1246	49.6	3.3	484	6	CB639653
1174	53.8	3.6	964	5	BO686539	BO686539	1247	49.6	3.3	543	7	CF340723
1175	53.6	3.6	287	4	BM654652	BM654652	1248	49.6	3.3	585	1	AU225865
1176	53.6	3.6	387	6	CB806010	CB806010	1249	49.6	3.3	631	6	CB653047
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1178	53.6	3.6	1404	5	BM907186	BM907186	1251	49.6	3.3	722	6	CB659406
1179	53.4	3.6	156	9	CG516394	CG516394	1252	49.6	3.3	842	7	CO435891
1180	53.4	3.6	229	2	AM422685	AM422685	1253	49.4	3.3	357	5	BY069623
1181	53.4	3.6	988	5	BO897984	BO897984	1254	49.2	3.3	372	5	BY050439
1182	53.2	3.6	458	1	BF151139	BF151139	1255	49.2	3.3	372	5	BY050439
1183	53.2	3.6	933	2	AL559613	AL559613	1256	49.2	3.3	383	5	BY059594
1184	52.6	3.6	1247	6	BU542112	BU542112	1257	49.2	3.3	393	3	CB717377
1185	52.6	3.6	343	6	CD102272	CD102272	1258	49.2	3.3	410	5	BY313404
1186	52.6	3.5	482	5	BY255020	BY255020	1259	49.2	3.3	415	6	CB799926
1187	52.6	3.5	662	2	AM097140	AM097140	1260	49.2	3.3	422	6	CB763144
1188	52.4	3.5	423	4	BG146767	BG146767	1261	49.2	3.3	430	6	CB758592
1189	52.4	3.5	513	7	CK689936	CK689936	1262	49.2	3.3	432	7	DI5295
1190	52.4	3.5	474	7	BM681050	UI-E-EIO-PD0	1263	49.2	3.3	440	6	CB749636
1191	52.4	3.5	658	7	CK189556	EST778871	1264	49.2	3.3	444	6	CI7719
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1268	49.2	3.3	505	6	CB783529	CB783529	AMGNNUC:N	1341	49	3.3	692	5	EX918886	EX918886
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1270	49.2	3.3	515	6	CB274539	CB274539	mai70d07.	1343	49	3.3	699	7	CN166011	CN166011
1271	49.2	3.3	517	6	CB716226	CB716226	AMGNNUC:N	1344	49	3.3	700	5	BQ598574	BQ598574
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1278	49.2	3.3	572	6	CB0058793	CB0058793	lt_PACIF	1350	49	3.3	948	4	BC331194	BC331194
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1280	49.2	3.3	580	7	CB039803	CB039803	DR_AOV.PL	1352	48.6	3.3	174	7	NA7817	NA7817
1281	49.2	3.3	584	7	CN203283	CN203283	TO3533.G	1353	48.6	3.3	536	7	CK898109	CK898109
1282	49.2	3.3	586	2	AM127954	AM127954	f105b08.y	1354	48.4	3.3	353	5	BY074771	BY074771
1283	49.2	3.3	586	2	AM127954	AM127954	f105b08.y	1355	48.4	3.3	506	6	CD297210	CD297210
1284	49.2	3.3	593	6	CB585582	CB585582	AMGNNUC:N	1356	48.4	3.3	785	5	AG594701	AG594701
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1286	49.2	3.3	596	7	CB0552415	CB0552415	AcLy525.S	1358	48.2	3.2	769	7	BY054236	BY054236
1287	49.2	3.3	600	7	CB0552474	CB0552474	AcLy1243	1359	48.2	3.2	543	7	CO506808	CO506808
1288	49.2	3.3	601	6	CB585235	CB585235	AMGNNUC:N	1360	48.2	3.2	568	7	CO507234	CO507234
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1290	49.2	3.3	644	7	CB0552741	CB0552741	AcLy936.S	1362	48.2	3.2	612	4	BI104905	BI104905
1291	49.2	3.3	645	7	CB0551959	CB0551959	AcLy1687	1363	48.2	3.2	769	7	BN582689	BN582689
1292	49.2	3.3	646	7	CB0552414	CB0552414	AcLy523.S	1364	48.2	3.2	988	2	BQ944424	BQ944424
1293	49.2	3.3	663	6	CD371813	CD371813	UI-R-GOO-	1365	48.2	3.2	1069	5	BF985859	BF985859
1294	49.2	3.3	761	7	CK693057	CK693057	ZF101-PO0	1366	48	3.2	442	7	CF279790	CF279790
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1296	49.2	3.3	775	7	CK966848	CK966848	AGENCOURT	1368	48	3.2	871	6	CB565614	CB565614
1297	49.2	3.3	801	7	CB039070	CB039070	AGENCOURT	1369	48	3.2	1004	1	AL513914	AL513914
1298	49.2	3.3	833	4	BG666609	BG666609	DRAPE10	1370	48	3.2	890	5	BE669589	BE669589
1299	49.2	3.3	855	5	BU962765	BU962765	AGENCOURT	1371	47.8	3.2	357	5	EX913914	EX913914
1300	49.2	3.3	871	7	CN331855	CN331855	AGENCOURT	1372	47.8	3.2	404	5	BK665959	BK665959
1301	49.2	3.3	884	7	CN832504	CN832504	AGENCOURT	1373	47.8	3.2	459	2	AM670310	AM670310
1302	49.2	3.3	890	7	CO927200	CO927200	AGENCOURT	1374	47.8	3.2	528	4	BE704681	BE704681
1303	49.2	3.3	946	1	AU079142	AU079142	LYEST1693	1375	47.8	3.2	1276	5	BQ944424	BQ944424
1304	49.2	3.3	949	7	CO546392	CO546392	LYEST1693	1376	47.6	3.2	240	2	BF985859	BF985859
1305	49.2	3.3	1000	7	CO543382	CO543382	LYEST1693	1377	47.6	3.2	346	5	BY099872	BY099872
1306	49.2	3.3	385	1	AJ604640	AJ604640	AMGNNUC:M	1378	47.6	3.2	352	5	BY208732	BY208732
1307	49.2	3.3	391	6	CB775169	CB775169	AMGNNUC:M	1379	47.6	3.2	352	5	BY208990	BY208990
1308	49.2	3.3	504	1	AJ604900	AJ604900	BM023619	1380	47.6	3.2	355	5	BY128100	BY128100
1309	49.2	3.3	518	4	BM023619	BM023619	ie82905.y	1381	47.6	3.2	355	5	BY293465	BY293465
1310	49.2	3.3	536	5	BK668559	BK668559	AGENCOURT	1382	47.6	3.2	357	5	BY294461	BY294461
1311	49.2	3.3	586	1	AJ604693	AJ604693	AGENCOURT	1383	47.6	3.2	359	5	BY310127	BY310127
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1314	49.2	3.3	614	1	AJ604742	AJ604742	AGENCOURT	1386	47.6	3.2	365	5	BY163806	BY163806
1315	49.2	3.3	622	5	BP016648	BP016648	AGENCOURT	1387	47.6	3.2	366	7	CF585782	CF585782
1316	49.2	3.3	636	5	BK673603	BK673603	AGENCOURT	1388	47.6	3.2	368	5	BY060827	BY060827
1317	49.2	3.3	637	1	AJ604861	AJ604861	AGENCOURT	1389	47.6	3.2	371	5	BY054153	BY054153
1318	49.2	3.3	640	5	BK676152	BK676152	AGENCOURT	1390	47.6	3.2	373	5	BY088761	BY088761
1319	49.2	3.3	644	7	CK459540	CK459540	929734.MA	1391	47.6	3.2	374	5	BY146384	BY146384
1320	49.2	3.3	652	1	AJ604884	AJ604884	AGENCOURT	1392	47.6	3.2	375	5	BI204723	BI204723
1321	49.2	3.3	655	1	BK668104	BK668104	AGENCOURT	1393	47.6	3.2	377	5	BY105886	BY105886
1322	49.2	3.3	673	4	BM190123	BM190123	POSM01000	1394	47.6	3.2	378	5	BY165606	BY165606
1323	49.2	3.3	674	5	BK916361	BK916361	AGENCOURT	1395	47.6	3.2	385	5	BY038667	BY038667
1324	49.2	3.3	674	5	BK921249	BK921249	AGENCOURT	1396	47.6	3.2	386	5	BY099594	BY099594
1325	49.2	3.3	676	5	BK918241	BK918241	AGENCOURT	1397	47.6	3.2	389	5	BY307826	BY307826
1326	49.2	3.3	677	5	BK914842	BK914842	AGENCOURT	1398	47.6	3.2	401	5	BY058690	BY058690
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1329	49.2	3.3	680	5	BK921231	BK921231	AGENCOURT	1401	47.6	3.2	407	6	CD546668	CD546668
1330	49.2	3.3	680	5	BK924652	BK924652	AGENCOURT	1402	47.6	3.2	413	5	BY155577	BY155577
1331	49.2	3.3	680	7	CK453887	CK453887	911133.MA	1403	47.6	3.2	425	5	BY260637	BY260637
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1333	49.2	3.3	682	5	BK924884	BK924884	AGENCOURT	1405	47.6	3.2	448	5	CD552435	CD552435
1334	49.2	3.3	682	7	CK459890	CK459890	930118.MA	1406	47.6	3.2	448	6	BY081002	BY081002
1335	49.2	3.3	683	5	BK668558	BK668558	AGENCOURT	1407	47.6	3.2	455	6	CB741218	CB741218
1336	49.2	3.3	683	5	BK924470	BK924470	AGENCOURT	1408	47.6	3.2	457	6	CB356292	CB356292
1337	49.2	3.3	686	5	BK673068	BK673068	AGENCOURT	1409	47.6	3.2	468	5	BY244998	BY244998
1338	49.2	3.3	686	5	BK920929	BK920929	AGENCOURT	1410	47.6	3.2	469	5	BE495028	BE495028
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1416	47.6	3.2	506	BQ840062	mhh73e12.
1417	47.6	3.2	513	CB361178	zF001..P00
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C1419	47.6	3.2	525	A1846611	fGqH005..X
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1421	47.6	3.2	530	AL913376	Al913376
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1425	47.6	3.2	543	CO552707	aCLy890..S
1426	47.6	3.2	547	CO552086	aCLy1871
1427	47.6	3.2	552	CO552554	aCLy698..S
1428	47.6	3.2	556	BG307182	fml3b02..Y
1429	47.6	3.2	562	BQ748121	UI-M-FD0-
1430	47.6	3.2	567	CK137814	maJ97f08..
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ORIGIN

Query Match	97.8%	Score 1453	DB 3	Length 3381
Best Local Similarity	100.0%	Pred. No. 0		
Best Local 1453, Conservative	0	Mismatches 0	Indels 0	Gaps 0

QY	18	UCCCGAGGCCCGAGCCAGGCGCTGTGGCTCTCTCTCTGTCTCTGTCCGCGGTCCGGAAGCC	77
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QY	618	CTTCTTGACACACTGTGATCTCTCTCTCTCATTTTGTGGTCAATTGAGGGTTGTG	677
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QY	918	CAAGTTCAAGGCTCACTAAGCTGGCTCTGACGAGAGCCCAAGGCCACTCTGAGAAAGCTT	977
Db	901	CAAGTTCAAGGCTCACTAAGCTGGCTCTGACGAGAGCCCAAGGCCACTCTGAGAAAGCTT	960
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QY	1038	GTGCTCTGGTGTCA	CCCAAGACA	CAGCCACTGGGGGCCGGCTG	CCCCAGCTGATCCCCA		10977
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QY	1218	CTGTGCAAGCAGT	GAGGAGGAGCGTCAGCCTTAC	TGTCCTTACTGGGCAACAAGG		1277	
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QY	1278	GCTTCGAGAGCA	MAAGTGAAGGCTTGGGGGTTTGGGGG	MAAGTCACTCAATGCTGTGTTCC		1337	
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Db	1441	AATCTGCTTGAAA		1453			

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	COMMENT
HSNM805198	Homo sapiens mRNA; cDNA DKFZp761N011 (from clone DKFZp761N011).	AL683896	AL683896.1	GI:21739417	HTC.	Homo sapiens (human)			
						Homo sapiens			
						Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
						1 (bases 1 to 3381)			
						Oertzenaeider, B., Obermaier, B., Deuschelbauer, S., Schaidp, A., Mewes, H.W., Weil, B., Amid, C., Oeanger, A., Fodor, G., Han, M. and Wiemann, S.			
						The German cDNA Consortium			
						Direct Submission			
						Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY			
						Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; Sequencing consortium of the German Genome Project.			
						This clone (DKFZp761N011) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.			
						Please contact RZPD for ordering:			
						http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneid=DKFZp761N011			
						Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.			

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JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 Evry cedex - FRANCE (E-mail : sequefgenoscope.cns.fr)

COMMENT - Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dn) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

FEATURES
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ORIGIN

Query Match 77.5%; Score 1151.6; DB 3; Length 1158;
Best Local Similarity 99.7%; Pred. No. 4,5e-293;
Matches 1154; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Oy 427 TTGTGAACATGATGCTGGGGGAAAGGTGGGTGCTCCATGTTGTCATGATGTTTGA 486
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Db 121 TTGTGAACATGATGCTGGGGGAAAGGTGGGTGCTCCATGTTGTCATGATGTTTGA 180
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CDNA clone CS0DK004YL21 5-PRIME, mRNA sequence.
ACCESSION AL556428
VERSION AL556428.3 GI:46181850
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 944)
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
JOURNAL
On Feb 15, 2001 this sequence version replaced gi.31278230.
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Creteil, CP 5706 - 91057 Evry cedex - FRANCE
Email: sequefgenoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dn) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
5100.f

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?b=CS0DK004CF11QPI&c=5100.f.
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES
source

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VERSION	BX400361.2			
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ORGANISM	Homo sapiens			
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AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
TITLE	1 (bases 1 to 894)			
JOURNAL	Li, W.B., Gruber, C., Jesssee, J. and Polayes, D.			
COMMENT	Unpublished (2001)			
	On May 13, 2003 this sequence version replaced gi:30622186.			
	Contact: Genoscope			
	Genoscope - Centre National de Sequencage			
	2 rue Gascon Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE			
	Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr			
	1st strand cDNA was primed with a NotI-Ligo (dt) primer. Five primers			
	enriched, double-strand cDNA was digested with Not I and cloned			
	into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library			
	was normalized. Library was constructed by life Technologies, a			
	division of Invitrogen. This sequence belongs to sequence cluster			
	5100.f			
	For more information about this cluster, see			
	http://www.genoscope.cns.fr/cdna?c=CS0D009BBD120P1&c=5100.f.			
	Location/Qualifiers			

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421	CTCTGGGTGCGGGATCTGAGACCTTGGGTCCCGCTCTTCTTCTCTCTCTCCCG	480		
787	CTCCCTGTGAGAAAGGCTGATATCAACAAAACTAAGAGGGGACAGGGCCAGGGACAG	846		
481	CTCCCTGTGAGAAAGGCTGATATCAACAAAACTAAGAGGGGACAGGGCCAGGGACAG	540		
847	GAGGTTCACACC-TGTGTTCCCTCACTTGGAGAA-CAAGCAATCTCCATCTTTAG	904		
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601	AAAGTTCACCAAGTTCAGAGCTCACTGACCTGGCTCTGACAGAGACCCCAAGCCACT	660		
965	CTGAGAGACCTTGAAGTGAAGGACAGGCTGAGGGCTCTTTGGGTTTCTTGGACAG	1022		
661	CTGAGAGACCTTGAAGTGAAGGACAGGCTGAGGGCTCTTTGGGTTTCTTGGACAG	720		
1025	TGCAATGGTTCACAGTCTCTGATGACCCAGAGACAGGCACTCGGGCCCGCTGCC	1082		
721	TGCAATGGTTCACAGTCTCTGATGACCCAGAGACAGGCACTCGGGCTCCGCTGCC	780		
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DEFINITION	AGENCOURT 14373241 NIH MGC 181 Homo sapiens cDNA clone IMAGE:30398267 5', mRNA sequence.				
ACCESSION	CD514425				
VERSION	CD514425.1 GI:31446143				
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Mammalia; Euteheria; Chordata; Craniata; Vertebrata; Euteleostomi; Eumarkaria; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 842)				
TITLE	NIH-MGC http://mgi.mgi.nih.gov/.				
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)				
COMMENT	Unpublished (1999) Contract: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics / NIH National Cancer Institute Bldg. 31 Rm10A07 Bethesda, MD 20892 Email: cga@bbs-remail.nih.gov Tissue Procurement: Dr. Michael Brownstein cDNA Library Preparation: Invitrogen Corp cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: NDAM482 row: 0 column: 12 High quality sequence stop: 721. Location/Qualifiers 1. 842 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:30398267" /tissue_type="White Matter" /dev_stage="Unknown" /lab_host="DH10B-Ton A (T1 and T5 phage resistances)" /clone_1ib="NIH MGC 181" /note="Vector: pCMV-Sport6.1; site 1: NotI; site 2: EcoRV (destroyed); Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.42 kb. Library was constructed by (Invitrogen). Note: this is a NIH_MGC Library."				
FEATURES	source				
ORIGIN	Query Match 50.6%; Score 751.4; DB 6; Length 842; Best Local Similarity 98.3%; Pred. No.3.1e-187; Matches 822; Conservative 0; Mismatches 7; Indels 7; Gaps 6				
QY	3 GGCCACACCCAGCTAGCCCGAGCCCGAGCCAGCGCTGCTCTCTCTGCTCTGCG 62				
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 Oy 779 CTTCCCGGCTCCCTGT-GCAGAGGGGCTGA--TATCAACCAAAAACTAGAGGGG 831
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RESULT 12
 BX421987
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

BX421987 755 bp RNA linear EST 01-MAY-2004
 BX421987 Homo sapiens T CELLS (JURKAT CELL LINE) Homo sapiens CDNA
 clone CS0DH006YD09 5-PRIME, mRNA sequence.
 BX421987
 BX421987.2 GI:46934324
 EST.
 Homo sapiens (human)
 Homo sapiens
 Hukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 755)
 Li, W.B., Gruber, C., Jeesee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On May 13, 2003 this sequence version replaced gi:30659228.

Contact: Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dAT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
 was not normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
 This sequence belongs to sequence cluster 5100.f
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna7s-CS0DH006CB05QPI&c=5100.f.
 Location/Qualifiers
 1..755

FEATURES
 source

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clone="CSDDH006YD09"  
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cell_line="JURKAT CELL LINE"  
clone_1lb="Homo sapiens T CELLS (JURKAT CELL LINE)"  
note="Vector: pCMVSPORT 6; 1st strand cDNA was primed  
with a NotI-oligo(dT) primer. Five prime end enriched,  
double-strand cDNA was digested with Not I and cloned into
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QY 437 TGATGCTGGGAAACGCTGGCTGCTCAAGTTATGTCATGATGTTGAAGAAAAGCCA 496
DB 424 TGAATGCTGGGAAACGCTGGCTGCTCAAGTTATGTCATGATGTTGAAGAAAAGCCA 483
QY 497 ACGAGAGAGAGCCCAAGCAGATTGGCCCCCTCCAGAGAGAGACATTGCTAGCCCT 556
DB 484 ACGAGAGAGAGCCCAAGCAGATTGGCCCCCTCCAGAGAGAGACATTGCTAGCCCT 543
QY 557 GAGAGACCCCGCTGAGCTCCCAAGCTCCCAAGCCCAATGCTCCCTCCATCTTGTGTC 616
DB 544 GAGAGACCCCGCTGAGCTCCCAAGCTCCCAAGCCCAATGCTCCCTCCATCTTGTGTC 603
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DB 604 CTTTCTTACACACATGATCTCTCTCTCTCTCAATTTGTTGTCATTGAGG-TTTTGT 663
QY 676 TGTGTTTTCATCATGT-CTTTGTAAGACAAATTAATGCTTAAAGGGGCTTGGG- 733
DB 664 TGTGTTTTCATCATGTCTTTGTAAGACAAATTAATGCTTAAAGGGGCTTGGG- 723
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RESULT 14
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DEFINITION UI-CF-FNO-aex-g-19-0-UI s1 UI-CF-FNO Homo sapiens cDNA clone
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VERSION CA312962.1 GI:24531060
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 701)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 9704477
PUBMED 8889548
COMMENT Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
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/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
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/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site_1: Bcor I; Site_2: Not I;
UI-CF-FNO is a subtracted cDNA library derived from two

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normalized Human lung epithelial cell libraries (EN1 and D01). The library was subtracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. For additional information, contact: bento-soares@uiowa.edu
TAG TISSUE=Human Lung Epithelial Cell Lines untreated LPS 6hr to LPS 24h
TAG LIB=UI-CF-FNO
TAG_SEQ=CTGCTCAGGT"

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ORIGIN
Query Match 47.2%; Score 701; DB 6; Length 701;
Best local Similarity 100.0%; Pred. No. 6.4e-174;
Matches 701; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 521 CTGAGAAACCTTGAGTGGGAGCAAGGCTGACGAGGCTCTTTCGGGTTTCTTGACAG 462
QY 1025 TGCCATGTTTCAGTGCTGTGTGTGTCACCCAGAGACAGGCACTCGGGGCTCCGCTGCC 1084
DB 461 TGCCATGTTTCAGTGCTGTGTGTGTCACCCAGAGACAGGCACTCGGGGCTCCGCTGCC 402
QY 1085 CAGCTGATCCCACTGATTCACACCTCTTCATCCTCAGTATGTAAGTGGAGAG 1144
DB 401 CAGCTGATCCCACTGATTCACACCTCTTCATCCTCAGTATGTAAGTGGAGAG 342
QY 1145 AAAGAGCTTGAGCTTGGAGAGCCCTTCAGAAAGTACCAAGAGAACCTTCAGTCTGC 1204
DB 341 AAAGAGCTTGAGCTTGGAGAGCCCTTCAGAAAGTACCAAGAGAACCTTCAGTCTGC 282
QY 1205 TCTGTGCGCACACTGTGTGTCAGGACGCTGAGAGGACAGGTGCAAGCCCTACT 1264
DB 281 TCTGTGCGCACACTGTGTGTCAGGACGCTGAGAGGACAGGTGCAAGCCCTACT 222
QY 1265 GGGGACAGAGAGGCTTCGAGAGGAGAGGCTGAGGCTTGGGGGAAAAGTCAAGC 1324
DB 221 GGGGACAGAGAGGCTTCGAGAGGAGAGGCTGAGGCTTGGGGGAAAAGTCAAGC 162
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DB 101 TAAATGCTCAGCGCAAAAGTACAGACCTGTAGGCAAGACATCAAAATACAGGTTG 42
QY 1445 CTGTCTGACCCCAATCTGCTTGAAGAAAAA 1485
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DEFINITION AU133192 NT2RP4 Homo sapiens cDNA clone NT2RP400514 5', mRNA
ACCESSION AU133192
VERSION AU133192.1 GI:10993731
KEYWORDS EST.
SOURCE Homo sapiens (human)

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using BW model

Run on: March 29, 2005, 03:23:39 ; Search time 2717 Seconds
(without alignments)
3257.125 Million cell updates/sec

Perfect score: 1485

Sequence: 1 gcgcgcacacgcagtagcc.....tgaaaaaaaaaaaaaa 1485

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 5552208 seqs, 2979665951 residues

Total number of hits satisfying chosen parameters: 1110416

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database :

Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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64	1485	100.0	1485	15	US-10-223-088-209 9-cv
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100	1485	100.0	1485	15	US-10-223-087-209 "
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194	192.2	12.9	658	14	US-10-300-257-5
195	192.2	12.9	760	18	US-10-723-860-5430
196	191	12.9	639	17	US-10-172-118-639
197	191	12.9	639	17	US-10-342-887-639
198	191	12.9	639	18	US-10-775-169-181
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C 243	54.4	3.7	500	9	US-09-864-761-2515
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C 256	45.2	3.0	433	18	US-10-674-124A-12589	Sequence 12589, A	329	41.2	2.8	1228	18	US-10-425-115-40607	Sequence 40607, A
257	45	3.0	1112	17	US-10-152-319A-1701	Sequence 1701, Ap	330	41.2	2.8	1296	18	US-10-425-115-40656	Sequence 40656, A
258	44.6	3.0	516	19	US-10-696-639-982	Sequence 982, App	331	41.2	2.8	1769	18	US-10-425-115-40698	Sequence 40698, A
259	44.6	3.0	863	17	US-10-424-599-39046	Sequence 39046, A	332	41.2	2.8	3450	18	US-10-425-115-129580	Sequence 129580, A
C 260	44.6	3.0	3372	14	US-10-067-457-2	Sequence 2, App1	333	41	2.8	975	9	US-09-938-842A-2193	Sequence 2193, Ap
C 261	44.6	3.0	3459	17	US-10-311-795-3	Sequence 3, App1	334	41	2.8	975	11	US-09-938-842A-2193	Sequence 2193, Ap
262	44.4	3.0	785	17	US-10-435-114-18116	Sequence 18116, A	335	41	2.8	1129	18	US-10-437-963-99465	Sequence 99465, Ap
263	44.4	3.0	787	15	US-10-259-165-594	Sequence 594, App	336	40.6	2.7	426	18	US-10-437-963-99465	Sequence 99465, Ap
264	44.4	3.0	802	17	US-10-260-238-5631	Sequence 5631, Ap	337	40.6	2.7	560	18	US-10-767-795-4912	Sequence 4912, Ap
265	44.4	3.0	802	17	US-10-260-238-5636	Sequence 3636, Ap	338	40.6	2.7	724	17	US-10-260-238-5936	Sequence 2936, Ap
266	44.4	3.0	841	17	US-10-260-238-5639	Sequence 3639, Ap	339	40.6	2.7	1794	18	US-10-437-963-66912	Sequence 66912, A
267	44.4	3.0	909	17	US-10-425-114-5085	Sequence 5085, Ap	340	40.6	2.7	16807	18	US-10-322-281-305	Sequence 305, App
268	44.4	3.0	910	17	US-10-425-114-28387	Sequence 28387, A	341	40.4	2.7	1974	11	US-09-876-143-1398	Sequence 1398, Ap
269	44.4	3.0	958	17	US-10-425-114-16262	Sequence 16262, A	342	40.4	2.7	974	11	US-09-876-143-1399	Sequence 1399, Ap
270	44.4	3.0	975	18	US-10-425-115-129585	Sequence 129585, A	343	40.4	2.7	2240	17	US-10-108-260A-1135	Sequence 11352, Ap
271	44.4	3.0	1196	18	US-10-425-115-129569	Sequence 129569, A	C 344	40.2	2.7	654	9	US-09-917-800A-1352	Sequence 10537, A
272	44	3.0	1251	10	US-09-989-025A-7	Sequence 7, App1	345	40.2	2.7	679	18	US-10-425-115-10537	Sequence 35458, A
273	44	3.0	2175	14	US-10-175-523-17	Sequence 17, App1	346	40.2	2.7	762	17	US-10-425-115-35458	Sequence 68350, A
274	44	3.0	2247	16	US-10-119-428-34	Sequence 34, App1	347	40.2	2.7	1070	18	US-10-425-115-68330	Sequence 31744, A
275	44	3.0	2247	17	US-10-291-172-31	Sequence 31, App1	348	40.2	2.7	2394	17	US-10-282-122A-31744	Sequence 5472, Ap
276	44	3.0	2247	17	US-10-221-278-31	Sequence 31, App1	349	40.2	2.7	3446	18	US-10-723-860-5472	Sequence 5, App1
277	44	2.9	255	10	US-09-237-183A-828	Sequence 828, App	350	40.2	2.7	3513	14	US-10-175-523-5	Sequence 102, App
278	43.8	2.9	1161	9	US-09-954-531-575	Sequence 575, App	351	40.2	2.7	3513	14	US-10-175-523-102	Sequence 1962, Ap
279	43.6	2.9	1170	18	US-10-411-910A-227	Sequence 227, App	352	40.2	2.7	3916	17	US-10-152-319A-1962	Sequence 67100, A
280	43.4	2.9	2466	15	US-09-953-348-83	Sequence 83, App1	353	40	2.7	1327	18	US-10-086-738A-1	Sequence 1, App1
281	43.4	2.9	2466	15	US-10-267-225-83	Sequence 83, App1	354	40	2.7	4166	18	US-10-086-738A-1	Sequence 76274, A
282	43.4	2.9	18034	10	US-09-953-348-75	Sequence 75, App1	355	40	2.7	289	18	US-10-437-963-76274	Sequence 90606, A
283	43.4	2.9	18034	10	US-10-267-225-75	Sequence 75, App1	C 356	39.8	2.7	4166	18	US-10-425-115-99606	Sequence 719, App
284	43.2	2.9	294	15	US-09-237-183A-618	Sequence 618, App	357	39.8	2.7	289	18	US-09-237-183A-719	Sequence 7504, Ap
285	43.2	2.9	447	10	US-09-989-025A-3	Sequence 3, App1	C 358	39.8	2.7	339	10	US-10-674-124A-7504	Sequence 709, App
286	43.2	2.9	878	17	US-10-425-114-4443	Sequence 4443, Ap	359	39.8	2.7	339	14	US-09-237-183A-709	Sequence 404, App
287	43.2	2.9	1227	17	US-10-425-114-725	Sequence 725, App	360	39.8	2.7	1139	17	US-10-191-803-111	Sequence 111, App
288	43.2	2.9	1926	17	US-10-425-114-33755	Sequence 33755, A	361	39.8	2.7	1139	17	US-10-152-319A-1704	Sequence 1704, App
289	43.2	2.9	2908	14	US-10-080-114A-6	Sequence 6, App1	362	39.8	2.7	1576	18	US-10-437-963-1369	Sequence 30745, Ap
290	43.2	2.9	3880	18	US-10-425-115-99607	Sequence 99607, A	363	39.8	2.7	1890	17	US-10-369-493-30745	Sequence 27989, A
291	43	2.9	285	10	US-09-237-183A-676	Sequence 676, App	364	39.8	2.7	1929	17	US-10-369-493-27989	Sequence 3634, Ap
292	43	2.9	299	18	US-10-674-124A-6609	Sequence 6609, Ap	365	39.6	2.7	541	17	US-10-260-238-3634	Sequence 36347, Ap
293	43	2.9	378	14	US-10-062-727-542	Sequence 542, App	366	39.6	2.7	545	18	US-10-767-701-6347	Sequence 745, App
294	43	2.9	450	14	US-10-062-727-395	Sequence 395, App	367	39.6	2.7	695	17	US-10-425-114-745	Sequence 2937, App
295	43	2.9	495	14	US-10-062-727-862	Sequence 862, App	368	39.6	2.7	709	17	US-10-260-238-2937	Sequence 2937, App
296	42.8	2.9	803	17	US-10-425-114-22255	Sequence 22255, A	369	39.6	2.7	727	17	US-10-425-114-3541	Sequence 3541, Ap
297	42.8	2.9	820	17	US-10-260-238-3635	Sequence 3635, Ap	370	39.6	2.7	727	17	US-10-424-599-40635	Sequence 40635, A
298	42.8	2.9	836	18	US-10-739-930-2210	Sequence 2210, Ap	371	39.6	2.7	735	18	US-10-739-930-3113	Sequence 3113, Ap
299	42.8	2.9	1668	18	US-10-411-910A-226	Sequence 226, App	372	39.6	2.7	915	18	US-10-425-115-125942	Sequence 25942, A
300	42.6	2.9	306	10	US-09-237-183A-622	Sequence 622, App	373	39.6	2.7	940	17	US-10-425-114-25780	Sequence 25780, A
301	42.6	2.9	313	10	US-09-237-183A-3952	Sequence 395, App	374	39.6	2.7	1039	17	US-10-424-599-40636	Sequence 40636, A
C 302	42.4	2.8	282	18	US-10-437-963-101008	Sequence 101008, A	375	39.6	2.7	1088	17	US-10-424-599-93719	Sequence 93719, A
303	42.4	2.8	756	18	US-10-425-115-43557	Sequence 43557, A	376	39.6	2.7	1170	17	US-10-437-963-35214	Sequence 35214, A
C 304	42.2	2.8	769	18	US-10-437-963-101040	Sequence 101040, A	377	39.6	2.7	1434	18	US-10-437-963-26803	Sequence 26803, A
C 305	42.2	2.8	1681	18	US-10-425-115-92916	Sequence 92916, A	378	39.6	2.7	1949	18	US-10-437-963-26803	Sequence 26803, A
306	41.6	2.8	390	17	US-10-425-114-35084	Sequence 35084, A	C 379	39.6	2.7	6120	15	US-10-240-453-314	Sequence 114, App1
307	41.6	2.8	1948	18	US-09-748-033-7	Sequence 7, App1	C 380	39.6	2.7	421	18	US-10-425-115-114139	Sequence 114139, A
308	41.4	2.8	905	9	US-10-425-115-31253	Sequence 31253, A	381	39.4	2.7	442	18	US-10-674-124A-23425	Sequence 23425, A
309	41.4	2.8	1647	18	US-10-259-165-688	Sequence 688, App	C 382	39.4	2.7	471	18	US-10-437-963-71075	Sequence 71075, A
310	41.2	2.8	447	15	US-10-259-165-688	Sequence 688, App	C 383	39.4	2.7	996	17	US-10-085-117-267	Sequence 267, App
311	41.2	2.8	727	17	US-10-425-114-28012	Sequence 28012, A	C 384	39.4	2.7	1830	13	US-10-027-632-99068	Sequence 99068, A
312	41.2	2.8	738	17	US-10-425-114-17862	Sequence 17862, A	C 385	39.4	2.7	1830	13	US-10-027-632-99068	Sequence 99068, A
313	41.2	2.8	744	18	US-10-425-115-89651	Sequence 89651, A	C 386	39.4	2.7	1830	13	US-10-027-632-99068	Sequence 99068, A
314	41.2	2.8	778	18	US-10-425-114-28655	Sequence 28655, A	387	39.4	2.7	20450	11	US-10-085-117-266	Sequence 266, App
315	41.2	2.8	796	17	US-10-425-114-25198	Sequence 25198, A	388	39.4	2.7	3396	17	US-09-997-722-771	Sequence 7271, App
316	41.2	2.8	817	17	US-10-425-114-28675	Sequence 28675, A	389	39.4	2.7	93011	18	US-10-719-993-6871	Sequence 6871, App
317	41.2	2.8	824	17	US-10-425-114-22150	Sequence 22150, A	390	39.2	2.6	551	13	US-10-027-632-11673	Sequence 71673, A
318	41.2	2.8	834	17	US-10-425-114-4388	Sequence 4388, Ap	391	39.2	2.6	551	17	US-10-425-114-18543	Sequence 18543, A
319	41.2	2.8	844	17	US-10-425-114-4296	Sequence 4296, App	C 392	39.2	2.6	716	17	US-10-437-963-61317	Sequence 61317, A
320	41.2	2.8	844	17	US-10-425-114-4296	Sequence 4296, App	C 393	39.2	2.6	1146	18	US-10-260-238-1264	Sequence 1264, Ap
321	41.2	2.8	877	17	US-10-425-114-31912	Sequence 31912, A	C 394	39.2	2.6	1308	17	US-10-260-238-1264	Sequence 1264, Ap
322	41.2	2.8	884	17	US-10-425-114-3887	Sequence 3887, App	C 395	39.2	2.6	1341	18	US-10-437-963-61316	Sequence 61316, A
323	41.2	2.8	884	17	US-10-425-114-2298	Sequence 2298, Ap	C 396	39.2	2.6	1814	18	US-10-425-115-129591	Sequence 129591, A
324	41.2	2.8	888	18	US-10-425-115-99652	Sequence 99652, A	C 397	39.2	2.6	33454	13	US-10-087-192-1111	Sequence 1111, Ap
325	41.2	2.8	888	18	US-10-425-115-99652	Sequence 99652, A	398	39.2	2.6	103012	19	US-10-741-600-17697	Sequence 17697, A
326	41.2	2.8	892	17	US-10-425-114-1352	Sequence 1352, Ap	399	39	2.6	402	10	US-09-918-995-3927	Sequence 3927, Ap

400	39	2.6	451	10	US-09-918-995-5666	Sequence 5666, Ap	579	38.4	2.6	99588	13	US-10-087-192-1780	Sequence 1780, Ap
401	39	2.6	663	18	US-10-739-930-4372	Sequence 4372, Ap	580	38.4	2.6	101241	13	US-10-087-192-1339	Sequence 1339, Ap
C 402	39	2.6	681	13	US-10-027-632-141458	Sequence 141458, A	581	38.2	2.6	281	10	US-09-237-183A-677	Sequence 677, Ap
C 403	39	2.6	681	13	US-10-027-632-141460	Sequence 141460, A	582	38.2	2.6	288	10	US-09-237-183A-650	Sequence 650, Ap
C 404	39	2.6	681	17	US-10-027-632-141458	Sequence 141458, A	583	38.2	2.6	307	10	US-09-237-183A-612	Sequence 612, Ap
C 405	39	2.6	681	17	US-10-027-632-141460	Sequence 141460, A	584	38.2	2.6	504	18	US-10-767-701-28690	Sequence 28690, A
406	39	2.6	844	14	US-10-116-802-53	Sequence 53, Appl	C 585	38.2	2.6	594	14	US-10-123-155-10	Sequence 10, Appl
407	39	2.6	846	10	US-09-919-039-319	Sequence 319, Appl	C 586	38.2	2.6	603	16	US-10-029-386-20492	Sequence 20492, A
408	39	2.6	1116	16	US-10-353-826-8	Sequence 8, Appl	601	38.2	2.6	735	18	US-10-425-115-86499	Sequence 86499, A
409	39	2.6	1158	10	US-09-919-039-320	Sequence 320, Appl	602	38.2	2.6	800	17	US-10-260-238-3633	Sequence 3633, Ap
410	39	2.6	1173	16	US-10-353-826-3	Sequence 3, Appl	C 603	38.2	2.6	1032	15	US-10-156-761-5323	Sequence 5323, Ap
411	39	2.6	1225	18	US-10-723-860-6099	Sequence 6099, Ap	C 604	38.2	2.6	1814	18	US-10-425-115-129591	Sequence 129591, A
412	39	2.6	1248	13	US-10-002-600-112	Sequence 112, Appl	605	38.2	2.6	2313	17	US-10-369-493-28024	Sequence 28024, A
413	39	2.6	1284	14	US-10-086-738A-2	Sequence 2, Appl	606	38.2	2.6	2313	17	US-10-369-493-30779	Sequence 30779, A
414	39	2.6	1284	14	US-10-086-738A-3	Sequence 3, Appl	607	38.2	2.6	2421	17	US-10-282-122A-11634	Sequence 11634, A
415	39	2.6	1929	9	US-09-554-000-1	Sequence 1, Appl	608	38.2	2.6	2421	17	US-10-282-122A-12945	Sequence 12945, A
416	39	2.6	1929	9	US-09-554-000-5	Sequence 5, Appl	609	38.2	2.6	3250	17	US-10-170-385-122	Sequence 122, Appl
417	39	2.6	1959	9	US-09-554-000-3	Sequence 3, Appl	610	38.2	2.6	4139	17	US-10-439-388-24	Sequence 24, Appl
418	39	2.6	1971	9	US-09-554-000-7	Sequence 7, Appl	611	38.2	2.6	50460	13	US-10-087-192-1633	Sequence 1633, Ap
C 419	39	2.6	6171	15	US-10-311-455-762	Sequence 762, Appl	C 612	38.2	2.6	9025608	15	US-10-156-761-1	Sequence 1, Appl
420	39	2.6	137560	18	US-10-481-112-1	Sequence 1, Appl	613	38	2.6	345	14	US-10-062-727-930	Sequence 930, Appl
421	38.8	2.6	278	14	US-10-062-727-818	Sequence 818, Appl	614	38	2.6	359	14	US-10-062-727-641	Sequence 641, Appl
422	38.8	2.6	396	18	US-10-437-963-3172	Sequence 3172, Appl	615	38	2.6	375	18	US-10-674-124A-1390	Sequence 1390, Appl
423	38.8	2.6	773	18	US-10-767-701-15509	Sequence 15509, A	616	38	2.6	404	14	US-10-062-727-415	Sequence 415, Appl
424	38.8	2.6	777	17	US-10-424-599-5665	Sequence 5665, A	617	38	2.6	414	14	US-10-062-727-669	Sequence 669, Appl
425	38.8	2.6	1008	17	US-10-191-803-732	Sequence 732, Appl	618	38	2.6	450	9	US-09-938-842A-2653	Sequence 2653, Appl
426	38.8	2.6	1008	17	US-10-152-319A-2103	Sequence 2103, Appl	619	38	2.6	450	11	US-09-938-842A-2653	Sequence 2653, Appl
427	38.8	2.6	2474	18	US-10-435-115-43967	Sequence 43967, A	C 620	38	2.6	486	18	US-10-767-701-238924	Sequence 238924, A
428	38.6	2.6	455	16	US-10-029-386-22746	Sequence 22746, A	C 621	38	2.6	501	13	US-10-027-632-195834	Sequence 195834, A
C 429	38.6	2.6	516	18	US-10-437-963-32307	Sequence 32307, A	C 622	38	2.6	501	17	US-10-027-632-195534	Sequence 195534, A
430	38.6	2.6	550	18	US-10-767-701-5385	Sequence 5385, Appl	C 623	38	2.6	695	9	US-09-770-149-985	Sequence 285, Appl
431	38.6	2.6	773	14	US-10-052-283-398	Sequence 398, Appl	624	38	2.6	868	17	US-10-425-114-6936	Sequence 6936, Appl
432	38.6	2.6	2107	9	US-09-981-353-49	Sequence 49, Appl	625	38	2.6	894	18	US-10-425-115-89655	Sequence 89655, A
433	38.6	2.6	2110	17	US-10-172-118-1846	Sequence 1846, Appl	626	38	2.6	903	18	US-10-437-963-26878	Sequence 26878, A
434	38.6	2.6	2110	17	US-10-342-887-1846	Sequence 1846, Appl	627	38	2.6	907	17	US-10-425-114-26943	Sequence 26943, A
435	38.6	2.6	2110	18	US-10-717-597-35	Sequence 35, Appl	628	38	2.6	1061	18	US-10-437-963-51439	Sequence 51439, A
436	38.6	2.6	2432	18	US-10-437-963-47424	Sequence 47424, A	C 629	38	2.6	1713	18	US-10-425-115-11862	Sequence 11862, A
445	38.6	2.6	2945	14	US-10-237-535-87	Sequence 87, Appl	630	38	2.6	1808	18	US-10-739-930-2978	Sequence 2978, Appl
444	38.6	2.6	2945	14	US-10-237-535-87	Sequence 87, Appl	C 631	38	2.6	1953	18	US-10-425-115-17586	Sequence 17586, A
454	38.6	2.6	95982	13	US-10-087-192-2029	Sequence 2029, Appl	C 632	38	2.6	3893	18	US-10-437-963-51441	Sequence 51441, A
545	38.6	2.6	233	10	US-09-237-183A-783	Sequence 783, Appl	C 633	38	2.6	6907	15	US-10-311-455-550	Sequence 540, Appl
546	38.4	2.6	257	10	US-09-237-183A-783	Sequence 783, Appl	634	38	2.6	62944	9	US-09-954-456-257	Sequence 2257, Appl
547	38.4	2.6	268	10	US-09-237-183A-783	Sequence 783, Appl	C 635	38	2.6	62944	11	US-09-968-007A-129	Sequence 129, Appl
548	38.4	2.6	274	10	US-09-237-183A-689	Sequence 689, Appl	C 636	38	2.6	109559	18	US-10-322-281-137	Sequence 137, Appl
549	38.4	2.6	286	10	US-09-237-183A-646	Sequence 646, Appl	C 637	38	2.6	3673778	16	US-10-312-841-2	Sequence 2, Appl
550	38.4	2.6	306	10	US-09-237-183A-576	Sequence 576, Appl	638	37.8	2.5	242	10	US-09-237-183A-812	Sequence 812, Appl
551	38.4	2.6	306	10	US-09-237-183A-576	Sequence 576, Appl	639	37.8	2.5	391	10	US-09-918-995-5449	Sequence 5449, Appl
552	38.4	2.6	360	10	US-09-237-183A-1058	Sequence 1058, Appl	640	37.8	2.5	449	10	US-09-918-995-11791	Sequence 11791, A
553	38.4	2.6	383	10	US-09-237-183A-1049	Sequence 1049, Appl	641	37.8	2.5	445	10	US-09-918-995-15644	Sequence 15644, A
554	38.4	2.6	392	17	US-10-260-238-2964	Sequence 2964, Appl	642	37.8	2.5	459	10	US-09-918-995-4655	Sequence 4655, Appl
555	38.4	2.6	413	10	US-09-237-183A-1063	Sequence 1063, Appl	643	37.8	2.5	465	10	US-09-918-995-3284	Sequence 3284, Appl
556	38.4	2.6	425	10	US-09-237-183A-1059	Sequence 1059, Appl	644	37.8	2.5	478	10	US-09-918-995-14016	Sequence 14016, A
557	38.4	2.6	433	10	US-09-237-183A-1047	Sequence 1047, Appl	645	37.8	2.5	581	13	US-09-930-213-168	Sequence 168, Appl
C 558	38.4	2.6	442	9	US-09-880-107-1917	Sequence 1917, Appl	C 646	37.8	2.5	681	17	US-10-027-632-141457	Sequence 141457, A
559	38.4	2.6	450	11	US-09-997-722-273	Sequence 722, Appl	C 647	37.8	2.5	724	18	US-10-425-115-50608	Sequence 50608, A
560	38.4	2.6	469	10	US-09-237-183A-1020	Sequence 1020, Appl	648	37.8	2.5	788	18	US-10-425-115-135851	Sequence 135851, A
561	38.4	2.6	512	10	US-09-237-183A-1021	Sequence 1021, Appl	649	37.8	2.5	906	17	US-10-425-114-1174	Sequence 1174, Appl
562	38.4	2.6	591	17	US-10-264-049-1660	Sequence 1660, Appl	650	37.8	2.5	906	17	US-10-425-114-1174	Sequence 1174, Appl
563	38.4	2.6	870	17	US-10-425-114-6017	Sequence 6017, Appl	651	37.8	2.5	906	17	US-10-425-114-1174	Sequence 1174, Appl
564	38.4	2.6	1227	17	US-10-425-114-19280	Sequence 19280, A	652	37.8	2.5	906	17	US-10-425-114-1174	Sequence 1174, Appl
565	38.4	2.6	1262	17	US-10-425-114-6219	Sequence 6219, A	653	37.8	2.5	957	15	US-10-425-115-150619	Sequence 150619, A
566	38.4	2.6	1431	17	US-10-425-114-16306	Sequence 16306, A	654	37.8	2.5	1199	17	US-10-321-278-102	Sequence 278, Appl
567	38.4	2.6	1436	17	US-10-425-114-1505	Sequence 1505, Appl	655	37.8	2.5	1261	15	US-10-119-926-59	Sequence 926, Appl
568	38.4	2.6	1436	17	US-10-425-114-1505	Sequence 1505, Appl	656	37.8	2.5	1261	15	US-10-119-926-59	Sequence 926, Appl
569	38.4	2.6	2307	17	US-10-425-114-35558	Sequence 35558, A	657	37.8	2.5	1312	15	US-10-084-817-13	Sequence 817, A
570	38.4	2.6	2505	17	US-10-425-114-35609	Sequence 35609, A	658	37.8	2.5	1404	17	US-10-282-122A-114163	Sequence 114163, A
571	38.4	2.6	2638	17	US-10-425-114-2574	Sequence 2574, Appl	659	37.8	2.5	1839	18	US-10-437-963-37206	Sequence 37206, A
572	38.4	2.6	2986	17	US-10-425-114-2283	Sequence 2283, Appl	660	37.8	2.5	1839	18	US-10-437-963-37206	Sequence 37206, A
573	38.4	2.6	2992	17	US-10-425-114-26430	Sequence 26430, A	661	37.8	2.5	3397	14	US-10-198-846-11555	Sequence 11555, A
574	38.4	2.6	3419	17	US-10-425-114-17556	Sequence 17556, A	662	37.8	2.5	9025608	15	US-09-997-722-199	Sequence 199, Appl
575	38.4	2.6	4106	18	US-10-425-115-90606	Sequence 90606, A	663	37.8	2.5	450	18	US-10-674-124A-13880	Sequence 13880, A
576	38.4	2.6	99232	18	US-10-331-053-16	Sequence 16, Appl	664	37.6	2.5	451	18	US-10-767-701-22400	Sequence 22400, A
577	38.4	2.6					C 665	37.6	2.5				

666	37.6	2.5	799	17	US-10-369-493-29947	Sequence 29947, A	741	36.8	2.5	534	18	US-10-437-963-53472	Sequence 53472, A
C 667	37.6	2.5	804	18	US-10-437-963-18891	Sequence 18891, A	742	36.8	2.5	636	9	US-09-770-149-646	Sequence 646, App
668	37.6	2.5	1107	18	US-10-425-115-78809	Sequence 78809, A	743	36.8	2.5	711	15	US-10-156-761-3275	Sequence 3275, App
669	37.6	2.5	1208	17	US-10-425-114-23365	Sequence 32365, A	744	36.8	2.5	1734	18	US-10-437-963-1188	Sequence 1188, App
670	37.6	2.5	1230	17	US-10-437-963-2927	Sequence 2927, App	745	36.8	2.5	3430	18	US-10-767-701-14869	Sequence 14869, A
671	37.6	2.5	1501	17	US-10-425-114-17427	Sequence 17427, A	746	36.8	2.5	9980	9	US-09-880-107-3352	Sequence 3352, App
672	37.6	2.5	1507	18	US-10-425-115-9354	Sequence 9354, App	747	36.8	2.5	9980	11	US-09-968-007-476	Sequence 476, App
673	37.6	2.5	1787	17	US-10-425-114-10952	Sequence 10952, A	748	36.8	2.5	35828	16	US-10-384-993-17	Sequence 17, App
C 674	37.6	2.5	1798	13	US-10-027-632-98757	Sequence 98757, A	749	36.8	2.5	35828	17	US-10-463-190-17	Sequence 17, App
C 675	37.6	2.5	1798	17	US-10-027-632-98757	Sequence 98757, A	750	36.8	2.5	35828	17	US-10-095-248A-17	Sequence 17, App
676	37.6	2.5	2255	18	US-10-739-930-1681	Sequence 1681, App	C 751	36.8	2.5	35828	18	US-10-788-606-17	Sequence 17, App
C 677	37.6	2.5	3355	9	US-09-855-722-4	Sequence 4, App	752	36.8	2.5	46878	19	US-10-741-600-17664	Sequence 17664, A
C 678	37.6	2.5	3355	14	US-10-219-248-4	Sequence 4, App	753	36.8	2.5	64467	19	US-10-274-409-3	Sequence 3, App
C 679	37.6	2.5	3955	14	US-10-219-247-4	Sequence 4, App	754	36.8	2.5	64467	19	US-10-932-135-3	Sequence 3, App
C 680	37.6	2.5	4749	16	US-10-091-625-3	Sequence 3, App	755	36.8	2.5	118067	15	US-10-081-327-32	Sequence 32, App
C 681	37.6	2.5	4749	16	US-10-091-625-3	Sequence 3, App	756	36.8	2.5	201239	19	US-10-278-698-246	Sequence 246, App
C 682	37.6	2.5	4749	17	US-10-096-399A-3	Sequence 3, App	757	36.8	2.5	201239	19	US-10-278-698-246	Sequence 246, App
C 683	37.6	2.5	4749	17	US-10-461-668-3	Sequence 3, App	758	36.8	2.5	201239	19	US-10-278-698-246	Sequence 246, App
C 684	37.6	2.5	4974	16	US-10-388-263-376	Sequence 376, App	759	36.6	2.5	295	10	US-10-278-698-760	Sequence 760, App
C 685	37.6	2.5	4974	16	US-10-091-625-10	Sequence 10, App	760	36.6	2.5	340	10	US-09-237-183A-615	Sequence 615, App
C 686	37.6	2.5	4974	16	US-10-096-399A-10	Sequence 10, App	761	36.6	2.5	438	9	US-09-237-183A-537	Sequence 537, App
C 687	37.6	2.5	4974	17	US-10-461-668-10	Sequence 10, App	C 762	36.6	2.5	490	13	US-09-983-965-7720	Sequence 7720, App
C 688	37.6	2.5	5077	18	US-10-388-263-380	Sequence 380, App	763	36.6	2.5	490	17	US-10-027-632-270955	Sequence 270955, App
C 689	37.6	2.5	5077	18	US-10-789-378-37	Sequence 37, App	764	36.6	2.5	689	17	US-10-260-238-2713	Sequence 2713, App
C 690	37.6	2.5	115780	18	US-10-367-094-96	Sequence 96, App	C 765	36.6	2.5	689	17	US-10-767-701-5750	Sequence 5750, App
C 691	37.6	2.5	175590	10	US-09-911-077A-13	Sequence 13, App	766	36.6	2.5	700	18	US-10-767-701-5750	Sequence 5750, App
C 692	37.6	2.5	175590	18	US-10-724-806-13	Sequence 13, App	767	36.6	2.5	792	13	US-10-027-632-168583	Sequence 168583, App
C 693	37.4	2.5	256493	13	US-10-087-192-1000	Sequence 1000, App	768	36.6	2.5	792	13	US-10-027-632-168583	Sequence 168583, App
C 694	37.4	2.5	536	17	US-10-338-110-119	Sequence 119, App	769	36.6	2.5	792	13	US-10-027-632-168585	Sequence 168585, App
C 695	37.4	2.5	681	13	US-10-027-632-141459	Sequence 141459, App	770	36.6	2.5	792	13	US-10-027-632-168585	Sequence 168585, App
C 696	37.4	2.5	681	17	US-10-027-632-141459	Sequence 141459, App	771	36.6	2.5	792	13	US-10-027-632-168585	Sequence 168585, App
C 697	37.4	2.5	806	18	US-10-437-963-414	Sequence 414, App	772	36.6	2.5	792	13	US-10-027-632-168585	Sequence 168585, App
C 698	37.4	2.5	806	18	US-10-425-115-60966	Sequence 60966, A	773	36.6	2.5	792	13	US-10-027-632-168585	Sequence 168585, App
C 699	37.4	2.5	806	18	US-10-425-115-60966	Sequence 60966, A	774	36.6	2.5	792	17	US-10-027-632-168585	Sequence 168585, App
C 700	37.4	2.5	1930	17	US-10-260-238-564	Sequence 564, App	775	36.6	2.5	792	17	US-10-027-632-168585	Sequence 168585, App
C 701	37.4	2.5	2052	18	US-10-437-963-58102	Sequence 58102, A	776	36.6	2.5	905	9	US-09-748-033-5	Sequence 5, App
C 702	37.4	2.5	2209	17	US-10-114-270-189	Sequence 189, App	C 777	36.6	2.5	1086	18	US-10-425-115-47026	Sequence 47026, A
C 703	37.4	2.5	2485	9	US-09-923-444A-1	Sequence 19, App	778	36.6	2.5	1182	17	US-10-260-238-882	Sequence 882, App
C 704	37.2	2.5	358	18	US-10-674-124A-9730	Sequence 9730, App	779	36.6	2.5	1294	9	US-09-748-033-2	Sequence 2, App
C 705	37.2	2.5	377	18	US-10-674-124A-9730	Sequence 9730, App	C 780	36.6	2.5	1367	18	US-10-437-963-16510	Sequence 16510, A
C 706	37.2	2.5	471	18	US-10-437-963-38537	Sequence 38537, A	C 781	36.6	2.5	1434	15	US-10-156-761-4335	Sequence 4335, App
C 707	37.2	2.5	476	18	US-10-856-499-1441	Sequence 1441, App	C 782	36.6	2.5	2460	18	US-10-437-963-7546	Sequence 7546, App
C 708	37.2	2.5	524	18	US-10-767-701-18076	Sequence 18076, A	783	36.6	2.5	2470	18	US-10-425-115-23592	Sequence 23592, App
C 709	37.2	2.5	1122	18	US-10-437-963-72816	Sequence 72816, A	784	36.6	2.5	2470	18	US-10-425-115-23592	Sequence 23592, App
C 710	37.2	2.5	1485	15	US-10-156-761-2495	Sequence 2495, App	C 785	36.6	2.5	49806	13	US-10-087-192-1021	Sequence 1021, App
C 711	37.2	2.5	1782	11	US-09-972-211-57	Sequence 57, App	C 786	36.6	2.5	215	18	US-10-087-192-1021	Sequence 1021, App
C 712	37.2	2.5	1782	17	US-10-096-625-57	Sequence 57, App	C 787	36.4	2.5	272	9	US-10-674-124A-20437	Sequence 20437, A
C 713	37.2	2.5	1881	17	US-10-210-130-147	Sequence 147, App	788	36.4	2.5	313	17	US-09-923-876-5713	Sequence 5713, App
C 714	37.2	2.5	1936	17	US-10-425-114-201	Sequence 201, App	789	36.4	2.5	313	17	US-09-923-876-5713	Sequence 5713, App
C 715	37.2	2.5	1936	18	US-10-425-115-9792	Sequence 9792, A	790	36.4	2.5	313	17	US-10-424-599-46165	Sequence 46165, A
C 716	37.2	2.5	7791	17	US-10-242-515-3700	Sequence 3700, App	791	36.4	2.5	313	17	US-10-424-599-46165	Sequence 46165, A
C 717	37.2	2.5	7791	17	US-10-242-515-3700	Sequence 3700, App	792	36.4	2.5	313	17	US-10-424-599-46165	Sequence 46165, A
C 718	37.2	2.5	21457	18	US-10-322-281-15	Sequence 15, App	C 793	36.4	2.5	450	17	US-10-260-238-5943	Sequence 5943, App
C 719	37.2	2.5	80959	9	US-09-858-546-3	Sequence 3, App	794	36.4	2.5	450	17	US-10-260-238-5943	Sequence 5943, App
C 720	37.2	2.5	261817	13	US-10-087-192-2002	Sequence 2002, App	C 795	36.4	2.5	516	18	US-10-437-963-82862	Sequence 82862, A
721	37	2.5	289	10	US-09-237-183A-632	Sequence 632, App	796	36.4	2.5	516	18	US-10-437-963-82862	Sequence 82862, A
722	37	2.5	572	13	US-10-027-632-215791	Sequence 215791, App	C 797	36.4	2.5	541	13	US-10-027-632-141919	Sequence 141919, App
723	37	2.5	572	17	US-10-027-632-215791	Sequence 215791, App	C 798	36.4	2.5	541	13	US-10-027-632-141919	Sequence 141919, App
724	37	2.5	623	17	US-10-425-114-21114	Sequence 21114, A	C 799	36.4	2.5	588	17	US-10-437-963-96529	Sequence 96529, App
C 725	37	2.5	1092	17	US-10-282-122A-11790	Sequence 11790, A	C 800	36.4	2.5	588	17	US-10-437-963-96529	Sequence 96529, App
726	37	2.5	1567	18	US-10-739-930-4900	Sequence 4900, App	801	36.4	2.5	606	17	US-10-260-238-3638	Sequence 3638, App
C 727	37	2.5	1934	10	US-09-882-227-201	Sequence 201, App	C 802	36.4	2.5	606	17	US-10-260-238-3638	Sequence 3638, App
728	37	2.5	2256	15	US-10-156-761-4122	Sequence 4122, App	C 803	36.4	2.5	649	17	US-10-425-115-13958	Sequence 13958, App
C 729	37	2.5	2496	18	US-10-468-335-3	Sequence 335, App	C 804	36.4	2.5	662	17	US-10-260-238-3638	Sequence 3638, App
C 730	37	2.5	3644	18	US-10-468-335-3	Sequence 335, App	C 805	36.4	2.5	662	17	US-10-260-238-3638	Sequence 3638, App
C 731	37	2.5	11910	15	US-10-156-761-2879	Sequence 2879, App	806	36.4	2.5	841	18	US-10-437-963-1368	Sequence 1368, App
732	37	2.5	44442	17	US-10-395-740-15	Sequence 740, App	C 807	36.4	2.5	841	18	US-10-437-963-1368	Sequence 1368, App
733	37	2.5	90541	9	US-09-759-359A-3	Sequence 3, App	808	36.4	2.5	868	17	US-10-260-238-3638	Sequence 3638, App
734	37	2.5	90541	16	US-10-207-973-3	Sequence 3, App	C 809	36.4	2.5	936	18	US-10-437-963-82873	Sequence 82873, App
735	37	2.5	90541	18	US-10-799-676-3	Sequence 3, App	810	36.4	2.5	987	15	US-10-156-761-3333	Sequence 3333, App
736	37	2.5	125746	15	US-10-156-761-15102	Sequence 15102, A	811	36.4	2.5	1306	9	US-09-954-456-732	Sequence 732, App
737	37	2.5	262	10	US-09-237-183A-836	Sequence 836, App	812	36.4	2.5	1306	9	US-09-954-456-732	Sequence 732, App
738	36.8	2.5	309	18	US-10-425-115-8163	Sequence 8163, App	C 813	36.4	2.5	1306	9	US-09-954-456-732	Sequence 732, App
739	36.8	2.5	518	16	US-10-029-386-11351	Sequence 11351, A	C 814	36.4	2.5	1306	9	US-09-954-456-732	Sequence 732, App
C 740	36.8	2.5	518	16	US-10-029-386-11770	Sequence 11770, A	815	36.4	2.5	1405	18	US-10-425-115-13967	Sequence 13967, App
							816	36.4	2.5	1541	18	US-10-739-930-2845	Sequence 2845, App
							C 817	36.4	2.5	1710	17	US-10-210-130-143	Sequence 143, App

818	36.4	2.5	1809	15	US-10-156-761-6413	Sequence 6413, Ap
819	36.4	2.5	2202	15	US-10-156-761-6617	Sequence 6617, Ap
820	36.4	2.5	2425	18	US-10-602-494-22	Sequence 22, Appl
821	36.4	2.5	2746	9	US-09-962-832-254	Sequence 254, Appl
822	36.4	2.5	5877	14	US-10-152-886-54	Sequence 54, Appl
823	36.4	2.5	3121	14	US-10-103-313-604	Sequence 604, Appl
824	36.4	2.5	35236	13	US-10-087-192-370	Sequence 370, Appl
825	36.4	2.5	90043	13	US-10-087-192-1141	Sequence 1141, Ap
826	36.4	2.5	97415	18	US-10-332-281-387	Sequence 287, Appl
827	36.4	2.5	107820	10	US-09-792-616-1	Sequence 1, Appl1
828	36.4	2.5	107820	18	US-10-764-328-1	Sequence 1, Appl1
829	36.4	2.5	151858	18	US-10-322-281-653	Sequence 653, Appl
830	36.4	2.5	17984	19	US-10-484-577-661	Sequence 661, Appl
831	36.4	2.5	186591	19	US-10-484-577-682	Sequence 682, Appl
832	36.4	2.5	208648	19	US-10-484-577-663	Sequence 663, Appl
833	36.4	2.5	208648	19	US-10-484-577-668	Sequence 668, Appl
834	36.2	2.4	294	10	US-09-237-183A-640	Sequence 640, Appl
835	36.2	2.4	399	18	US-10-674-124A-3003	Sequence 3003, Appl
836	36.2	2.4	399	17	US-10-242-535A-10965	Sequence 10965, A
837	36.2	2.4	399	17	US-10-085-783A-10965	Sequence 10965, A
838	36.2	2.4	403	18	US-10-674-124A-1445	Sequence 14245, A
839	36.2	2.4	433	18	US-10-674-124A-21413	Sequence 21413, A
840	36.2	2.4	738	17	US-10-424-599-11781	Sequence 11781, A
841	36.2	2.4	756	18	US-10-425-115-1179220	Sequence 179220, A
842	36.2	2.4	805	18	US-10-425-115-4153	Sequence 4153, Ap
843	36.2	2.4	870	15	US-10-156-761-4573	Sequence 4573, Ap
844	36.2	2.4	901	18	US-10-437-963-47879	Sequence 47879, A
845	36.2	2.4	1011	18	US-10-437-963-88631	Sequence 88631, A
846	36.2	2.4	1086	14	US-10-083-168-78	Sequence 78, Appl
847	36.2	2.4	1120	9	US-09-969-708-340	Sequence 320, Appl
848	36.2	2.4	1120	18	US-09-873-367C-686	Sequence 686, Appl
849	36.2	2.4	1120	18	US-10-717-597-134	Sequence 134, Appl
850	36.2	2.4	1303	18	US-10-723-860-5468	Sequence 5468, Appl
851	36.2	2.4	1629	17	US-10-425-114-33620	Sequence 33660, A
852	36.2	2.4	1907	18	US-10-425-115-156020	Sequence 156020, A
853	36.2	2.4	1941	10	US-09-814-353-20998	Sequence 20998, A
854	36.2	2.4	2044	17	US-10-094-749-90	Sequence 90, Appl1
855	36.2	2.4	2355	17	US-10-282-122A-39279	Sequence 39279, A
856	36.2	2.4	2429	17	US-10-425-114-3569	Sequence 3569, Ap
857	36.2	2.4	2642	18	US-10-425-115-156016	Sequence 156016, A
858	36.2	2.4	2651	17	US-10-425-114-33369	Sequence 23369, A
859	36.2	2.4	2808	18	US-10-425-115-32466	Sequence 32466, A
860	36.2	2.4	5230	18	US-10-475-476-20	Sequence 20, Appl1
861	36.2	2.4	11771	17	US-10-415-620-1	Sequence 1, Appl1
862	36.2	2.4	14117	18	US-10-482-936-1	Sequence 1, Appl1
863	36.2	2.4	14117	18	US-10-482-936-3	Sequence 1, Appl1
864	36.2	2.4	15872	9	US-09-861-289-1	Sequence 1, Appl1
865	36.2	2.4	15872	9	US-09-860-846-1	Sequence 1, Appl1
866	36.2	2.4	15872	10	US-09-988-384B-1	Sequence 1, Appl1
867	36.2	2.4	15872	16	US-10-836-821-1	Sequence 1, Appl1
868	36.2	2.4	15872	16	US-10-271-889-44	Sequence 44, Appl1
869	36.2	2.4	2262	13	US-10-087-192-1063	Sequence 1063, Appl
870	36.2	2.4	27485	18	US-10-332-281-196	Sequence 196, Appl
871	36.2	2.4	89829	18	US-10-332-281-359	Sequence 359, Appl
872	36.2	2.4	183334	19	US-10-741-600-17646	Sequence 17646, A
873	36.2	2.4	317	18	US-10-674-124A-12042	Sequence 12042, A
874	36.2	2.4	327	18	US-10-425-115-75246	Sequence 75246, A
875	36.2	2.4	433	18	US-10-674-124A-8934	Sequence 8934, Ap
876	36.2	2.4	452	18	US-10-723-860-1904	Sequence 1904, Ap
877	36.2	2.4	602	18	US-10-425-115-40695	Sequence 40695, A
878	36.2	2.4	738	18	US-10-437-963-88086	Sequence 88086, A
879	36.2	2.4	813	18	US-10-437-963-9395	Sequence 9395, Ap
880	36.2	2.4	1032	15	US-10-156-761-1110	Sequence 1110, Ap
881	36.2	2.4	1063	18	US-10-767-701-13615	Sequence 13615, A
882	36.2	2.4	1431	18	US-10-437-963-26802	Sequence 26802, A
883	36.2	2.4	1649	17	US-10-425-114-26399	Sequence 26399, A
884	36.2	2.4	1766	18	US-10-437-963-66848	Sequence 66848, A
885	36.2	2.4	1914	18	US-10-437-963-88485	Sequence 88485, A
886	36.2	2.4	2235	17	US-10-359-493-42996	Sequence 42996, A
887	36.2	2.4	2280	18	US-10-437-963-96359	Sequence 96359, A
888	36.2	2.4	2892	18	US-10-437-963-40093	Sequence 40093, A
889	36.2	2.4	3099	17	US-10-282-122A-29968	Sequence 29968, A
890	36.2	2.4	3779	9	US-09-925-300-712	Sequence 712, Appl
891	36.2	2.4	15362	9	US-09-764-877-2856	Sequence 2856, Ap
892	36.2	2.4	15362	17	US-10-242-515-2856	Sequence 2856, Ap
893	36.2	2.4	19303	18	US-10-433-287-81	Sequence 81, Appl
894	36.2	2.4	22000	16	US-10-091-625-11	Sequence 11, Appl
895	36.2	2.4	28000	16	US-10-096-399A-11	Sequence 11, Appl
896	36.2	2.4	28000	17	US-10-461-668-11	Sequence 11, Appl
897	36.2	2.4	28000	17	US-10-388-263-381	Sequence 381, Appl
898	36.2	2.4	69090	13	US-10-087-192-1123	Sequence 1123, Appl
899	36.2	2.4	189158	13	US-10-087-192-415	Sequence 415, Appl
900	36.2	2.4	192673	18	US-10-331-053-1	Sequence 1, Appl1
901	36.2	2.4	217409	13	US-10-087-192-1954	Sequence 1954, Ap
902	35.8	2.4	469	10	US-09-918-995-31647	Sequence 31647, A
903	35.8	2.4	561	15	US-10-259-165-357	Sequence 357, Appl
904	35.8	2.4	564	15	US-10-259-165-3	Sequence 3, Appl1
905	35.8	2.4	602	13	US-10-027-632-213538	Sequence 213538, A
906	35.8	2.4	602	13	US-10-027-632-213539	Sequence 213539, A
907	35.8	2.4	602	13	US-10-027-632-213540	Sequence 213540, A
908	35.8	2.4	602	17	US-10-027-632-213538	Sequence 213538, A
909	35.8	2.4	602	17	US-10-027-632-213539	Sequence 213539, A
910	35.8	2.4	602	17	US-10-027-632-213540	Sequence 213540, A
911	35.8	2.4	646	18	US-10-767-701-24140	Sequence 24140, A
912	35.8	2.4	646	17	US-10-152-819A-21406	Sequence 21406, Ap
913	35.8	2.4	747	17	US-10-424-599-136586	Sequence 136586, A
915	35.8	2.4	751	18	US-10-425-115-88093	Sequence 88093, A
917	35.8	2.4	774	13	US-10-042-417-39	Sequence 39, Appl1
919	35.8	2.4	1457	15	US-10-037-270-408	Sequence 408, Appl
920	35.8	2.4	1457	17	US-10-117-722-408	Sequence 408, Appl
921	35.8	2.4	2247	18	US-10-437-963-83588	Sequence 83588, A
922	35.8	2.4	2281	17	US-10-108-660A-57	Sequence 57, Appl1
923	35.8	2.4	2394	17	US-10-112-944-54	Sequence 54, Appl1
924	35.8	2.4	2490	17	US-10-112-944-53	Sequence 53, Appl1
925	35.8	2.4	2546	17	US-10-425-114-32586	Sequence 32586, A
926	35.8	2.4	2572	17	US-10-319-315-2	Sequence 2, Appl1
927	35.8	2.4	2785	18	US-10-425-115-48930	Sequence 48930, A
928	35.8	2.4	2874	15	US-10-259-165-251	Sequence 251, Appl
929	35.8	2.4	3168	17	US-10-120-988-409	Sequence 409, Appl
930	35.8	2.4	4080	17	US-10-172-118-1520	Sequence 1520, Ap
931	35.8	2.4	4080	17	US-10-342-887-1850	Sequence 1850, Ap
932	35.8	2.4	4263	18	US-10-437-963-26800	Sequence 26800, A
933	35.8	2.4	43950	9	US-09-735-934A-3	Sequence 1340, Ap
934	35.8	2.4	43950	13	US-10-060-332-3	Sequence 3, Appl1
935	35.8	2.4	43950	15	US-10-339-657-3	Sequence 3, Appl1
936	35.8	2.4	43950	18	US-10-885-879-3	Sequence 3, Appl1
937	35.8	2.4	62658	18	US-10-322-281-420	Sequence 420, Appl
938	35.8	2.4	160556	18	US-10-719-993-6827	Sequence 6827, Ap
939	35.8	2.4	174	9	US-09-922-217-325	Sequence 325, Appl
940	35.8	2.4	174	9	US-09-922-217-368	Sequence 368, Appl
941	35.8	2.4	174	9	US-09-833-263-325	Sequence 325, Appl
942	35.8	2.4	174	9	US-09-833-263-368	Sequence 368, Appl
943	35.8	2.4	174	13	US-10-025-380-325	Sequence 325, Appl
944	35.8	2.4	174	13	US-10-025-380-368	Sequence 368, Appl
945	35.8	2.4	242	9	US-09-923-876-2699	Sequence 2699, Ap
946	35.8	2.4	242	10	US-09-923-876-2699	Sequence 2699, Ap
947	35.8	2.4	309	10	US-09-237-183A-570	Sequence 570, Appl
948	35.8	2.4	326	18	US-10-674-124A-21108	Sequence 21108, A
949	35.8	2.4	369	18	US-10-674-124A-6702	Sequence 6702, Ap
950	35.8	2.4	458	18	US-10-021-323-6663	Sequence 6663, Appl
951	35.8	2.4	478	18	US-10-425-115-134316	Sequence 134316, A
952	35.8	2.4	486	13	US-10-027-632-135836	Sequence 135836, A
953	35.8	2.4	486	17	US-10-027-632-135836	Sequence 135836, A
954	35.8	2.4	504	10	US-09-918-995-32397	Sequence 32397, A
955	35.8	2.4	546	18	US-10-425-115-5031	Sequence 5031, A
956	35.8	2.4	546	9	US-09-864-761-10733	Sequence 20733, A
957	35.8	2.4	575	13	US-10-027-632-50030	Sequence 50030, A
958	35.8	2.4	575	13	US-10-027-632-50031	Sequence 50031, A
959	35.8	2.4	575	13	US-10-027-632-5003015	Sequence 5003015, A
960	35.8	2.4	575	17	US-10-027-632-302015	Sequence 302015, A
961	35.8	2.4	575	17	US-10-027-632-81841	Sequence 81841, A
962	35.8	2.4	575	17	US-10-027-632-302015	Sequence 302015, A
963	35.8	2.4	607	18	US-10-425-115-6919	Sequence 6919, Ap
964	35.8	2.4	626	17	US-10-424-599-44383	Sequence 44383, A
965	35.8	2.4	663	18	US-10-425-115-117063	Sequence 117063, A

C 966	35.6	2.4	687	18	US-10-363-345A-5817	Sequence 5817, Ap	1039	35.4	2.4	1501	17	US-10-425-114-18635	Sequence 18635, A
C 967	35.6	2.4	682	18	US-10-363-345A-5818	Sequence 5818, Ap	1040	35.4	2.4	1526	15	US-10-177-293-34	Sequence 34, Appl
C 968	35.6	2.4	697	18	US-10-425-115-117059	Sequence 117059, A	C1041	35.4	2.4	1701	18	US-10-437-963-101326	Sequence 101326, A
C 969	35.6	2.4	700	13	US-10-027-632-148457	Sequence 148457, A	1042	35.4	2.4	1770	17	US-10-282-1222-27524	Sequence 27524, A
C 970	35.6	2.4	700	13	US-10-027-632-148458	Sequence 148458, A	1043	35.4	2.4	2573	18	US-10-437-963-5223	Sequence 5223, Ap
C 971	35.6	2.4	700	17	US-10-027-632-148457	Sequence 148457, A	1044	35.4	2.4	2809	18	US-10-425-115-115247	Sequence 115247, A
C 972	35.6	2.4	700	17	US-10-027-632-148458	Sequence 148458, A	1045	35.4	2.4	3535	14	US-10-198-446-13957	Sequence 13957, A
C 973	35.6	2.4	744	18	US-10-437-963-37931	Sequence 37931, A	1046	35.4	2.4	3734	18	US-10-425-115-113388	Sequence 113388, A
C 974	35.6	2.4	745	13	US-10-027-632-144367	Sequence 144367, A	C1047	35.4	2.4	5012	18	US-10-719-993-252	Sequence 252, App
C 975	35.6	2.4	747	17	US-10-369-493-41119	Sequence 41119, A	C1048	35.4	2.4	5099	18	US-10-719-993-255	Sequence 255, App
C 976	35.6	2.4	747	17	US-10-369-493-41119	Sequence 41119, A	C1049	35.4	2.4	5186	18	US-10-719-993-257	Sequence 257, App
C 977	35.6	2.4	851	17	US-10-425-114-14245	Sequence 14245, A	1050	35.4	2.4	23318	18	US-10-322-921-504	Sequence 504, App
C 978	35.6	2.4	851	18	US-10-425-115-141528	Sequence 141528, A	C1051	35.4	2.4	26000	18	US-10-476-022-150	Sequence 10, Appl
C 979	35.6	2.4	977	18	US-10-437-963-90300	Sequence 90300, A	C1052	35.4	2.4	42027	18	US-10-417-375-58	Sequence 58, Appl
C 980	35.6	2.4	977	18	US-10-425-115-117057	Sequence 117057, A	1053	35.4	2.4	84410	18	US-10-322-281-747	Sequence 281, Appl
C 981	35.6	2.4	1175	18	US-10-425-115-117058	Sequence 117058, A	C1054	35.4	2.4	90026	13	US-10-087-192-229	Sequence 229, App
C 982	35.6	2.4	1215	18	US-10-425-115-117064	Sequence 117064, A	1055	35.4	2.4	96597	11	US-09-997-722-73	Sequence 73, Appl
C 983	35.6	2.4	1265	18	US-10-425-115-117064	Sequence 117064, A	C1056	35.4	2.4	659158	9	US-09-771-208-70	Sequence 20, Appl
C 984	35.6	2.4	1265	18	US-10-425-115-117064	Sequence 117064, A	C1057	35.4	2.4	775062	18	US-10-719-993-6844	Sequence 6844, Ap
C 985	35.6	2.4	1271	18	US-10-437-963-38282	Sequence 38282, A	C1058	35.2	2.4	325	18	US-10-674-124A-1933	Sequence 14933, A
C 986	35.6	2.4	1428	15	US-10-156-761-5428	Sequence 5428, Ap	1059	35.2	2.4	406	9	US-09-960-352-5045	Sequence 5045, Ap
C 987	35.6	2.4	1469	18	US-10-739-930-1975	Sequence 1975, Ap	1060	35.2	2.4	406	9	US-09-960-352-5045	Sequence 2762, A
C 988	35.6	2.4	1469	18	US-10-437-963-22612	Sequence 22612, A	1061	35.2	2.4	506	17	US-10-369-493-2762	Sequence 70077, A
C 989	35.6	2.4	1369	9	US-09-864-761-3972	Sequence 3972, Ap	C1062	35.2	2.4	655	17	US-10-437-963-70077	Sequence 10435, A
C 990	35.6	2.4	2035	19	US-10-959-539-65	Sequence 65, Appl	1063	35.2	2.4	879	15	US-10-424-599-10435	Sequence 3503, Ap
C 991	35.6	2.4	2066	17	US-10-210-130-151	Sequence 151, Appl	1064	35.2	2.4	927	15	US-10-156-761-6692	Sequence 6692, Ap
C 992	35.6	2.4	2305	17	US-10-369-493-44269	Sequence 44269, A	C1065	35.2	2.4	967	13	US-10-027-632-25326	Sequence 25326, A
C 993	35.6	2.4	2216	14	US-10-123-036-1	Sequence 1, Appl	C1066	35.2	2.4	967	17	US-10-027-632-25326	Sequence 25326, A
C 994	35.6	2.4	2216	14	US-10-123-036-1	Sequence 1, Appl	C1067	35.2	2.4	967	17	US-10-027-632-25326	Sequence 25326, A
C 995	35.6	2.4	2219	15	US-10-007-926A-333	Sequence 333, Appl	C1068	35.2	2.4	966	15	US-10-156-761-7246	Sequence 7246, Ap
C 996	35.6	2.4	2244	18	US-10-437-963-68841	Sequence 68841, A	1068	35.2	2.4	999	15	US-10-156-761-3794	Sequence 3794, Ap
C 997	35.6	2.4	2487	13	US-10-027-632-103365	Sequence 103365, A	C1069	35.2	2.4	1030	17	US-10-343-348-17	Sequence 17, Appl
C 998	35.6	2.4	2487	17	US-10-027-632-103365	Sequence 103365, A	C1070	35.2	2.4	1325	18	US-10-425-115-52338	Sequence 52338, A
C 999	35.6	2.4	2586	17	US-10-369-493-31958	Sequence 31958, A	1071	35.2	2.4	2289	17	US-10-437-963-45451	Sequence 45451, A
C 999	35.6	2.4	6997	18	US-10-335-053-242	Sequence 242, App	1072	35.2	2.4	2403	11	US-09-997-722-111	Sequence 11, App
1000	35.6	2.4	27980	18	US-10-719-993-6935	Sequence 6935, Ap	1073	35.2	2.4	2887	11	US-09-997-722-110	Sequence 110, App
1001	35.6	2.4	49087	18	US-10-322-696-1	Sequence 1, Appl	C1074	35.2	2.4	17934	15	US-10-311-455-1631	Sequence 16931, Ap
1002	35.6	2.4	49175	18	US-10-367-094-4	Sequence 4, Appl	C1075	35.2	2.4	58038	19	US-10-741-600-17942	Sequence 17942, A
1003	35.6	2.4	92219	18	US-10-322-281-805	Sequence 805, App	C1076	35.2	2.4	66972	13	US-10-087-192-574	Sequence 574, App
1004	35.6	2.4	110079	14	US-10-175-523-96	Sequence 96, Appl	C1077	35.2	2.4	76846	13	US-10-087-192-799	Sequence 799, App
1005	35.6	2.4	118931	13	US-10-087-192-1108	Sequence 1108, Ap	1078	35.2	2.4	142947	18	US-10-719-993-6967	Sequence 6967, Ap
1006	35.6	2.4	201143	17	US-10-240-425-1099	Sequence 1099, Ap	C1079	35.2	2.4	333811	19	US-10-741-600-17681	Sequence 17681, A
1007	35.6	2.4	203127	18	US-10-741-601-5654	Sequence 5654, Ap	1080	35.2	2.4	744802	17	US-10-929-729-1369	Sequence 1369, Ap
1008	35.6	2.4	203127	19	US-10-741-601-5654	Sequence 5654, Ap	1081	35.2	2.4	224	10	US-09-237-182A-899	Sequence 899, App
C1009	35.6	2.4	493999	18	US-10-719-993-6787	Sequence 6787, A	1082	35.2	2.4	235	10	US-09-237-182A-840	Sequence 840, App
C1010	35.4	2.4	293	18	US-10-674-124A-10333	Sequence 10333, A	1083	35.2	2.4	270	10	US-09-237-182A-695	Sequence 695, App
C1011	35.4	2.4	310	18	US-10-674-124A-10333	Sequence 10333, A	C1084	35.2	2.4	281	18	US-10-674-124A-24544	Sequence 24544, A
1012	35.4	2.4	325	17	US-10-242-535A-519	Sequence 519, App	1085	35.2	2.4	305	18	US-10-674-124A-12289	Sequence 12289, A
1013	35.4	2.4	325	17	US-10-085-783A-519	Sequence 519, App	1086	35.2	2.4	344	9	US-09-960-352-5692	Sequence 5692, Ap
1014	35.4	2.4	365	18	US-10-674-124A-1930	Sequence 1930, Ap	1087	35.2	2.4	393	18	US-10-723-860-2396	Sequence 2396, Ap
1015	35.4	2.4	385	9	US-09-960-352-4013	Sequence 4013, Ap	1088	35.2	2.4	418	13	US-10-674-124A-25651	Sequence 25651, A
1016	35.4	2.4	413	9	US-09-960-352-7745	Sequence 7745, Ap	C1089	35.2	2.4	453	18	US-10-027-632-135018	Sequence 135018, A
1017	35.4	2.4	416	9	US-09-960-352-2019	Sequence 2019, Ap	C1090	35.2	2.4	453	17	US-10-027-632-135018	Sequence 135018, A
1018	35.4	2.4	428	9	US-09-960-352-2677	Sequence 2677, Ap	C1091	35.2	2.4	460	18	US-10-027-632-135018	Sequence 135018, A
1019	35.4	2.4	450	9	US-09-960-352-335	Sequence 335, App	C1092	35.2	2.4	487	10	US-10-674-124A-18980	Sequence 18980, A
1020	35.4	2.4	492	18	US-09-918-995-1737	Sequence 1737, Ap	1093	35.2	2.4	520	10	US-09-918-995-3215	Sequence 32154, A
C1021	35.4	2.4	565	18	US-10-767-701-7758	Sequence 7758, Ap	C1094	35.2	2.4	598	16	US-10-767-701-25899	Sequence 25899, A
1022	35.4	2.4	606	15	US-10-767-701-25686	Sequence 25686, A	1095	35.2	2.4	648	18	US-10-029-386-5741	Sequence 5741, Ap
C1023	35.4	2.4	675	18	US-10-156-761-3903	Sequence 3903, Ap	1096	35.2	2.4	648	17	US-10-027-632-18469	Sequence 18469, A
1024	35.4	2.4	701	19	US-10-278-698-426	Sequence 426, App	1097	35.2	2.4	663	17	US-10-027-632-18469	Sequence 18469, A
1025	35.4	2.4	701	19	US-10-278-698-940	Sequence 940, App	C1098	35.2	2.4	714	18	US-10-425-114-3517	Sequence 3517, Ap
1026	35.4	2.4	735	18	US-10-437-963-101335	Sequence 101335, A	1099	35.2	2.4	744	17	US-10-437-963-68621	Sequence 68621, A
C1027	35.4	2.4	807	18	US-10-437-963-101330	Sequence 101330, A	1100	35.2	2.4	744	17	US-10-425-114-1318	Sequence 1318, Ap
1028	35.4	2.4	866	18	US-10-437-963-12852	Sequence 12852, A	1101	35.2	2.4	759	17	US-10-425-114-23009	Sequence 23009, A
1029	35.4	2.4	889	17	US-10-424-599-11763	Sequence 11763, A	1102	35.2	2.4	794	17	US-10-425-114-24501	Sequence 24501, A
C1030	35.4	2.4	955	18	US-10-425-115-30638	Sequence 30638, A	1103	35.2	2.4	797	17	US-10-425-114-1010	Sequence 1010, Ap
C1031	35.4	2.4	973	18	US-10-437-963-40397	Sequence 40397, A	1104	35.2	2.4	797	17	US-10-425-114-18888	Sequence 18888, A
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1033	35.4	2.4	1087	18	US-10-767-701-5388	Sequence 5388, Ap	1106	35.2	2.4	814	17	US-10-291-177-55	Sequence 55, Appl
1034	35.4	2.4	1135	18	US-10-437-963-73222	Sequence 73222, A	1107	35.2	2.4	816	17	US-10-221-278-55	Sequence 5533, Appl
1035	35.4	2.4	1146	18	US-10-437-963-80370	Sequence 80370, A	1108	35.2	2.4	884	18	US-10-767-701-5533	Sequence 5533, Appl
C1036	35.4	2.4	1190	18	US-10-437-963-80370	Sequence 80370, A	1109	35.2	2.4	888	15	US-10-119-926-6	Sequence 6, Appl
1037	35.4	2.4	1301	17	US-10-424-599-85423	Sequence 85423, A	1110	35.2	2.4	870	17	US-10-369-493-43223	Sequence 42323, A
1038	35.4	2.4	1320	18	US-10-437-963-13534	Sequence 13534, A	1111	35.2	2.4	1020	18	US-10-425-115-149778	Sequence 149778, A

1112	35	2.4	1216	17	US-10-310-154-210	Sequence 310, App	1185	34.8	2.3	3237	17	US-10-369-493-25803	Sequence 25803, A
1113	35	2.4	1481	17	US-10-425-114-31221	Sequence 31221, A	1186	34.8	2.3	4172	9	US-09-764-860-1024	Sequence 1024, Ap
1114	35	2.4	1498	10	US-09-919-039-99	Sequence 99, Appl	1187	34.8	2.3	4172	14	US-10-074-095-1024	Sequence 1024, Ap
1115	35	2.4	1517	17	US-10-425-114-8896	Sequence 8896, Ap	1188	34.8	2.3	4172	17	US-10-212-872-1024	Sequence 1024, Ap
1116	35	2.4	1579	18	US-10-437-963-43328	Sequence 43328, A	1189	34.8	2.3	5100	10	US-09-954-883A-14	Sequence 14, Appl
1117	35	2.4	1607	18	US-10-425-115-89472	Sequence 89472, A	1190	34.8	2.3	32152	9	US-09-764-855-328	Sequence 328, Ap
1118	35	2.4	1698	17	US-10-210-130-149	Sequence 149, Appl	1191	34.8	2.3	33152	14	US-09-764-872-518	Sequence 518, App
1119	35	2.4	1890	17	US-10-276-774-68	Sequence 68, Appl	1192	34.8	2.3	33152	14	US-10-072-449-328	Sequence 328, App
1120	35	2.4	2011	10	US-09-981-151A-15	Sequence 15, Appl	1193	34.8	2.3	96672	13	US-10-087-192-655	Sequence 655, App
1121	35	2.4	2011	17	US-10-004-378A-23	Sequence 23, Appl	1194	34.8	2.3	96672	13	US-10-087-192-1069	Sequence 1069, App
1122	35	2.4	2139	17	US-10-369-493-41751	Sequence 41751, A	1195	34.8	2.3	116561	18	US-10-723-860-409	Sequence 409, App
1123	35	2.4	2182	18	US-10-425-115-79752	Sequence 79752, A	1196	34.8	2.3	138115	18	US-10-322-281-377	Sequence 377, App
1124	35	2.4	2200	10	US-09-849-138-25	Sequence 25, Appl	1197	34.8	2.3	128139	13	US-10-087-192-232	Sequence 232, App
1125	35	2.4	2200	11	US-09-972-211-59	Sequence 59, Appl	1198	34.8	2.3	493631	13	US-10-087-192-205	Sequence 205, App
1126	35	2.4	2200	11	US-09-972-211-61	Sequence 61, Appl	1199	34.8	2.3	684187	18	US-10-367-094-71	Sequence 71, Appl
1127	35	2.4	2200	17	US-10-210-130-141	Sequence 141, App	1200	34.6	2.3	267	9	US-09-823-101-9	Sequence 9, Appl
1128	35	2.4	2200	17	US-10-036-625-59	Sequence 59, Appl	1201	34.6	2.3	336	18	US-10-674-124A-14888	Sequence 14888, A
1129	35	2.4	2200	17	US-10-036-625-61	Sequence 61, Appl	1202	34.6	2.3	372	18	US-10-425-115-177235	Sequence 177235, A
1130	35	2.4	2535	18	US-10-425-115-18723	Sequence 18723, A	1203	34.6	2.3	422	9	US-09-864-761-1041	Sequence 1041, Ap
1131	35	2.4	2645	18	US-10-437-963-11058	Sequence 31058, A	1204	34.6	2.3	422	18	US-10-425-115-22626	Sequence 22626, A
1132	35	2.4	2768	18	US-10-723-860-8321	Sequence 8321, Ap	1205	34.6	2.3	549	18	US-10-425-115-74784	Sequence 74784, A
1133	35	2.4	3570	17	US-10-336-472-15	Sequence 15, Appl	1206	34.6	2.3	549	18	US-10-425-115-74784	Sequence 74784, A
1134	35	2.4	4318	18	US-10-437-963-21360	Sequence 21360, A	1207	34.6	2.3	636	13	US-10-027-632-308921	Sequence 308921, A
1135	35	2.4	4595	18	US-10-437-963-53324	Sequence 53324, A	1208	34.6	2.3	636	13	US-10-027-632-308922	Sequence 308922, A
1136	35	2.4	4775	17	US-10-336-472-17	Sequence 17, Appl	1209	34.6	2.3	636	17	US-10-027-632-308921	Sequence 308921, A
1137	35	2.4	5780	17	US-10-336-472-19	Sequence 19, Appl	1210	34.6	2.3	665	17	US-10-027-632-308922	Sequence 308922, A
1138	35	2.4	6008	17	US-10-336-472-21	Sequence 21, Appl	1211	34.6	2.3	665	18	US-10-425-115-63700	Sequence 63700, A
1139	35	2.4	6008	18	US-10-717-597-197	Sequence 197, App	1212	34.6	2.3	693	14	US-10-123-155-406	Sequence 406, App
1140	35	2.4	6269	17	US-10-292-798-1421	Sequence 1421, Ap	1213	34.6	2.3	698	13	US-10-027-632-25570	Sequence 25570, A
1141	35	2.4	6647	10	US-09-764-891-8442	Sequence 8442, Ap	1214	34.6	2.3	698	13	US-10-027-632-25571	Sequence 25571, A
1142	35	2.4	8360	15	US-10-017-161-1633	Sequence 1633, Ap	1215	34.6	2.3	698	17	US-10-027-632-25570	Sequence 25570, A
1143	35	2.4	8360	17	US-10-292-798-1303	Sequence 1303, Ap	1216	34.6	2.3	698	17	US-10-027-632-25571	Sequence 25571, A
1144	35	2.4	11211	15	US-10-017-161-1765	Sequence 1765, Ap	1217	34.6	2.3	730	13	US-10-027-632-151953	Sequence 151953, A
1145	35	2.4	15579	10	US-09-764-891-8443	Sequence 8443, Ap	1218	34.6	2.3	730	17	US-10-027-632-151953	Sequence 151953, A
1146	35	2.4	30535	18	US-10-451-503A-7	Sequence 7, Appl	1219	34.6	2.3	740	17	US-10-260-338-3630	Sequence 3630, Ap
1147	35	2.4	33454	13	US-10-087-192-1111	Sequence 1111, Ap	1220	34.6	2.3	807	17	US-10-425-114-30318	Sequence 30318, A
1148	35	2.4	44748	13	US-10-087-192-325	Sequence 325, App	1221	34.6	2.3	861	18	US-10-437-963-56550	Sequence 56550, A
1149	35	2.4	56258	13	US-10-087-192-913	Sequence 913, App	1222	34.6	2.3	870	17	US-10-425-114-18555	Sequence 18555, A
1150	35	2.4	57181	19	US-10-741-600-17781	Sequence 17781, A	1223	34.6	2.3	899	18	US-10-437-963-182750	Sequence 182750, A
1151	35	2.4	96599	11	US-09-997-722-13	Sequence 13, Appl	1224	34.6	2.3	929	18	US-10-425-115-180964	Sequence 180964, A
1152	35	2.4	121434	18	US-10-303-165-11	Sequence 11, Appl	1225	34.6	2.3	978	18	US-10-437-963-64115	Sequence 64115, A
1153	35	2.4	154504	18	US-10-322-696-67	Sequence 67, Appl	1226	34.6	2.3	1086	9	US-09-995-225-7	Sequence 7, Appl
1154	34.8	2.3	166	18	US-10-674-124A-21458	Sequence 21458, A	1227	34.6	2.3	1086	10	US-09-995-225-7	Sequence 7, Appl
1155	34.8	2.3	389	18	US-10-674-124A-20448	Sequence 20448, A	1228	34.6	2.3	1086	10	US-09-995-225-7	Sequence 7, Appl
1156	34.8	2.3	437	18	US-10-674-124A-4968	Sequence 4968, Ap	1229	34.6	2.3	1086	13	US-10-086-181-3	Sequence 3, Appl
1157	34.8	2.3	471	18	US-10-437-963-77773	Sequence 77773, A	1230	34.6	2.3	1086	14	US-10-083-168-11	Sequence 11, Appl
1158	34.8	2.3	498	18	US-10-674-124A-14540	Sequence 14540, A	1231	34.6	2.3	1086	14	US-10-083-168-80	Sequence 80, Appl
1159	34.8	2.3	568	9	US-09-770-152-319	Sequence 89207, A	1232	34.6	2.3	1086	15	US-10-262-113-1	Sequence 1, Appl
1160	34.8	2.3	568	18	US-10-437-963-89217	Sequence 89217, A	1233	34.6	2.3	1086	18	US-10-768-878-1	Sequence 1, Appl
1161	34.8	2.3	673	18	US-10-437-963-89217	Sequence 89217, A	1234	34.6	2.3	1160	13	US-10-015-498-1	Sequence 1, Appl
1162	34.8	2.3	733	18	US-10-767-701-12439	Sequence 12439, A	1235	34.6	2.3	1203	18	US-10-437-963-36937	Sequence 36937, A
1163	34.8	2.3	747	17	US-10-260-238-1637	Sequence 3637, Ap	1236	34.6	2.3	1252	18	US-10-425-115-31573	Sequence 31573, A
1164	34.8	2.3	781	13	US-10-027-632-155529	Sequence 155529, A	1237	34.6	2.3	1278	17	US-10-369-493-45417	Sequence 45417, A
1165	34.8	2.3	821	18	US-10-767-701-15527	Sequence 15527, A	1238	34.6	2.3	1321	18	US-10-149-826-59	Sequence 59, Appl
1166	34.8	2.3	860	18	US-10-425-115-131510	Sequence 131510, A	1239	34.6	2.3	1349	10	US-09-988-462-20	Sequence 20, Appl
1167	34.8	2.3	1057	18	US-10-437-963-1511	Sequence 1511, Ap	1240	34.6	2.3	1368	17	US-10-369-493-43288	Sequence 43288, A
1168	34.8	2.3	1149	15	US-10-156-761-1907	Sequence 1907, Ap	1241	34.6	2.3	1372	15	US-10-017-161-2187	Sequence 2187, Ap
1169	34.8	2.3	1176	18	US-10-626-445-6	Sequence 6, Appl	1242	34.6	2.3	1558	17	US-10-292-798-1833	Sequence 1833, Ap
1170	34.8	2.3	1375	15	US-09-770-621-1	Sequence 1, Appl	1243	34.6	2.3	1558	17	US-10-424-599-82488	Sequence 82488, A
1171	34.8	2.3	1375	15	US-10-286-993-1	Sequence 1, Appl	1244	34.6	2.3	1599	19	US-10-762-107-66	Sequence 66, Appl
1172	34.8	2.3	1542	18	US-10-739-930-4426	Sequence 4426, Ap	1245	34.6	2.3	1743	13	US-10-086-181-1	Sequence 1, Appl
1173	34.8	2.3	1566	18	US-10-437-963-15117	Sequence 15117, A	1246	34.6	2.3	1743	14	US-10-077-698-2	Sequence 2, Appl
1174	34.8	2.3	1599	18	US-10-437-963-74134	Sequence 74134, A	1247	34.6	2.3	1743	14	US-10-171-027-2	Sequence 2, Appl
1175	34.8	2.3	1756	18	US-10-425-115-64321	Sequence 64321, A	1248	34.6	2.3	1743	15	US-10-075-987-2	Sequence 2, Appl
1176	34.8	2.3	1837	17	US-10-282-122A-15275	Sequence 15275, A	1249	34.6	2.3	2070	16	US-10-156-761-8	Sequence 8, Appl
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1178	34.8	2.3	2028	17	US-10-282-122A-15212	Sequence 15212, A	1251	34.6	2.3	2355	17	US-10-382-122A-38710	Sequence 38710, A
1179	34.8	2.3	2077	17	US-10-104-047-1221	Sequence 1221, Ap	1252	34.6	2.3	2368	18	US-10-437-963-78123	Sequence 78123, A
1180	34.8	2.3	2484	17	US-10-369-493-44347	Sequence 44347, A	1253	34.6	2.3	2447	18	US-10-437-963-69806	Sequence 69806, A
1181	34.8	2.3	2632	18	US-10-425-115-33249	Sequence 33249, A	1254	34.6	2.3	2628	17	US-10-424-599-37843	Sequence 37843, A
1182	34.8	2.3	2679	9	US-09-815-242-9667	Sequence 9667, Ap	1255	34.6	2.3	2650	17	US-10-104-047-1710	Sequence 1710, Ap
1183	34.8	2.3	2679	17	US-10-282-122A-39456	Sequence 39456, A	1256	34.6	2.3	3141	18	US-10-723-860-6407	Sequence 6407, Ap
1184	34.8	2.3	2679	17	US-10-282-122A-39456	Sequence 39456, A	1259	34.6	2.3	3141	18	US-10-723-860-6407	Sequence 6407, Ap

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C1271	34.6	2.3	4411	18	US-10-451-503A-5	Sequence 5, Appl1	C1347	34.4	2.3	744002	17	US-10-292-798-1369	Sequence 1369, Ap
C1272	34.6	2.3	5960	19	US-10-762-107-64	Sequence 64, Appl1	C1348	34.2	2.3	238	9	US-09-923-876-2694	Sequence 2694, Ap
C1273	34.6	2.3	23059	18	US-10-719-993-6878	Sequence 6878, Ap	C1349	34.2	2.3	238	10	US-09-923-876-2694	Sequence 2694, Ap
C1275	34.6	2.3	32591	17	US-10-085-117-187	Sequence 187, App	C1350	34.2	2.3	283	11	US-09-732-627A-345	Sequence 345, Ap
C1276	34.6	2.3	33944	18	US-10-719-993-6978	Sequence 6978, Ap	C1351	34.2	2.3	286	11	US-10-085-106-42	Sequence 42, Appl1
C1277	34.6	2.3	34245	18	US-10-367-094-102	Sequence 102, App	C1352	34.2	2.3	363	18	US-10-437-963-8633	Sequence 8632, A
C1278	34.6	2.3	53828	18	US-10-322-281-369	Sequence 369, App	C1353	34.2	2.3	372	18	US-10-674-124A-14216	Sequence 14216, A
C1279	34.6	2.3	55155	13	US-09-735-933-3	Sequence 3, Appl1	C1354	34.2	2.3	398	18	US-10-357-930-38493	Sequence 38493, A
C1280	34.6	2.3	223556	13	US-10-087-192-394	Sequence 394, App	C1355	34.2	2.3	420	14	US-10-074-475-127	Sequence 127, App
C1281	34.6	2.3	295096	13	US-10-087-192-331	Sequence 331, App	C1356	34.2	2.3	422	18	US-10-425-115-106976	Sequence 106976, A
C1282	34.4	2.3	256	18	US-10-425-115-123084	Sequence 123084, A	C1357	34.2	2.3	459	15	US-10-156-761-6202	Sequence 6202, Ap
C1283	34.4	2.3	385	18	US-10-425-115-88396	Sequence 88396, A	C1358	34.2	2.3	492	18	US-10-425-115-161395	Sequence 161395, A
C1284	34.4	2.3	432	10	US-10-425-115-140944	Sequence 140944, A	C1359	34.2	2.3	527	9	US-09-796-692-9347	Sequence 9347, Ap
C1285	34.4	2.3	432	10	US-09-925-299-648	Sequence 648, App	C1360	34.2	2.3	527	14	US-10-040-862-9347	Sequence 9347, Ap
C1286	34.4	2.3	434	9	US-09-960-352-2445	Sequence 2445, Ap	C1361	34.2	2.3	527	17	US-10-057-475B-9347	Sequence 9347, Ap
C1287	34.4	2.3	463	18	US-10-674-124A-26428	Sequence 26428, A	C1362	34.2	2.3	527	17	US-10-154-884A-9347	Sequence 9347, Ap
C1288	34.4	2.3	471	18	US-10-674-124A-3024	Sequence 3024, Ap	C1363	34.2	2.3	527	18	US-10-764-324-9347	Sequence 9347, Ap
C1289	34.4	2.3	479	18	US-10-674-124A-18991	Sequence 18991, A	C1364	34.2	2.3	567	18	US-10-653-047-259	Sequence 259, App
C1290	34.4	2.3	519	18	US-10-437-963-24023	Sequence 24023, A	C1365	34.2	2.3	583	18	US-10-767-701-3129	Sequence 3129, Ap
C1294	34.4	2.3	612	18	US-10-767-701-3698	Sequence 3698, Ap	C1366	34.2	2.3	624	18	US-10-674-124A-14216	Sequence 14216, A
C1295	34.4	2.3	650	18	US-10-767-701-29530	Sequence 29530, A	C1367	34.2	2.3	645	16	US-10-181-447A-57	Sequence 57, Appl1
C1296	34.4	2.3	707	13	US-10-027-632-14161	Sequence 14161, A	C1368	34.2	2.3	695	9	US-09-867-701-10647	Sequence 10647, A
C1297	34.4	2.3	707	17	US-10-027-632-14161	Sequence 14161, A	C1369	34.2	2.3	842	13	US-10-027-632-164272	Sequence 164272, A
C1298	34.4	2.3	717	13	US-10-027-632-14161	Sequence 14161, A	C1370	34.2	2.3	842	17	US-10-027-632-164271	Sequence 164271, A
C1299	34.4	2.3	712	17	US-10-027-632-23464	Sequence 23464, A	C1371	34.2	2.3	842	17	US-10-027-632-164272	Sequence 164272, A
C1300	34.4	2.3	740	9	US-09-728-721-48	Sequence 48, Appl1	C1372	34.2	2.3	978	18	US-10-437-963-1345	Sequence 1345, Ap
C1301	34.4	2.3	740	9	US-09-996-617-7	Sequence 48, Appl1	C1373	34.2	2.3	978	17	US-10-437-963-1345	Sequence 1345, Ap
C1302	34.4	2.3	740	9	US-09-996-617-10	Sequence 10, Appl1	C1374	34.2	2.3	1027	18	US-10-425-115-163195	Sequence 163195, A
C1303	34.4	2.3	740	9	US-09-841-879B-19	Sequence 19, Appl1	C1375	34.2	2.3	1164	15	US-10-156-761-2363	Sequence 2363, Ap
C1304	34.4	2.3	740	9	US-09-841-879B-19	Sequence 19, Appl1	C1376	34.2	2.3	1230	15	US-10-156-761-2363	Sequence 2363, Ap
C1306	34.4	2.3	740	15	US-10-295-981-48	Sequence 48, Appl1	C1377	34.2	2.3	1299	18	US-10-437-963-6605	Sequence 6605, Ap
C1307	34.4	2.3	740	18	US-10-756-097-48	Sequence 48, Appl1	C1378	34.2	2.3	1548	18	US-10-437-963-26804	Sequence 26804, A
C1308	34.4	2.3	740	18	US-10-756-097-48	Sequence 48, Appl1	C1379	34.2	2.3	1548	18	US-10-437-963-26804	Sequence 26804, A
C1309	34.4	2.3	740	18	US-10-843-188-48	Sequence 18, Appl1	C1380	34.2	2.3	1761	17	US-10-376-947-9	Sequence 947, A
C1310	34.4	2.3	745	17	US-10-240-145-12	Sequence 12, Appl1	C1381	34.2	2.3	2028	15	US-10-156-761-3359	Sequence 3359, A
C1311	34.4	2.3	771	18	US-10-437-963-42980	Sequence 42980, A	C1382	34.2	2.3	2028	17	US-10-369-493-47118	Sequence 47118, A
C1312	34.4	2.3	779	17	US-10-131-410-21	Sequence 21, Appl1	C1383	34.2	2.3	2419	18	US-10-425-115-89362	Sequence 89362, A
C1313	34.4	2.3	786	18	US-10-425-115-64617	Sequence 64617, A	C1384	34.2	2.3	2634	18	US-10-437-963-72016	Sequence 72016, A
C1314	34.4	2.3	806	15	US-10-106-698-1144	Sequence 1144, Ap	C1385	34.2	2.3	2922	18	US-10-425-115-92259	Sequence 92259, A
C1315	34.4	2.3	811	9	US-09-925-301-278	Sequence 278, App	C1386	34.2	2.3	3012	15	US-10-156-761-7256	Sequence 7256, Ap
C1316	34.4	2.3	855	18	US-10-762-107-43	Sequence 43, Appl1	C1387	34.2	2.3	3354	18	US-10-425-115-158032	Sequence 158032, A
C1317	34.4	2.3	855	18	US-10-425-115-16730	Sequence 16730, A	C1388	34.2	2.3	3573	18	US-10-437-963-5583	Sequence 5583, Ap
C1318	34.4	2.3	979	18	US-10-437-963-5535	Sequence 5535, A	C1389	34.2	2.3	6573	18	US-09-942-025-16	Sequence 16, Appl1
C1319	34.4	2.3	141	18	US-10-437-963-5535	Sequence 5535, A	C1390	34.2	2.3	11358	10	US-10-057-726-16	Sequence 16, Appl1
C1320	34.4	2.3	1140	13	US-10-027-632-253750	Sequence 253750, A	C1391	34.2	2.3	16011	14	US-10-057-726-16	Sequence 16, Appl1
C1321	34.4	2.3	1140	13	US-10-027-632-253750	Sequence 253750, A	C1392	34.2	2.3	18800	18	US-10-741-601-5748	Sequence 5748, Ap
C1322	34.4	2.3	1140	17	US-10-027-632-253750	Sequence 253750, A	C1393	34.2	2.3	18800	18	US-10-741-601-5748	Sequence 5748, Ap
C1323	34.4	2.3	1140	17	US-10-027-632-253750	Sequence 253750, A	C1394	34.2	2.3	20922	10	US-09-942-025-14	Sequence 14, Appl1
C1324	34.4	2.3	1164	17	US-10-359-493-45267	Sequence 45267, A	C1395	34.2	2.3	22492	13	US-10-087-192-850	Sequence 850, App
C1325	34.4	2.3	1305	15	US-10-156-761-3516	Sequence 3516, Ap	C1396	34.2	2.3	27246	18	US-10-741-601-5676	Sequence 5676, Ap
C1326	34.4	2.3	1470	9	US-09-815-242-7855	Sequence 7855, Ap	C1397	34.2	2.3	32069	16	US-10-719-993-6851	Sequence 6851, A
C1327	34.4	2.3	1619	9	US-09-764-868-400	Sequence 400, App	C1398	34.2	2.3	42772	12	US-10-004-113-7	Sequence 7, Appl1
C1328	34.4	2.3	1619	14	US-10-103-313-74	Sequence 74, Appl1	C1399	34.2	2.3	42939	9	US-10-087-192-1903	Sequence 1903, Ap
C1329	34.4	2.3	1659	17	US-10-425-114-21811	Sequence 21811, A	C1400	34.2	2.3	42939	10	US-09-836-911A-17	Sequence 17, Appl1
C1330	34.4	2.3	1714	18	US-10-437-963-43882	Sequence 43882, A	C1401	34.2	2.3	42939	10	US-09-836-911A-17	Sequence 17, Appl1
C1331	34.4	2.3	1744	17	US-10-425-114-34867	Sequence 34867, A	C1402	34.2	2.3	42939	13	US-10-125-767-17	Sequence 17, Appl1
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C 30	44.6	3.0	31868	4	US-09-949-016-11907	Sequence 11907, A
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C 32	43.6	2.9	1161	4	US-09-949-016-579	Sequence 579, App
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C 38	43.4	2.9	2466	4	US-09-266-965-83	Sequence 83, Appl
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C 40	43.2	2.9	447	4	US-09-989-025A-3	Sequence 3, Appl1
C 41	43.2	2.9	564	4	US-09-513-999C-3836	Sequence 3836, Ap
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C 62	39	2.6	1971	2	US-08-818-253-7	Sequence 7, Appl1
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C 81	37.6	2.5	1344	4	US-09-252-991A-5239	Sequence 5239, Ap
C 82	37.6	2.5	1794	4	US-09-252-991A-5181	Sequence 5181, Ap
C 83	37.6	2.5	2547	4	US-09-252-991A-5294	Sequence 5294, Ap
C 84	37.6	2.5	3955	3	US-09-214-218-4	Sequence 4, Appl1
C 85	37.6	2.5	3955	4	US-09-855-722-4	Sequence 4, Appl1
C 86	37.4	2.5	2485	4	US-08-424-444B-1	Sequence 1, Appl1
C 87	37.4	2.5	2485	5	PCT-US94-05163A-1	Sequence 1, Appl1
C 88	37.4	2.5	387	4	US-09-902-540-8061	Sequence 8061, Ap
C 89	37.2	2.5	476	4	US-09-640-211A-1441	Sequence 1441, Ap
C 90	37.2	2.5	864	4	US-09-252-991A-15661	Sequence 15661, Ap
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C 103	37	2.5	1218	4	US-09-902-540-9113	Sequence 9113, Ap	176	35.8	2.4	43950	3	US-09-735-934A-3	Sequence 3, Appl1
C 104	37	2.5	1434	4	US-09-252-991A-7601	Sequence 7601, Ap	177	35.8	2.4	43950	4	US-10-060-332-3	Sequence 3, Appl1
C 105	37	2.5	1626	4	US-09-902-540A-7950	Sequence 7950, Ap	178	35.8	2.4	43950	4	US-10-339-657-3	Sequence 3, Appl1
C 106	37	2.5	1995	4	US-09-902-540-9209	Sequence 9209, Ap	179	35.8	2.4	258775	4	US-09-949-016-16435	Sequence 16435, A
C 107	37	2.5	2169	4	US-09-252-991A-7531	Sequence 7531, Ap	180	35.6	2.4	174	4	US-09-401-064-325	Sequence 325, App
C 108	37	2.5	8820	4	US-09-902-540-974	Sequence 974, App	181	35.6	2.4	174	4	US-09-401-064-368	Sequence 368, App
C 109	37	2.5	10301	4	US-09-902-540-985	Sequence 985, App	182	35.6	2.4	2136	4	US-09-600-991-19	Sequence 19, Appl
C 110	37	2.5	41927	4	US-09-902-540-1268	Sequence 1268, Ap	183	35.6	2.4	2136	4	US-09-601-040A-11	Sequence 11, Appl
C 111	37	2.5	90541	4	US-09-759-359A-3	Sequence 3, Appl1	184	35.6	2.4	2219	2	US-08-666-082B-2	Sequence 2, Appl
C 112	37	2.5	90541	4	US-10-207-973-3	Sequence 1766, Ap	185	35.6	2.4	2219	1	US-07-882-925A-1	Sequence 1, Appl
C 113	36.8	2.5	873	4	US-09-252-991A-1766	Sequence 16018, A	186	35.6	2.4	2262	1	US-07-882-925A-7	Sequence 7, Appl
C 114	36.8	2.5	2169	4	US-09-252-991A-1910	Sequence 17, Appl	187	35.6	2.4	2219	1	US-08-184-012C-1	Sequence 1, Appl
C 115	36.8	2.5	2946	4	US-09-252-991A-2045	Sequence 2045, Ap	188	35.6	2.4	2219	1	US-08-184-012C-2	Sequence 2, Appl
C 116	36.8	2.5	4123	4	US-09-252-991A-12852	Sequence 12852, A	189	35.6	2.4	2219	4	US-09-949-016-1110	Sequence 1110, Ap
C 117	36.8	2.5	6100	1	US-07-882-925A-6	Sequence 6, Appl1	190	35.6	2.4	2232	5	US-08-334-177-1	Sequence 1, Appl
C 118	36.8	2.5	6100	1	US-08-184-012C-6	Sequence 15018, A	191	35.6	2.4	2262	1	PCT-US95-13830-1	Sequence 1, Appl
C 119	36.8	2.5	17922	4	US-09-949-016-15018	Sequence 17, Appl	192	35.6	2.4	2262	1	US-08-184-012C-7	Sequence 7, Appl
C 120	36.8	2.5	35828	3	US-09-449-218D-17	Sequence 17, Appl	193	35.6	2.4	2262	1	US-08-785-420-1	Sequence 1, Appl
C 121	36.8	2.5	35828	4	US-09-668-037A-17	Sequence 17, Appl	194	35.6	2.4	15378	3	US-09-949-016-14080	Sequence 14080, A
C 122	36.8	2.5	35828	4	US-09-668-037A-17	Sequence 17, Appl	195	35.6	2.4	60990	4	US-09-949-016-12277	Sequence 12277, A
C 123	36.8	2.5	35828	4	US-09-668-037A-17	Sequence 17, Appl	196	35.6	2.4	113967	4	US-09-949-016-17051	Sequence 17051, A
C 124	36.8	2.5	64467	4	US-09-803-671B-3	Sequence 3, Appl1	197	35.6	2.4	113967	4	US-09-949-016-15127	Sequence 15127, A
C 125	36.8	2.5	64467	4	US-10-274-409-3	Sequence 32, Appl	198	35.4	2.4	142783	4	US-09-949-016-15127	Sequence 10252, A
C 126	36.8	2.5	118067	4	US-09-497-855A-32	Sequence 17349, A	199	35.4	2.4	423	4	US-09-252-991A-10025	Sequence 16637, A
C 127	36.8	2.5	156651	4	US-09-949-016-17349	Sequence 161657, A	200	35.4	2.4	1116	4	US-09-949-016-196637	Sequence 3384, Ap
C 128	36.6	2.5	601	4	US-09-949-016-161657	Sequence 2, Appl1	201	35.4	2.4	1116	4	US-09-902-540-384	Sequence 4412, Ap
C 129	36.6	2.5	1294	3	US-09-025-691-2	Sequence 12887, A	202	35.4	2.4	1320	4	US-09-902-540-4812	Sequence 899, App
C 130	36.6	2.5	20537	4	US-09-949-016-12887	Sequence 17052, A	203	35.4	2.4	1526	4	US-09-949-016-899	Sequence 1636, Ap
C 131	36.6	2.5	20538	4	US-09-949-016-17052	Sequence 16267, A	204	35.4	2.4	1526	4	US-09-949-016-1636	Sequence 7, Appl1
C 132	36.6	2.5	54531	4	US-09-949-016-16267	Sequence 14803, A	205	35.4	2.4	1559	3	US-09-019-095A-7	Sequence 1160, Ap
C 133	36.6	2.5	421491	4	US-09-949-016-12805	Sequence 18033, A	206	35.4	2.4	16427	4	US-09-902-540-1160	Sequence 1218, Ap
C 134	36.6	2.5	421491	4	US-09-949-016-14060	Sequence 14803, A	207	35.4	2.4	23677	4	US-09-902-540-1218	Sequence 17308, A
C 135	36.4	2.5	474	4	US-09-621-976-18033	Sequence 82606, A	208	35.4	2.4	25992	4	US-09-949-016-17308	Sequence 12505, A
C 136	36.4	2.5	601	4	US-09-949-016-82606	Sequence 13666, A	209	35.4	2.4	26000	4	US-09-843-376-10	Sequence 14207, A
C 137	36.4	2.5	19237	4	US-09-949-016-13666	Sequence 15462, A	210	35.4	2.4	670689	4	US-09-949-016-12505	Sequence 12345, A
C 138	36.4	2.5	44208	4	US-09-949-016-12240	Sequence 15403, A	211	35.4	2.4	670689	4	US-09-949-016-12505	Sequence 15758, A
C 139	36.4	2.5	44208	4	US-09-949-016-15941	Sequence 1, Appl1	212	35.2	2.4	342	4	US-09-902-540-6243	Sequence 5828, Ap
C 140	36.4	2.5	107820	4	US-09-792-616-1	Sequence 14138, A	213	35.2	2.4	717	4	US-09-902-540-5828	Sequence 7412, Ap
C 141	36.4	2.5	121068	4	US-09-949-016-11138	Sequence 15845, A	214	35.2	2.4	1854	4	US-09-902-540-5828	Sequence 99, Appl
C 142	36.4	2.5	133559	4	US-09-949-016-15845	Sequence 18976, Ap	215	35.2	2.4	8083	3	US-09-383-630-4	Sequence 5058, Ap
C 143	36.2	2.4	399	4	US-09-621-976-8976	Sequence 15371, A	216	35.2	2.4	8083	3	US-09-383-630-4	Sequence 1094, Ap
C 144	36.2	2.4	1989	4	US-09-252-991A-15371	Sequence 15371, A	217	35.2	2.4	72704	4	US-09-949-016-17578	Sequence 16960, A
C 145	36.2	2.4	2058	4	US-09-252-991A-15462	Sequence 15462, A	218	35.2	2.4	86414	4	US-09-949-016-17578	Sequence 14129, A
C 146	36.2	2.4	2637	4	US-09-252-991A-15462	Sequence 15403, A	219	35.2	2.4	86414	4	US-09-949-016-17578	Sequence 17920, A
C 147	36.2	2.4	2637	4	US-09-252-991A-15462	Sequence 735, App	220	35.2	2.4	86414	4	US-09-949-016-17578	Sequence 17920, A
C 148	36.2	2.4	5467	4	US-09-976-594-735	Sequence 735, App	221	35	2.4	601	4	US-09-949-016-17921	Sequence 41810, A
C 149	36.2	2.4	6640	4	US-09-949-016-797	Sequence 13, Appl	222	35	2.4	1488	4	US-09-252-991A-7333	Sequence 41811, A
C 150	36.2	2.4	9515	1	US-08-920-812-13	Sequence 13, Appl	223	35	2.4	1488	4	US-09-252-991A-7333	Sequence 67157, A
C 151	36.2	2.4	9515	1	US-08-920-812-13	Sequence 13, Appl	224	35	2.4	1488	4	US-09-252-991A-7333	Sequence 18276, A
C 152	36.2	2.4	9515	1	US-08-921-177-13	Sequence 13, Appl	225	35	2.4	1488	4	US-09-252-991A-7333	Sequence 359, App
C 153	36.2	2.4	9515	2	US-08-362-577C-13	Sequence 13, Appl	226	35	2.4	15782	4	US-09-902-540-1094	Sequence 5848, App
C 154	36.2	2.4	9515	2	US-08-920-828-13	Sequence 13, Appl	227	35	2.4	31713	4	US-09-949-016-16560	Sequence 11921, A
C 155	36.2	2.4	15872	3	US-09-105-537-1	Sequence 1, Appl1	228	34.8	2.3	530	4	US-09-513-999-14129	Sequence 17920, A
C 156	36.2	2.4	15872	4	US-09-091-609-3	Sequence 1, Appl1	229	34.8	2.3	601	4	US-09-949-016-17920	Sequence 41810, A
C 157	36.2	2.4	43280	2	US-09-091-609-3	Sequence 1, Appl1	230	34.8	2.3	601	4	US-09-949-016-17920	Sequence 41811, A
C 158	36.2	2.4	253345	4	US-08-804-227C-1	Sequence 1, Appl1	231	34.8	2.3	601	4	US-09-949-016-17920	Sequence 67157, A
C 159	36.2	2.4	253345	4	US-09-949-016-12656	Sequence 1635, A	232	34.8	2.3	601	4	US-09-949-016-17920	Sequence 18276, A
C 160	36	2.4	601	4	US-09-949-016-13639	Sequence 1635, A	233	34.8	2.3	601	4	US-09-949-016-17920	Sequence 359, App
C 161	36	2.4	601	4	US-09-949-016-17919	Sequence 17919, A	234	34.8	2.3	601	4	US-09-949-016-17920	Sequence 5848, App
C 162	36	2.4	601	4	US-09-949-016-17919	Sequence 17919, A	235	34.8	2.3	601	4	US-09-949-016-17920	Sequence 11921, A
C 163	36	2.4	894	4	US-09-949-016-82607	Sequence 82607, A	236	34.8	2.3	601	4	US-09-949-016-17920	Sequence 41810, A
C 164	36	2.4	1512	4	US-09-252-991A-10016	Sequence 10016, A	237	34.8	2.3	1285	4	US-09-902-540-137	Sequence 5848, App
C 165	36	2.4	1512	4	US-09-252-991A-1551	Sequence 1551, Ap	238	34.8	2.3	1285	4	US-09-902-540-137	Sequence 11921, A
C 166	36	2.4	2271	3	US-09-252-991A-1616	Sequence 1616, Ap	239	34.8	2.3	1375	2	US-08-468-812-1	Sequence 1, Appl1
C 167	36	2.4	4315	3	US-08-882-046-3	Sequence 6006, Ap	240	34.8	2.3	1375	2	US-08-468-812-1	Sequence 1, Appl1
C 168	36	2.4	4315	3	US-08-882-046-3	Sequence 3, Appl1	241	34.8	2.3	1375	4	US-09-770-621-1	Sequence 1, Appl1
C 169	36	2.4	23902	4	US-09-566-047-3	Sequence 3, Appl1	242	34.8	2.3	1375	4	US-09-770-621-1	Sequence 1, Appl1
C 170	35.8	2.4	774	4	US-09-949-016-14220	Sequence 14220, A	243	34.8	2.3	1512	4	US-09-902-540-3874	Sequence 3874, Ap
C 171	35.8	2.4	774	4	US-09-385-219A-39	Sequence 3367, Ap	244	34.8	2.3	11666	4	US-09-949-016-14668	Sequence 11468, Ap
C 172	35.8	2.4	783	4	US-09-902-540-367	Sequence 3367, Ap	245	34.8	2.3	21133	4	US-09-902-540-1191	Sequence 1191, Ap
C 173	35.8	2.4	1457	4	US-09-252-991A-6882	Sequence 6882, Ap	246	34.8	2.3	30782	4	US-09-949-016-13724	Sequence 13724, A
					US-09-620-312D-408	Sequence 408, App				31391	4	US-09-949-016-14319	Sequence 14319, A

C 247	34.8	2.3	34539	4	US-09-949-016-12226	Sequence 12226, A
C 248	34.8	2.3	34540	4	US-09-949-016-13156	Sequence 13156, A
C 249	34.8	2.3	45546	3	US-09-146-053-6	Sequence 6, Appl1
250	34.8	2.3	135058	4	US-09-949-016-12565	Sequence 12565, A
251	34.8	2.3	136480	4	US-09-949-016-17064	Sequence 17064, A
252	34.8	2.3	144158	4	US-09-949-016-11755	Sequence 11755, A
253	34.8	2.3	144158	4	US-09-949-016-12936	Sequence 12936, A
254	34.8	2.3	203475	4	US-09-949-016-14516	Sequence 14516, A
255	34.8	2.3	203475	4	US-09-949-016-14517	Sequence 14517, A
256	34.8	2.3	203475	4	US-09-949-016-14518	Sequence 14518, A
257	34.8	2.3	203475	4	US-09-949-016-14519	Sequence 14519, A
258	34.8	2.3	203475	4	US-09-949-016-17226	Sequence 17226, A
259	34.8	2.3	203475	4	US-09-949-016-17227	Sequence 17227, A
260	34.8	2.3	203475	4	US-09-949-016-17228	Sequence 17228, A
261	34.8	2.3	203475	4	US-09-949-016-17229	Sequence 17229, A
262	34.8	2.3	212139	4	US-09-949-016-16065	Sequence 16065, A
263	34.6	2.3	289	3	US-09-007-005-17	Sequence 17, Appl1
264	34.6	2.3	289	3	US-09-244-796-17	Sequence 17, Appl1
265	34.6	2.3	601	4	US-09-949-016-199458	Sequence 199458, A
266	34.6	2.3	601	4	US-09-949-016-199459	Sequence 199459, A
267	34.6	2.3	601	4	US-09-949-016-199460	Sequence 199460, A
268	34.6	2.3	601	4	US-09-949-016-199461	Sequence 199461, A
C 269	34.6	2.3	984	4	US-09-252-991A-2298	Sequence 2298, Ap
C 270	34.6	2.3	1036	4	US-09-902-540-4309	Sequence 4309, Ap
271	34.6	2.3	1349	1	US-07-951-715A-20	Sequence 20, Appl1
272	34.6	2.3	1349	2	US-08-459-448A-20	Sequence 20, Appl1
273	34.6	2.3	1349	3	US-08-459-504B-20	Sequence 20, Appl1
274	34.6	2.3	1349	3	US-08-459-504B-20	Sequence 20, Appl1
275	34.6	2.3	1349	3	US-08-459-504B-20	Sequence 20, Appl1
276	34.6	2.3	1349	3	US-08-459-504B-20	Sequence 20, Appl1
277	34.6	2.3	1349	3	US-08-459-504B-20	Sequence 20, Appl1
278	34.6	2.3	1349	3	US-08-459-504B-20	Sequence 20, Appl1
279	34.6	2.3	1349	3	US-08-459-504B-20	Sequence 20, Appl1
C 280	34.6	2.3	1743	3	US-09-261-559B-2	Sequence 2, Appl1
C 281	34.6	2.3	1743	3	US-09-456-455A-2	Sequence 2, Appl1
C 282	34.6	2.3	2073	4	US-09-252-991A-10279	Sequence 10279, A
C 283	34.6	2.3	2782	4	US-09-902-540-512	Sequence 512, App
284	34.6	2.3	11199	4	US-09-252-991A-10577	Sequence 10577, A
C 285	34.6	2.3	22807	4	US-09-902-540-1017	Sequence 1017, Ap
286	34.6	2.3	61178	4	US-09-949-016-17369	Sequence 17369, A
287	34.4	2.3	601	4	US-09-949-016-29117	Sequence 29117, A
288	34.4	2.3	601	4	US-09-949-016-37984	Sequence 37984, A
289	34.4	2.3	601	4	US-09-949-016-65230	Sequence 65230, A
290	34.4	2.3	601	4	US-09-949-016-65237	Sequence 65237, A
291	34.4	2.3	601	4	US-09-949-016-121300	Sequence 121300, A
292	34.4	2.3	740	4	US-09-840-620A-48	Sequence 48, Appl1
293	34.4	2.3	740	4	US-09-841-879B-4	Sequence 4, Appl1
C 294	34.4	2.3	740	4	US-09-841-879B-4	Sequence 4, Appl1
C 295	34.4	2.3	740	4	US-09-841-879B-4	Sequence 4, Appl1
C 296	34.4	2.3	740	4	US-09-841-879B-4	Sequence 4, Appl1
C 297	34.4	2.3	740	4	US-09-841-879B-4	Sequence 4, Appl1
C 298	34.4	2.3	740	4	US-09-841-879B-4	Sequence 4, Appl1
C 299	34.4	2.3	740	4	US-09-841-879B-4	Sequence 4, Appl1
C 300	34.4	2.3	740	4	US-09-841-879B-4	Sequence 4, Appl1
C 301	34.4	2.3	740	4	US-09-841-879B-4	Sequence 4, Appl1
C 302	34.4	2.3	740	4	US-09-841-879B-4	Sequence 4, Appl1
C 303	34.4	2.3	740	4	US-09-841-879B-4	Sequence 4, Appl1
C 304	34.4	2.3	740	4	US-09-841-879B-4	Sequence 4, Appl1
C 305	34.4	2.3	740	4	US-09-841-879B-4	Sequence 4, Appl1
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C 307	34.4	2.3	740	4	US-09-841-879B-4	Sequence 4, Appl1
C 308	34.4	2.3	740	4	US-09-841-879B-4	Sequence 4, Appl1
C 309	34.4	2.3	740	4	US-09-841-879B-4	Sequence 4, Appl1
C 310	34.4	2.3	740	4	US-09-841-879B-4	Sequence 4, Appl1
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C 313	34.4	2.3	740	4	US-09-841-879B-4	Sequence 4, Appl1
C 314	34.4	2.3	740	4	US-09-841-879B-4	Sequence 4, Appl1
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C 317	34.4	2.3	740	4	US-09-841-879B-4	Sequence 4, Appl1
C 318	34.4	2.3	740	4	US-09-841-879B-4	Sequence 4, Appl1
C 319	34.4	2.3	740	4	US-09-841-879B-4	Sequence 4, Appl1

393	33.6	2.3	1437	4	US-09-252-991A-8463	Sequence 8463, Ap	466	33.4	2.2	390890	4	US-09-949-016-14720	Sequence 14720, A
394	33.6	2.3	1575	1	US-09-949-016-4211	Sequence 4211, Ap	467	33.4	2.2	455726	4	US-09-949-016-14157	Sequence 14157, A
395	33.6	2.3	1728	1	US-08-427-097-1	Sequence 1, Appl1	468	33.4	2.2	481115	4	US-09-949-016-11940	Sequence 11940, A
396	33.6	2.3	1728	2	US-08-878-957-1	Sequence 1, Appl1	469	33.2	2.2	601	4	US-09-949-016-105288	Sequence 105288, A
397	33.6	2.3	1746	2	US-08-427-097-29	Sequence 29, Appl	470	33.2	2.2	601	4	US-09-949-016-151464	Sequence 151464, A
398	33.6	2.3	1752	1	US-08-878-957-29	Sequence 29, Appl	471	33.2	2.2	601	4	US-09-949-016-167541	Sequence 167541, A
399	33.6	2.3	1752	1	US-08-427-097-13	Sequence 13, Appl	472	33.2	2.2	601	4	US-09-949-016-167542	Sequence 167542, A
400	33.6	2.3	1752	1	US-08-427-097-15	Sequence 15, Appl	473	33.2	2.2	601	4	US-09-949-016-167543	Sequence 167543, A
401	33.6	2.3	1752	1	US-08-427-097-19	Sequence 19, Appl	474	33.2	2.2	601	4	US-09-949-016-167648	Sequence 167648, A
402	33.6	2.3	1752	1	US-08-427-097-27	Sequence 27, Appl	475	33.2	2.2	601	4	US-09-949-016-167649	Sequence 167649, A
403	33.6	2.3	1752	2	US-08-878-957-13	Sequence 13, Appl	476	33.2	2.2	1251	4	US-09-949-016-167650	Sequence 167650, A
404	33.6	2.3	1752	2	US-08-878-957-15	Sequence 15, Appl	477	33.2	2.2	1563	4	US-09-949-016-167651	Sequence 167651, A
405	33.6	2.3	1752	2	US-08-878-957-19	Sequence 19, Appl	478	33.2	2.2	1721	1	US-07-688-352C-13	Sequence 37, Appl
406	33.6	2.3	1752	2	US-08-878-957-27	Sequence 27, Appl	479	33.2	2.2	1721	2	US-08-474-379C-13	Sequence 13, Appl
407	33.6	2.3	1785	4	US-09-252-991A-2704	Sequence 2593, Ap	480	33.2	2.2	1721	3	US-09-146-249A-13	Sequence 13, Appl
408	33.6	2.3	1851	4	US-09-252-991A-2593	Sequence 1, Appl1	481	33.2	2.2	1721	3	US-08-206-188B-13	Sequence 13, Appl
409	33.6	2.3	2027	1	US-08-150-203A-1	Sequence 1, Appl1	482	33.2	2.2	1721	5	PCT-US91-02714-13	Sequence 13, Appl
410	33.6	2.3	2027	3	US-08-949-788-1	Sequence 1, Appl1	483	33.2	2.2	1734	6	5352575-8	Patent No. 5352575
411	33.6	2.3	2027	3	US-08-949-788-1	Sequence 36, Appl	484	33.2	2.2	1734	6	5352575-8	Patent No. 5352575
412	33.6	2.3	2040	1	US-08-247-475-36	Sequence 36, Appl	485	33.2	2.2	3452	4	US-09-949-016-1233	Sequence 3333, Ap
413	33.6	2.3	2040	1	US-08-191-86CD-57	Sequence 57, Appl	486	33.2	2.2	3957	4	US-10-237-551-193	Sequence 193, Ap
414	33.6	2.3	2040	1	US-08-674-169-36	Sequence 36, Appl	487	33.2	2.2	4286	4	US-09-899-634C-1	Sequence 1, Appl1
415	33.6	2.3	2040	1	US-08-185-949B-57	Sequence 57, Appl	488	33.2	2.2	6424	4	US-09-902-540-584	Sequence 584, Ap
416	33.6	2.3	2161	5	PCT-US93-08386-4	Sequence 4, Appl1	489	33.2	2.2	6714	3	US-09-299-141-6	Sequence 6, Appl1
417	33.6	2.3	2172	4	US-09-252-991A-2325	Sequence 2325, Ap	490	33.2	2.2	6924	3	US-09-299-141-9	Sequence 9, Appl1
418	33.6	2.3	4190	3	US-08-924-345-1	Sequence 1, Appl1	491	33.2	2.2	6924	3	US-09-299-141-10	Sequence 10, Appl
419	33.6	2.3	4190	3	US-08-875-435B-5	Sequence 5, Appl1	492	33.2	2.2	6924	3	US-09-299-141-11	Sequence 11, Appl
420	33.6	2.3	9840	4	US-09-534-638-1	Sequence 1, Appl1	493	33.2	2.2	8033	4	US-09-574-779B-134	Sequence 134, Ap
421	33.6	2.3	9840	4	US-09-534-638-1	Sequence 1, Appl1	494	33.2	2.2	10528	4	US-09-902-540-945	Sequence 945, App
422	33.6	2.3	41594	4	US-09-949-016-12998	Sequence 1, Appl1	495	33.2	2.2	12424	4	US-09-949-016-14975	Sequence 14975, A
423	33.6	2.3	41684	4	US-09-536-059-1	Sequence 1, Appl1	496	33.2	2.2	14367	4	US-09-902-540-1113	Sequence 1113, Ap
424	33.6	2.3	49144	4	US-09-949-016-15343	Sequence 15343, A	497	33.2	2.2	18917	4	US-09-949-016-13129	Sequence 13129, A
425	33.6	2.3	55703	4	US-09-949-016-12007	Sequence 12007, A	498	33.2	2.2	18917	4	US-09-949-016-13130	Sequence 13130, A
426	33.6	2.3	55703	4	US-09-949-016-15781	Sequence 15781, A	499	33.2	2.2	18917	4	US-09-949-016-13131	Sequence 13131, A
427	33.6	2.3	96240	4	US-09-949-016-1863	Sequence 1863, A	500	33.2	2.2	41617	4	US-09-949-016-14356	Sequence 14356, A
428	33.6	2.3	137753	4	US-09-949-016-17404	Sequence 17404, A	501	33.2	2.2	41617	4	US-09-949-016-14661	Sequence 14661, A
429	33.6	2.3	169334	4	US-09-949-016-15999	Sequence 15999, A	502	33.2	2.2	53500	4	US-09-266-965-76	Sequence 76, Appl
430	33.6	2.3	300598	4	US-09-949-016-11868	Sequence 11868, A	503	33.2	2.2	54601	4	US-09-949-016-14173	Sequence 14173, A
431	33.6	2.3	302604	4	US-09-949-016-14588	Sequence 14588, A	504	33.2	2.2	60424	4	US-09-949-016-12175	Sequence 12175, A
432	33.6	2.3	302604	4	US-09-949-016-14589	Sequence 14589, A	505	33.2	2.2	78157	4	US-09-949-016-16466	Sequence 16466, A
433	33.6	2.3	308362	4	US-09-949-016-17112	Sequence 17119, A	506	33.2	2.2	78157	4	US-09-949-016-16467	Sequence 16467, A
434	33.6	2.3	4403765	3	US-09-103-840A-2	Sequence 2, Appl1	507	33.2	2.2	83428	4	US-09-949-016-16467	Sequence 16467, A
435	33.6	2.3	4411529	3	US-09-103-840A-1	Sequence 1, Appl1	508	33.2	2.2	154746	4	US-09-949-016-13610	Sequence 13610, A
436	33.4	2.2	123	3	US-09-007-005-1	Sequence 1, Appl1	509	33.2	2.2	154746	4	US-09-827-688-8	Sequence 8, Appl1
437	33.4	2.2	123	3	US-09-244-796-1	Sequence 1, Appl1	510	33.2	2.2	319608	4	US-09-539-333D-1	Sequence 8, Appl1
438	33.4	2.2	573	4	US-09-902-540-7511	Sequence 7511, Ap	511	33.2	2.2	319608	4	US-09-679-409-1	Sequence 1, Appl1
439	33.4	2.2	601	4	US-09-949-016-124997	Sequence 124997, A	512	33.2	2.2	480	4	US-09-621-976-14850	Sequence 14850, A
440	33.4	2.2	601	4	US-09-949-016-144805	Sequence 3914, Ap	513	33.2	2.2	537	4	US-09-252-991A-15911	Sequence 15911, A
441	33.4	2.2	852	4	US-09-252-991A-3914	Sequence 3914, Ap	514	33.2	2.2	601	4	US-09-949-016-68791	Sequence 68791, A
442	33.4	2.2	988	4	US-09-949-016-2888	Sequence 2888, Ap	515	33.2	2.2	601	4	US-09-949-016-68791	Sequence 68791, A
443	33.4	2.2	1002	4	US-09-252-991A-3539	Sequence 3539, Ap	516	33.2	2.2	870	4	US-09-949-016-87534	Sequence 87534, A
444	33.4	2.2	1011	4	US-09-252-991A-4029	Sequence 4029, Ap	517	33.2	2.2	931	4	US-09-252-991A-15882	Sequence 15882, A
445	33.4	2.2	1030	4	US-09-902-540-73	Sequence 73, Appl	518	33.2	2.2	1264	4	US-09-902-540-4292	Sequence 4292, Ap
446	33.4	2.2	1111	4	US-09-949-016-4856	Sequence 4856, Ap	519	33.2	2.2	1317	4	US-09-902-540-11536	Sequence 11536, A
447	33.4	2.2	1137	4	US-09-724-797-53	Sequence 53, Appl	520	33.2	2.2	1651	4	US-09-573-080A-131	Sequence 131, Appl
448	33.4	2.2	1436	4	US-09-252-991A-3888	Sequence 3888, Ap	521	33.2	2.2	2277	1	US-08-676-967-5	Sequence 15779, A
449	33.4	2.2	1581	4	US-09-252-991A-3962	Sequence 3962, Ap	522	33.2	2.2	2056	4	US-09-976-594-413	Sequence 413, Appl
450	33.4	2.2	1644	4	US-09-252-991A-3548	Sequence 3548, Ap	523	33.2	2.2	2056	4	US-09-976-594-413	Sequence 413, Appl
451	33.4	2.2	1788	4	US-09-902-540-8800	Sequence 8800, Ap	524	33.2	2.2	2056	4	US-09-976-594-413	Sequence 413, Appl
452	33.4	2.2	2076	4	US-09-252-991A-2935	Sequence 2935, Ap	525	33.2	2.2	2277	1	US-08-676-967-5	Sequence 15779, A
453	33.4	2.2	2211	4	US-09-902-540-5403	Sequence 5403, Ap	526	33.2	2.2	2277	1	US-08-676-967-5	Sequence 15779, A
454	33.4	2.2	2839	4	US-09-252-991A-3523	Sequence 3523, Ap	527	33.2	2.2	13668	4	US-09-902-540-1082	Sequence 1082, Ap
455	33.4	2.2	2852	4	US-09-252-991A-3523	Sequence 3523, Ap	528	33.2	2.2	20250	4	US-09-902-540-1213	Sequence 1213, Ap
456	33.4	2.2	3437	3	US-08-450-962-3	Sequence 3, Appl1	529	33.2	2.2	43577	4	US-09-949-016-16594	Sequence 16594, A
457	33.4	2.2	3437	3	US-08-848-631-3	Sequence 2933, Appl	530	33.2	2.2	47476	4	US-09-949-016-16767	Sequence 16767, A
458	33.4	2.2	3876	4	US-09-252-991A-2933	Sequence 2933, Appl	531	33.2	2.2	47476	4	US-09-949-016-16767	Sequence 16767, A
459	33.4	2.2	6645	4	US-09-902-540-8819	Sequence 8819, Ap	532	33.2	2.2	74177	4	US-09-949-016-11472	Sequence 11472, A
460	33.4	2.2	10603	4	US-09-949-016-16598	Sequence 16598, A	533	33.2	2.2	74177	4	US-09-949-016-11472	Sequence 11472, A
461	33.4	2.2	11282	4	US-09-902-540-1039	Sequence 1039, Ap	534	33.2	2.2	74177	4	US-09-949-016-11472	Sequence 11472, A
462	33.4	2.2	12898	4	US-09-902-540-1000	Sequence 1000, Ap	535	33.2	2.2	119762	4	US-09-949-016-17313	Sequence 17313, A
463	33.4	2.2	20235	1	US-07-642-734C-3	Sequence 3, Appl1	536	33.2	2.2	137226	4	US-09-949-016-17313	Sequence 17313, A
464	33.4	2.2	20235	1	US-08-439-009A-3	Sequence 3, Appl1	537	33.2	2.2	171130	4	US-09-949-016-14861	Sequence 14861, A
465	33.4	2.2	23535	4	US-09-949-016-14630	Sequence 14630, A	538	33.2	2.2	171130	4	US-09-949-016-14861	Sequence 14861, A

539	33	2.2	191433	4	US-09-949-016-16144	Sequence 16144, A	C 612	32.8	2.2	818128	4	US-09-949-016-14548	Sequence 14548, A
540	33	2.2	256287	4	US-09-949-016-14608	Sequence 14608, A	C 613	32.8	2.2	818128	4	US-09-949-016-14549	Sequence 14549, A
541	33.8	2.2	495	4	US-09-902-540-7060	Sequence 7060, Ap	C 614	32.8	2.2	818128	4	US-09-949-016-14550	Sequence 14550, A
542	32.8	2.2	499	4	US-09-621-976-13716	Sequence 13716, A	C 615	32.8	2.2	818128	4	US-09-949-016-14551	Sequence 14551, A
543	32.8	2.2	601	4	US-09-949-016-63989	Sequence 63989, A	C 616	32.8	2.2	818128	4	US-09-949-016-14552	Sequence 14552, A
544	32.8	2.2	601	4	US-09-949-016-96510	Sequence 96510, A	C 617	32.8	2.2	818128	4	US-09-949-016-14553	Sequence 14553, A
545	32.8	2.2	601	4	US-09-949-016-96776	Sequence 96776, A	C 618	32.8	2.2	818128	4	US-09-949-016-14554	Sequence 14554, A
546	32.8	2.2	601	4	US-09-949-016-97042	Sequence 97042, A	C 619	32.8	2.2	818128	4	US-09-949-016-14555	Sequence 14555, A
547	32.8	2.2	601	4	US-09-949-016-97308	Sequence 97308, A	C 620	32.8	2.2	818128	4	US-09-949-016-14556	Sequence 14556, A
548	32.8	2.2	601	4	US-09-949-016-97574	Sequence 97574, A	C 621	32.8	2.2	818128	4	US-09-949-016-14557	Sequence 14557, A
549	32.8	2.2	601	4	US-09-949-016-97840	Sequence 97840, A	C 622	32.8	2.2	818128	4	US-09-949-016-14558	Sequence 14558, A
550	32.8	2.2	601	4	US-09-949-016-98106	Sequence 98106, A	C 623	32.8	2.2	818128	4	US-09-949-016-14559	Sequence 14559, A
551	32.8	2.2	601	4	US-09-949-016-98372	Sequence 98372, A	C 624	32.8	2.2	818128	4	US-09-949-016-14560	Sequence 14560, A
552	32.8	2.2	601	4	US-09-949-016-98638	Sequence 98638, A	C 625	32.8	2.2	818128	4	US-09-949-016-14561	Sequence 14561, A
553	32.8	2.2	601	4	US-09-949-016-98904	Sequence 98904, A	C 626	32.8	2.2	818128	4	US-09-949-016-14562	Sequence 14562, A
554	32.8	2.2	601	4	US-09-949-016-99170	Sequence 99170, A	C 627	32.8	2.2	818128	4	US-09-949-016-14564	Sequence 14564, A
555	32.8	2.2	601	4	US-09-949-016-99436	Sequence 99436, A	C 628	32.8	2.2	818128	4	US-09-949-016-14565	Sequence 14565, A
556	32.8	2.2	601	4	US-09-949-016-99702	Sequence 99702, A	C 629	32.8	2.2	818128	4	US-09-949-016-14566	Sequence 14566, A
557	32.8	2.2	601	4	US-09-949-016-99968	Sequence 99968, A	C 630	32.8	2.2	818128	4	US-09-949-016-14567	Sequence 14567, A
558	32.8	2.2	601	4	US-09-949-016-100234	Sequence 100234, A	C 631	32.6	2.2	495	4	US-09-902-540-3913	Sequence 3913, Ap
559	32.8	2.2	601	4	US-09-949-016-100500	Sequence 100500, A	C 632	32.6	2.2	601	4	US-09-949-016-53740	Sequence 53740, A
560	32.8	2.2	601	4	US-09-949-016-100766	Sequence 100766, A	C 633	32.6	2.2	601	4	US-09-949-016-111591	Sequence 111591, A
561	32.8	2.2	601	4	US-09-949-016-101070	Sequence 101070, A	C 634	32.6	2.2	601	4	US-09-949-016-111592	Sequence 111592, A
562	32.8	2.2	601	4	US-09-949-016-101336	Sequence 101336, A	C 635	32.6	2.2	601	4	US-09-949-016-111593	Sequence 111593, A
563	32.8	2.2	601	4	US-09-949-016-101602	Sequence 101602, A	C 636	32.6	2.2	601	4	US-09-949-016-111594	Sequence 111594, A
564	32.8	2.2	601	4	US-09-949-016-101868	Sequence 101868, A	C 637	32.6	2.2	601	4	US-09-949-016-111595	Sequence 111595, A
565	32.8	2.2	601	4	US-09-949-016-102288	Sequence 102288, A	C 638	32.6	2.2	601	4	US-09-949-016-111596	Sequence 111596, A
566	32.8	2.2	601	4	US-09-949-016-102428	Sequence 102428, A	C 639	32.6	2.2	601	4	US-09-949-016-111597	Sequence 111597, A
567	32.8	2.2	741	4	US-09-902-540-9589	Sequence 9589, Ap	C 640	32.6	2.2	601	4	US-09-949-016-111730	Sequence 111730, A
568	32.8	2.2	904	4	US-09-620-312D-495	Sequence 495, App	C 641	32.6	2.2	601	4	US-09-949-016-111740	Sequence 111740, A
569	32.8	2.2	1434	4	US-09-266-965-67	Sequence 67, App	C 642	32.6	2.2	601	4	US-09-949-016-111741	Sequence 111741, A
570	32.8	2.2	1641	4	US-08-726-214-17	Sequence 17, App	C 643	32.6	2.2	601	4	US-09-949-016-111742	Sequence 111742, A
571	32.8	2.2	1652	3	US-08-468-811-3	Sequence 3, App	C 644	32.6	2.2	601	4	US-09-949-016-111743	Sequence 111743, A
572	32.8	2.2	1864	2	US-08-590-563-3	Sequence 3, App	C 645	32.6	2.2	601	4	US-09-949-016-111744	Sequence 111744, A
573	32.8	2.2	1864	4	US-09-770-621-3	Sequence 3, App	C 646	32.6	2.2	601	4	US-09-949-016-111745	Sequence 111745, A
574	32.8	2.2	1864	4	US-09-235-833-3	Sequence 3, App	C 647	32.6	2.2	601	4	US-09-949-016-111865	Sequence 111865, A
575	32.8	2.2	1864	4	US-09-489-039A-4682	Sequence 4682, Ap	C 648	32.6	2.2	601	4	US-09-949-016-111866	Sequence 111866, A
576	32.8	2.2	2187	4	US-09-489-039A-4783	Sequence 4783, Ap	C 649	32.6	2.2	601	4	US-09-949-016-111867	Sequence 111867, A
577	32.8	2.2	2555	4	US-09-949-016-12110	Sequence 2310, Ap	C 650	32.6	2.2	601	4	US-09-949-016-111868	Sequence 111868, A
578	32.8	2.2	2891	4	US-09-620-312D-753	Sequence 753, App	C 651	32.6	2.2	601	4	US-09-949-016-111869	Sequence 111869, A
579	32.8	2.2	2990	3	US-09-009-816-19	Sequence 19, App	C 652	32.6	2.2	601	4	US-09-949-016-111890	Sequence 111890, A
580	32.8	2.2	3198	4	US-09-902-540-2522	Sequence 2522, Ap	C 653	32.6	2.2	601	4	US-09-949-016-111891	Sequence 111891, A
581	32.8	2.2	3757	2	US-09-016-366A-13	Sequence 13, App	C 654	32.6	2.2	601	4	US-09-949-016-112030	Sequence 112030, A
582	32.8	2.2	3757	2	US-08-978-404B-19	Sequence 19, App	C 655	32.6	2.2	601	4	US-09-949-016-112031	Sequence 112031, A
583	32.8	2.2	4008	3	US-08-307-896-5	Sequence 5, App	C 656	32.6	2.2	601	4	US-09-949-016-112032	Sequence 112032, A
584	32.8	2.2	4008	3	US-08-726-214-3	Sequence 3, App	C 657	32.6	2.2	601	4	US-09-949-016-112033	Sequence 112033, A
585	32.8	2.2	4008	5	PCT-US95-11808-5	Sequence 5, App	C 658	32.6	2.2	601	4	US-09-949-016-112034	Sequence 112034, A
586	32.8	2.2	4060	1	US-08-308-949A-1	Sequence 1, App	C 659	32.6	2.2	601	4	US-09-949-016-112035	Sequence 112035, A
587	32.8	2.2	4060	4	US-09-902-540-639	Sequence 629, App	C 660	32.6	2.2	601	4	US-09-949-016-112036	Sequence 112036, A
588	32.8	2.2	9867	4	US-09-902-540-1008	Sequence 1008, Ap	C 661	32.6	2.2	978	4	US-09-949-016-16456	Sequence 16456, A
589	32.8	2.2	14207	4	US-09-949-016-13775	Sequence 13775, A	C 662	32.6	2.2	1839	1	US-08-070-165F-7	Sequence 7, App
590	32.8	2.2	15664	1	US-08-402-282-3	Sequence 3, App	C 663	32.6	2.2	1839	2	US-08-885-418-7	Sequence 7, App
591	32.8	2.2	15664	1	US-08-508-004-3	Sequence 3, App	C 664	32.6	2.2	2016	4	US-09-902-540-8274	Sequence 8274, Ap
592	32.8	2.2	15664	1	US-08-402-066-3	Sequence 3, App	C 665	32.6	2.2	2214	3	US-08-943-731-57	Sequence 57, App
593	32.8	2.2	15664	1	US-08-402-066-3	Sequence 3, App	C 666	32.6	2.2	2532	4	US-09-252-991A-12912	Sequence 12912, A
594	32.8	2.2	17503	4	US-09-902-540-1114	Sequence 1114, Ap	C 667	32.6	2.2	2533	4	US-09-902-540-2867	Sequence 2867, Ap
595	32.8	2.2	18917	4	US-09-949-016-14052	Sequence 14052, A	C 668	32.6	2.2	2880	2	US-08-500-857A-3	Sequence 3, App
596	32.8	2.2	18917	4	US-09-949-016-15129	Sequence 15129, A	C 669	32.6	2.2	3770	4	US-09-397-550-21	Sequence 21, App
597	32.8	2.2	18917	4	US-09-949-016-13130	Sequence 13130, A	C 670	32.6	2.2	2880	4	US-09-902-540-856	Sequence 856, App
598	32.8	2.2	18917	4	US-09-949-016-13131	Sequence 13131, A	C 671	32.6	2.2	6930	4	US-09-902-540-987	Sequence 987, App
599	32.8	2.2	18917	4	US-09-949-016-13131	Sequence 13131, A	C 672	32.6	2.2	9818	4	US-09-902-540-987	Sequence 987, App
600	32.8	2.2	32010	4	US-09-949-016-13127	Sequence 13127, A	C 673	32.6	2.2	11801	4	US-09-534-072C-8	Sequence 8, App
601	32.8	2.2	51723	4	US-09-949-016-11152	Sequence 11152, A	C 674	32.6	2.2	11801	4	US-09-949-016-16447	Sequence 16447, A
602	32.8	2.2	51723	4	US-09-949-016-16991	Sequence 16991, A	C 675	32.6	2.2	11916	4	US-09-949-016-16448	Sequence 16448, A
603	32.8	2.2	69701	4	US-09-949-016-11187	Sequence 11187, A	C 676	32.6	2.2	17592	4	US-09-902-540-11138	Sequence 11138, Ap
604	32.8	2.2	72278	4	US-09-949-016-16113	Sequence 16113, A	C 677	32.6	2.2	18609	3	US-08-943-731-1	Sequence 1, App
605	32.8	2.2	73308	4	US-09-949-016-15326	Sequence 15326, A	C 678	32.6	2.2	21375	4	US-09-902-540-11193	Sequence 11193, Ap
606	32.8	2.2	101558	4	US-09-949-016-12243	Sequence 12243, A	C 679	32.6	2.2	28374	4	US-09-949-016-17508	Sequence 17508, A
607	32.8	2.2	150394	4	US-09-949-016-13042	Sequence 13042, A	C 680	32.6	2.2	42574	4	US-09-949-016-17525	Sequence 17525, A
608	32.8	2.2	393753	4	US-09-949-016-14573	Sequence 14573, A	C 681	32.6	2.2	44789	4	US-09-949-016-13909	Sequence 13909, A
609	32.8	2.2	393753	4	US-09-949-016-14574	Sequence 14574, A	C 682	32.6	2.2	53562	4	US-09-949-016-16386	Sequence 16386, A
610	32.8	2.2	818128	4	US-09-949-016-14546	Sequence 14546, A	C 683	32.6	2.2	84171	4	US-09-949-016-16356	Sequence 16356, A
611	32.8	2.2	818128	4	US-09-949-016-14547	Sequence 14547, A	C 684	32.6	2.2	88557	4	US-09-949-016-17028	Sequence 17028, A

685	32.6	2.2	113876	4	US-09-949-016-14828	Sequence 14828, A	758	32.4	2.2	35935	3	US-09-244-752-1	Sequence 1, Appl1
686	32.6	2.2	113876	4	US-09-949-016-14829	Sequence 14829, A	759	32.4	2.2	35935	3	US-09-245-497-1	Sequence 1, Appl1
687	32.6	2.2	115508	4	US-09-949-016-11800	Sequence 11800, A	760	32.4	2.2	35935	3	US-09-400-670-43	Sequence 43, Appl1
688	32.6	2.2	115508	4	US-09-949-016-14826	Sequence 14826, A	761	32.4	2.2	35935	3	US-09-562-919-1	Sequence 1, Appl1
689	32.6	2.2	115508	4	US-09-949-016-14827	Sequence 14827, A	762	32.4	2.2	35935	3	US-09-562-919-1	Sequence 1, Appl1
690	32.6	2.2	169998	3	US-09-676-610B-24	Sequence 24, Appl1	763	32.4	2.2	35978	4	US-09-956-335-1	Sequence 30, Appl1
691	32.6	2.2	197336	4	US-09-949-016-15584	Sequence 15584, A	764	32.4	2.2	36620	4	US-09-952-060-30	Sequence 28, Appl1
692	32.6	2.2	197336	4	US-09-949-016-15881	Sequence 15881, A	765	32.4	2.2	37474	4	US-09-952-060-25	Sequence 28, Appl1
693	32.6	2.2	197337	4	US-09-949-016-15376	Sequence 15376, A	766	32.4	2.2	38519	4	US-09-952-060-28	Sequence 28, Appl1
694	32.6	2.2	197496	4	US-09-877-177A-10	Sequence 10, Appl1	767	32.4	2.2	119930	4	US-09-949-016-12677	Sequence 12677, A
695	32.6	2.2	199945	4	US-09-949-016-15336	Sequence 15336, A	768	32.4	2.2	119931	4	US-09-949-016-16319	Sequence 16319, A
696	32.6	2.2	234288	4	US-09-949-016-11272	Sequence 11272, A	769	32.4	2.2	122772	4	US-09-949-016-14132	Sequence 14132, A
697	32.6	2.2	250715	4	US-09-949-016-13294	Sequence 13294, A	770	32.4	2.2	123536	4	US-09-949-016-14186	Sequence 14186, A
698	32.6	2.2	276237	4	US-09-949-016-17504	Sequence 17504, A	771	32.4	2.2	136163	4	US-09-949-016-15824	Sequence 15824, A
699	32.4	2.2	546	4	US-09-902-540-8130	Sequence 8130, Ap	772	32.4	2.2	141560	4	US-09-949-016-16476	Sequence 16476, A
700	32.4	2.2	601	4	US-09-949-016-36290	Sequence 36290, A	773	32.2	2.2	187136	4	US-09-949-016-17231	Sequence 17231, A
701	32.4	2.2	601	4	US-09-949-016-36291	Sequence 36291, A	774	32.2	2.2	390	4	US-09-583-110-835	Sequence 835, App
702	32.4	2.2	601	4	US-09-949-016-86553	Sequence 86553, A	775	32.2	2.2	405	4	US-09-107-433-2234	Sequence 2234, Ap
703	32.4	2.2	601	4	US-09-949-016-86554	Sequence 86554, A	776	32.2	2.2	601	4	US-09-949-016-59382	Sequence 59382, A
704	32.4	2.2	601	4	US-09-949-016-163246	Sequence 163246, A	777	32.2	2.2	601	4	US-09-949-016-59383	Sequence 59383, A
705	32.4	2.2	601	4	US-09-949-016-163247	Sequence 163247, A	778	32.2	2.2	601	4	US-09-949-016-92991	Sequence 92991, A
706	32.4	2.2	601	4	US-09-949-016-168683	Sequence 168683, A	779	32.2	2.2	601	4	US-09-949-016-92991	Sequence 92991, A
707	32.4	2.2	601	4	US-09-949-001-405	Sequence 405, App	780	32.2	2.2	606	4	US-09-252-991A-11529	Sequence 11529, A
708	32.4	2.2	880	3	US-09-056-285A-5	Sequence 5, Appl1	781	32.2	2.2	729	4	US-09-252-991A-8930	Sequence 8930, Ap
709	32.4	2.2	954	4	US-09-252-991A-5722	Sequence 5722, Ap	782	32.2	2.2	729	4	US-09-252-991A-8930	Sequence 8930, Ap
710	32.4	2.2	954	4	US-09-902-540-3679	Sequence 3679, Ap	783	32.2	2.2	741	4	US-09-902-540-6761	Sequence 6761, Ap
711	32.4	2.2	1070	3	US-09-470-443-7	Sequence 7, Appl1	784	32.2	2.2	741	4	US-09-902-540-7127	Sequence 7127, Ap
712	32.4	2.2	1278	4	US-09-252-991A-5750	Sequence 5750, Ap	785	32.2	2.2	945	4	US-09-252-991A-8444	Sequence 8444, Ap
713	32.4	2.2	1401	3	US-09-235-909-1	Sequence 1, Appl1	786	32.2	2.2	1128	4	US-09-023-655-1464	Sequence 1464, App
714	32.4	2.2	1623	4	US-09-902-540-2051	Sequence 2051, Ap	787	32.2	2.2	1161	4	US-09-919-039-388	Sequence 388, App
715	32.4	2.2	1974	4	US-09-902-540-4766	Sequence 4766, Ap	788	32.2	2.2	1209	4	US-09-902-540-9332	Sequence 4332, Ap
716	32.4	2.2	2176	6	5320958-1	Patent No. 5320958	789	32.2	2.2	1229	4	US-09-976-594-1058	Sequence 1058, Ap
717	32.4	2.2	2176	6	5320958-1	Patent No. 5320958	790	32.2	2.2	1239	4	US-09-902-540-5817	Sequence 5817, Ap
718	32.4	2.2	2218	4	US-09-350-457A-1	Sequence 1, Appl1	791	32.2	2.2	1356	4	US-09-252-991A-9233	Sequence 9233, Ap
719	32.4	2.2	3186	4	US-09-397-550-1	Sequence 1, Appl1	792	32.2	2.2	1423	1	US-07-829-954-1	Sequence 1, Appl1
720	32.4	2.2	3248	4	US-09-397-550-2	Sequence 2, Appl1	793	32.2	2.2	1423	1	US-07-994-423-1	Sequence 1, Appl1
721	32.4	2.2	3327	4	US-09-397-550-3	Sequence 3, Appl1	794	32.2	2.2	1423	1	US-08-421-891-1	Sequence 1, Appl1
722	32.4	2.2	5463	3	US-09-470-443-1	Sequence 1, Appl1	795	32.2	2.2	1476	4	US-09-949-016-1726	Sequence 1726, Ap
723	32.4	2.2	5482	3	US-09-470-443-3	Sequence 3, Appl1	796	32.2	2.2	1632	4	US-09-248-796A-599	Sequence 599, App
724	32.4	2.2	5482	4	US-09-397-550-19	Sequence 19, Appl1	797	32.2	2.2	2260	4	US-09-919-039-10	Sequence 10, Appl1
725	32.4	2.2	5674	1	US-07-807-043B-8	Sequence 8, Appl1	798	32.2	2.2	2363	4	US-09-818-780-22	Sequence 22, Appl1
726	32.4	2.2	5674	1	US-08-190-411A-1	Sequence 1, Appl1	799	32.2	2.2	2496	4	US-09-252-991A-8330	Sequence 8330, Ap
727	32.4	2.2	5674	4	US-08-299-849B-8	Sequence 8, Appl1	800	32.2	2.2	2674	3	US-09-513-783A-173	Sequence 173, App
728	32.4	2.2	5674	2	US-08-560-024-1	Sequence 1, Appl1	801	32.2	2.2	2685	4	US-09-949-016-4734	Sequence 4734, Ap
729	32.4	2.2	5674	4	US-08-142-368A-8	Sequence 8, Appl1	802	32.2	2.2	2715	4	US-09-252-991A-8715	Sequence 8715, Ap
730	32.4	2.2	5674	3	US-08-967-727-8	Sequence 8, Appl1	803	32.2	2.2	3126	4	US-09-252-991A-9066	Sequence 9066, Ap
731	32.4	2.2	5674	3	US-08-037-2230D-8	Sequence 8, Appl1	804	32.2	2.2	3960	4	US-09-902-540-8918	Sequence 8918, Ap
732	32.4	2.2	5674	4	US-09-583-850-8	Sequence 8, Appl1	805	32.2	2.2	4326	4	US-09-252-991A-11572	Sequence 11572, A
733	32.4	2.2	5674	4	US-09-579-197-8	Sequence 8, Appl1	806	32.2	2.2	4473	4	US-09-252-991A-11871	Sequence 11871, A
734	32.4	2.2	5674	4	US-09-404-026-8	Sequence 8, Appl1	807	32.2	2.2	6186	3	US-08-961-527-131	Sequence 131, App
735	32.4	2.2	5674	4	US-09-312-464-8	Sequence 8, Appl1	808	32.2	2.2	9097	4	US-09-902-540-947	Sequence 947, App
736	32.4	2.2	5699	4	US-09-949-016-14445	Sequence 14445, A	809	32.2	2.2	9367	4	US-09-902-540-951	Sequence 951, App
737	32.4	2.2	8352	4	US-09-902-540-832	Sequence 14430, A	810	32.2	2.2	11101	4	US-09-902-540-1005	Sequence 1005, App
738	32.4	2.2	8352	4	US-09-902-540-832	Sequence 832, App	811	32.2	2.2	15271	4	US-09-902-540-1051	Sequence 1051, App
739	32.4	2.2	16924	4	US-09-902-540-1178	Sequence 1178, Ap	812	32.2	2.2	26396	4	US-09-949-016-13348	Sequence 1348, A
740	32.4	2.2	32166	4	US-09-562-930-11	Sequence 1235, Ap	813	32.2	2.2	26894	4	US-09-949-016-16800	Sequence 16800, A
741	32.4	2.2	32798	4	US-09-604-694B-1	Sequence 11, Appl1	814	32.2	2.2	28509	4	US-09-902-540-1240	Sequence 1240, Ap
742	32.4	2.2	34303	2	US-08-735-609-4	Sequence 4, Appl1	815	32.2	2.2	30780	4	US-09-902-540-1243	Sequence 1243, Ap
743	32.4	2.2	34303	2	US-08-735-609-4	Sequence 4, Appl1	816	32.2	2.2	30922	4	US-09-949-016-16700	Sequence 16700, A
744	32.4	2.2	34303	2	US-08-735-609-4	Sequence 4, Appl1	817	32.2	2.2	36223	4	US-09-949-016-14417	Sequence 14417, A
745	32.4	2.2	34303	3	US-09-315-372-4	Sequence 4, Appl1	818	32.2	2.2	42276	4	US-09-949-016-17218	Sequence 17218, A
746	32.4	2.2	34303	3	US-09-244-752-4	Sequence 4, Appl1	819	32.2	2.2	61158	4	US-09-949-016-16971	Sequence 16971, A
747	32.4	2.2	34303	3	US-09-245-497-4	Sequence 4, Appl1	820	32.2	2.2	71989	3	US-09-949-016-15041	Sequence 15041, A
748	32.4	2.2	34303	3	US-09-562-919-4	Sequence 4, Appl1	821	32.2	2.2	72704	4	US-09-443-501A-2	Sequence 2, Appl1
749	32.4	2.2	34303	3	US-08-374-483-6	Sequence 6, Appl1	822	32.2	2.2	75431	4	US-09-902-540-1273	Sequence 1273, Ap
750	32.4	2.2	34303	3	US-08-973-334-3	Sequence 3, Appl1	823	32.2	2.2	75431	4	US-09-949-016-15122	Sequence 15122, A
751	32.4	2.2	35408	3	US-09-563-869A-3	Sequence 3, Appl1	824	32.2	2.2	97196	4	US-09-949-016-12212	Sequence 12212, A
752	32.4	2.2	35408	3	US-08-549-489-3	Sequence 3, Appl1	825	32.2	2.2	97196	4	US-09-949-016-16971	Sequence 16971, A
753	32.4	2.2	35871	4	US-09-956-335-2	Sequence 2, Appl1	826	32.2	2.2	118136	4	US-09-949-016-12439	Sequence 12439, A
754	32.4	2.2	35935	2	US-08-735-609-1	Sequence 1, Appl1	827	32.2	2.2	126982	4	US-09-949-016-16597	Sequence 16597, A
755	32.4	2.2	35935	2	US-08-735-609-1	Sequence 1, Appl1	828	32.2	2.2	200	4	US-09-513-999C-22029	Sequence 22029, A
756	32.4	2.2	35935	2	US-08-379-452-43	Sequence 43, Appl1	829	32.2	2.2	363	3	US-09-060-756-159	Sequence 159, App
757	32.4	2.2	35935	3	US-09-315-372-1	Sequence 1, Appl1	830	32.2	2.2	434	4	US-09-670-514-159	Sequence 159, App

C 831	32	2.2	434	4	US-09-270-767-20086	Sequence 20086, A	904	32	2.2	266748	4	US-09-949-016-13188	Sequence 13188, A
C 832	32	2.2	522	4	US-09-252-991A-12063	Sequence 12063, A	905	32	2.2	283538	4	US-09-949-016-13506	Sequence 13506, A
C 833	32	2.2	601	4	US-09-949-016-16344	Sequence 16344, A	906	31.8	2.1	540	4	US-09-252-991A-15565	Sequence 15565, A
C 834	32	2.2	601	4	US-09-949-016-16345	Sequence 16345, A	907	31.8	2.1	564	4	US-09-902-540-4648	Sequence 4648, Ap
C 835	32	2.2	601	4	US-09-949-016-16883	Sequence 16883, A	908	31.8	2.1	601	4	US-09-949-016-19161	Sequence 19161, A
C 836	32	2.2	601	4	US-09-949-016-19011	Sequence 19011, A	909	31.8	2.1	601	4	US-09-949-016-18412	Sequence 18412, A
C 837	32	2.2	601	4	US-09-949-016-19183	Sequence 19183, A	910	31.8	2.1	601	4	US-09-949-016-18116	Sequence 18116, A
C 838	32	2.2	601	4	US-09-949-016-19359	Sequence 19359, A	911	31.8	2.1	601	4	US-09-949-016-15361	Sequence 15361, A
C 839	32	2.2	601	4	US-09-949-016-19662	Sequence 19662, A	912	31.8	2.1	601	4	US-09-949-016-13619	Sequence 13619, A
C 840	32	2.2	601	4	US-09-949-016-19662	Sequence 19662, A	913	31.8	2.1	601	4	US-09-949-016-15361	Sequence 15361, A
C 841	32	2.2	601	4	US-09-949-016-16331	Sequence 16331, A	914	31.8	2.1	601	4	US-09-949-016-15361	Sequence 15361, A
C 842	32	2.2	601	4	US-09-949-016-16331	Sequence 16331, A	915	31.8	2.1	601	4	US-09-949-016-15361	Sequence 15361, A
C 843	32	2.2	622	4	US-09-311-021-161	Sequence 161, Ap	916	31.8	2.1	601	4	US-09-949-016-19406	Sequence 19406, A
C 844	32	2.2	630	4	US-09-252-991A-1585	Sequence 1585, Ap	917	31.8	2.1	601	4	US-09-949-016-19406	Sequence 19406, A
C 845	32	2.2	693	4	US-09-252-991A-12003	Sequence 12003, A	918	31.8	2.1	601	4	US-09-949-016-19406	Sequence 19406, A
C 846	32	2.2	1026	4	US-09-902-540-4562	Sequence 4562, Ap	919	31.8	2.1	601	4	US-09-949-016-14479	Sequence 14479, A
C 847	32	2.2	1071	4	US-09-252-991A-1635	Sequence 1635, Ap	920	31.8	2.1	601	4	US-09-949-016-14480	Sequence 14480, A
C 848	32	2.2	1266	4	US-09-252-991A-15869	Sequence 15869, A	921	31.8	2.1	601	4	US-09-949-016-14480	Sequence 14480, A
C 849	32	2.2	1290	4	US-09-902-540-5641	Sequence 5641, Ap	922	31.8	2.1	601	4	US-09-949-016-14480	Sequence 14480, A
C 850	32	2.2	1292	4	US-09-902-540-127	Sequence 127, Ap	923	31.8	2.1	601	4	US-09-949-016-14480	Sequence 14480, A
C 851	32	2.2	1335	4	US-09-252-991A-1685	Sequence 1685, Ap	924	31.8	2.1	601	4	US-09-949-016-14480	Sequence 14480, A
C 852	32	2.2	1422	4	US-09-489-039A-4425	Sequence 4425, Ap	925	31.8	2.1	601	4	US-09-949-016-14480	Sequence 14480, A
C 853	32	2.2	1695	4	US-09-252-991A-1686	Sequence 1686, Ap	926	31.8	2.1	601	4	US-09-949-016-15151	Sequence 15151, A
C 854	32	2.2	1704	4	US-09-252-991A-11910	Sequence 11910, A	927	31.8	2.1	601	4	US-09-949-016-19181	Sequence 19181, A
C 855	32	2.2	1740	4	US-09-252-991A-1492	Sequence 1492, Ap	928	31.8	2.1	663	4	US-09-252-991A-12910	Sequence 12910, A
C 856	32	2.2	1746	4	US-09-902-540-2679	Sequence 2679, Ap	929	31.8	2.1	918	4	US-09-252-991A-9633	Sequence 9633, Ap
C 857	32	2.2	1746	4	US-09-489-039A-4325	Sequence 4325, Ap	930	31.8	2.1	919	4	US-09-902-540-6400	Sequence 6400, Ap
C 858	32	2.2	1806	4	US-09-252-991A-1534	Sequence 1534, Ap	931	31.8	2.1	951	4	US-09-252-991A-12576	Sequence 12576, A
C 859	32	2.2	1916	4	US-09-252-991A-12032	Sequence 12032, A	932	31.8	2.1	1116	4	US-09-902-540-1551	Sequence 1551, Ap
C 860	32	2.2	2113	4	US-09-573-080A-70	Sequence 70, Ap	933	31.8	2.1	1422	4	US-09-252-991A-15636	Sequence 15636, Ap
C 861	32	2.2	2481	4	US-09-894-998A-35	Sequence 35, Ap	934	31.8	2.1	1689	4	US-09-252-991A-12883	Sequence 12883, A
C 862	32	2.2	2481	4	US-10-237-551-35	Sequence 35, Ap	935	31.8	2.1	1689	4	US-09-902-540-6020	Sequence 6020, Ap
C 863	32	2.2	2560	4	US-09-902-540-7617	Sequence 7617, Ap	936	31.8	2.1	1692	4	US-09-902-540-7344	Sequence 7344, Ap
C 864	32	2.2	2588	2	US-08-796-414B-6	Sequence 6, Ap	937	31.8	2.1	1718	4	US-09-962-665-10	Sequence 10, Ap
C 865	32	2.2	3066	4	US-10-237-551-152	Sequence 152, Ap	938	31.8	2.1	1718	4	US-09-963-333-10	Sequence 10, Ap
C 866	32	2.2	3252	4	US-09-902-540-9254	Sequence 9254, Ap	939	31.8	2.1	1722	4	US-09-962-677-10	Sequence 10, Ap
C 867	32	2.2	3293	4	US-09-949-016-14658	Sequence 14658, Ap	940	31.8	2.1	1722	4	US-09-902-540-1332	Sequence 1332, Ap
C 868	32	2.2	3314	4	US-09-949-016-836	Sequence 836, Ap	941	31.8	2.1	2082	4	US-09-818-780-67	Sequence 67, Ap
C 869	32	2.2	3372	4	US-09-949-016-165	Sequence 165, Ap	942	31.8	2.1	2453	4	US-09-902-540-129	Sequence 129, Ap
C 870	32	2.2	3390	4	US-09-252-991A-11961	Sequence 11961, A	943	31.8	2.1	3592	4	US-09-814-351-7	Sequence 7, Ap
C 871	32	2.2	3396	3	US-08-974-549A-638	Sequence 638, Ap	944	31.8	2.1	3654	4	US-09-252-991A-9533	Sequence 9533, Ap
C 872	32	2.2	3396	4	US-09-721-456-638	Sequence 638, Ap	945	31.8	2.1	3957	4	US-10-237-551-193	Sequence 193, Ap
C 873	32	2.2	3716	4	US-09-949-016-14682	Sequence 14682, Ap	946	31.8	2.1	4084	4	US-09-949-016-570	Sequence 570, Ap
C 874	32	2.2	5017	4	US-09-902-540-748	Sequence 748, Ap	947	31.8	2.1	4084	4	US-09-949-016-1163	Sequence 1163, Ap
C 875	32	2.2	5773	4	US-09-566-921-112	Sequence 112, Ap	948	31.8	2.1	4561	4	US-09-902-540-700	Sequence 700, Ap
C 876	32	2.2	10322	4	US-09-902-540-989	Sequence 989, Ap	949	31.8	2.1	5847	4	US-09-962-665-11	Sequence 11, Ap
C 877	32	2.2	17622	4	US-09-902-540-1125	Sequence 1125, Ap	950	31.8	2.1	5847	4	US-09-963-333-11	Sequence 11, Ap
C 878	32	2.2	20187	4	US-09-902-540-1186	Sequence 1186, Ap	951	31.8	2.1	5847	4	US-09-962-677-11	Sequence 11, Ap
C 879	32	2.2	24905	4	US-09-902-540-1225	Sequence 1225, Ap	952	31.8	2.1	8310	4	US-09-902-540-1001	Sequence 1001, Ap
C 880	32	2.2	28804	2	US-08-592-874-1	Sequence 1, Ap	953	31.8	2.1	8438	1	US-07-945-283-1	Sequence 1, Ap
C 881	32	2.2	28804	3	US-09-056-942-2	Sequence 2, Ap	954	31.8	2.1	11321	4	US-09-949-016-13466	Sequence 13466, A
C 882	32	2.2	28804	3	US-09-056-867-2	Sequence 2, Ap	955	31.8	2.1	12703	4	US-09-949-016-16685	Sequence 16685, A
C 883	32	2.2	29927	4	US-09-949-016-1814	Sequence 1814, A	956	31.8	2.1	12703	4	US-09-949-016-16339	Sequence 16339, A
C 884	32	2.2	29927	4	US-09-949-016-17474	Sequence 17474, A	957	31.8	2.1	16073	4	US-09-949-016-12312	Sequence 12312, A
C 885	32	2.2	29927	4	US-09-949-016-17475	Sequence 17475, A	958	31.8	2.1	16073	4	US-09-949-016-12905	Sequence 12905, A
C 886	32	2.2	31111	4	US-09-949-016-15628	Sequence 15628, A	959	31.8	2.1	17228	4	US-09-902-540-1170	Sequence 1170, Ap
C 887	32	2.2	31440	4	US-09-949-016-12578	Sequence 12578, A	960	31.8	2.1	20966	4	US-09-776-976-7	Sequence 7, Ap
C 888	32	2.2	31440	4	US-09-949-016-16400	Sequence 16400, A	961	31.8	2.1	20966	4	US-09-909-547-7	Sequence 7, Ap
C 889	32	2.2	37804	4	US-09-949-016-12639	Sequence 12639, A	962	31.8	2.1	20966	4	US-09-559-8528-1	Sequence 1, Ap
C 890	32	2.2	38954	4	US-09-949-016-12292	Sequence 12292, A	963	31.8	2.1	22218	4	US-09-949-016-14280	Sequence 14280, A
C 891	32	2.2	53332	4	US-09-801-861-3	Sequence 3, Ap	964	31.8	2.1	24984	4	US-09-949-016-14950	Sequence 14950, A
C 892	32	2.2	53332	4	US-10-224-562-3	Sequence 3, Ap	965	31.8	2.1	26930	4	US-09-902-540-1228	Sequence 1228, Ap
C 893	32	2.2	100863	4	US-09-949-016-17031	Sequence 17031, A	966	31.8	2.1	32379	4	US-09-949-016-15217	Sequence 15217, A
C 894	32	2.2	102409	4	US-09-949-016-15148	Sequence 15148, A	967	31.8	2.1	32379	4	US-09-949-016-15218	Sequence 15218, A
C 895	32	2.2	119930	4	US-09-949-016-12677	Sequence 12677, A	968	31.8	2.1	32379	4	US-09-949-016-15219	Sequence 15219, A
C 896	32	2.2	119931	4	US-09-949-016-16319	Sequence 16319, A	969	31.8	2.1	32379	4	US-09-949-016-15220	Sequence 15220, A
C 897	32	2.2	125536	4	US-09-949-016-14186	Sequence 14186, A	970	31.8	2.1	32379	4	US-09-949-016-15221	Sequence 15221, A
C 898	32	2.2	141560	4	US-09-949-016-15475	Sequence 15475, A	971	31.8	2.1	32379	4	US-09-949-016-15222	Sequence 15222, A
C 899	32	2.2	177251	4	US-09-949-016-15841	Sequence 15841, A	972	31.8	2.1	32379	4	US-09-949-016-15223	Sequence 15223, A
C 900	32	2.2	192302	4	US-09-949-016-15270	Sequence 15270, A	973	31.8	2.1	32379	4	US-09-949-016-15224	Sequence 15224, A
C 901	32	2.2	251769	4	US-09-949-016-13185	Sequence 13185, A	974	31.8	2.1	32379	4	US-09-949-016-15225	Sequence 15225, A
C 902	32	2.2	251769	4	US-09-949-016-13186	Sequence 13186, A	975	31.8	2.1	32379	4	US-09-949-016-15226	Sequence 15226, A
C 903	32	2.2	266748	4	US-09-949-016-13187	Sequence 13187, A	976	31.8	2.1	45587	4	US-09-949-016-15836	Sequence 15836, A

977	31.8	2.1	57392	4	US-09-949-016-12070	Sequence 12070, A	1050	31.6	2.1	2795	4	US-09-291-417D-25	Sequence 25, Appl
978	31.8	2.1	57400	4	US-09-949-016-13293	Sequence 13293, A	1051	31.6	2.1	2962	4	US-09-688-188B-106	Sequence 106, App
979	31.8	2.1	59240	4	US-09-949-016-11933	Sequence 11933, A	1052	31.6	2.1	2962	4	US-09-291-417D-106	Sequence 106, App
980	31.8	2.1	64377	4	US-09-949-016-15212	Sequence 15212, A	1053	31.6	2.1	3664	4	US-09-949-016-633	Sequence 433, App
981	31.8	2.1	64377	4	US-09-949-016-15213	Sequence 15213, A	1054	31.6	2.1	3674	4	US-09-902-540-9155	Sequence 9155, App
982	31.8	2.1	64377	4	US-09-949-016-15214	Sequence 15214, A	1055	31.6	2.1	4056	4	US-09-489-039A-3861	Sequence 3861, App
983	31.8	2.1	64377	4	US-09-949-016-15215	Sequence 15215, A	1056	31.6	2.1	4221	4	US-09-949-016-809	Sequence 809, App
984	31.8	2.1	64377	4	US-09-949-016-15216	Sequence 15216, A	1057	31.6	2.1	4495	3	US-09-417-822-6	Sequence 6, Appl
985	31.8	2.1	87350	3	US-09-781-891-79	Sequence 79, Appl	1058	31.6	2.1	4495	4	US-09-957-837A-6	Sequence 6, Appl
986	31.8	2.1	87350	4	US-09-618-166-79	Sequence 79, Appl	1059	31.6	2.1	4534	3	US-09-417-822-7	Sequence 7, Appl
987	31.8	2.1	87543	3	US-09-791-211-3	Sequence 3, Appl	1060	31.6	2.1	4534	4	US-09-957-837A-7	Sequence 7, Appl
988	31.8	2.1	113701	4	US-09-949-016-13214	Sequence 13214, A	1061	31.6	2.1	4535	3	US-09-417-822-8	Sequence 8, Appl
989	31.8	2.1	134890	4	US-09-949-016-15602	Sequence 15602, A	1062	31.6	2.1	4808	4	US-09-957-837A-8	Sequence 8, Appl
990	31.8	2.1	156324	4	US-09-949-016-13749	Sequence 13749, A	1063	31.6	2.1	4808	4	US-09-902-540-689	Sequence 689, App
991	31.8	2.1	187916	4	US-09-949-016-12980	Sequence 12980, A	1064	31.6	2.1	4825	4	US-09-902-540-692	Sequence 692, App
992	31.8	2.1	190078	4	US-09-949-016-12707	Sequence 12707, A	1065	31.6	2.1	4944	1	US-08-623-679-6	Sequence 6, Appl
993	31.8	2.1	190078	4	US-09-949-016-17026	Sequence 17026, A	1066	31.6	2.1	4944	3	US-08-933-774-6	Sequence 6, Appl
994	31.8	2.1	192956	4	US-09-949-016-14382	Sequence 14382, A	1067	31.6	2.1	4944	3	US-09-181-030-6	Sequence 6, Appl
995	31.8	2.1	237510	4	US-09-949-016-14273	Sequence 14273, A	1068	31.6	2.1	4944	3	US-09-534-242-6	Sequence 6, Appl
996	31.8	2.1	784019	4	US-09-949-016-14033	Sequence 14033, A	1069	31.6	2.1	4944	3	US-09-454-854-6	Sequence 6, Appl
997	31.8	2.1	828152	4	US-09-949-016-12777	Sequence 12777, A	1070	31.6	2.1	4944	4	US-09-154-671-6	Sequence 6, Appl
998	31.6	2.1	217	2	US-08-332-766A-4	Sequence 4, Appl	1071	31.6	2.1	4944	4	US-09-182-113-6	Sequence 6, Appl
999	31.6	2.1	284	2	US-09-621-976-13655	Sequence 13655, A	1072	31.6	2.1	4944	4	US-08-862-442-6	Sequence 6, Appl
C 1000	31.6	2.1	348	2	US-08-623-906A-14	Sequence 14, Appl	1073	31.6	2.1	5055	1	US-08-623-679-8	Sequence 8, Appl
C 1001	31.6	2.1	432	4	US-09-252-991A-3530	Sequence 3530, Ap	1074	31.6	2.1	5055	3	US-08-933-774-8	Sequence 8, Appl
1002	31.6	2.1	489	4	US-09-902-540-19754	Sequence 19754, A	1075	31.6	2.1	5055	3	US-09-181-030-8	Sequence 8, Appl
1003	31.6	2.1	601	4	US-09-949-016-19754	Sequence 19754, A	1076	31.6	2.1	5055	3	US-09-534-242-8	Sequence 8, Appl
C 1004	31.6	2.1	601	4	US-09-949-016-28142	Sequence 28142, A	1077	31.6	2.1	5055	3	US-09-454-854-8	Sequence 8, Appl
C 1005	31.6	2.1	601	4	US-09-949-016-28143	Sequence 28143, A	1078	31.6	2.1	5055	3	US-09-164-671-8	Sequence 8, Appl
C 1006	31.6	2.1	601	4	US-09-949-016-28144	Sequence 28144, A	1079	31.6	2.1	5055	4	US-09-182-113-8	Sequence 8, Appl
C 1007	31.6	2.1	601	4	US-09-949-016-28145	Sequence 28145, A	1080	31.6	2.1	5055	4	US-08-862-442-8	Sequence 8, Appl
C 1008	31.6	2.1	601	4	US-09-949-016-41097	Sequence 41097, A	1081	31.6	2.1	5408	1	US-08-441-139-15	Sequence 15, Appl
C 1009	31.6	2.1	601	4	US-09-949-016-41098	Sequence 41098, A	1082	31.6	2.1	7336	4	US-09-949-016-13935	Sequence 13935, A
C 1010	31.6	2.1	601	4	US-09-949-016-41099	Sequence 41099, A	1083	31.6	2.1	8321	4	US-09-902-540-979	Sequence 979, App
C 1011	31.6	2.1	601	4	US-09-949-016-41100	Sequence 41100, A	1084	31.6	2.1	8838	3	US-09-417-822-1	Sequence 1, Appl
C 1012	31.6	2.1	601	4	US-09-949-016-81973	Sequence 81973, A	1085	31.6	2.1	8838	4	US-09-957-837A-1	Sequence 1, Appl
C 1013	31.6	2.1	601	4	US-09-949-016-174173	Sequence 174173, A	1086	31.6	2.1	10280	4	US-09-902-540-980	Sequence 980, App
C 1014	31.6	2.1	601	4	US-09-949-016-174174	Sequence 174174, A	1087	31.6	2.1	13335	4	US-09-949-016-14676	Sequence 14676, A
C 1015	31.6	2.1	601	4	US-09-949-016-174365	Sequence 174365, A	1088	31.6	2.1	15535	4	US-09-949-016-17225	Sequence 17225, A
C 1016	31.6	2.1	601	4	US-09-949-016-174366	Sequence 174366, A	1089	31.6	2.1	16073	4	US-09-949-016-12312	Sequence 12312, A
C 1017	31.6	2.1	601	4	US-09-949-016-191466	Sequence 191466, A	1090	31.6	2.1	16073	4	US-09-949-016-12905	Sequence 12905, A
C 1018	31.6	2.1	601	4	US-09-949-016-191467	Sequence 191467, A	1091	31.6	2.1	16387	4	US-09-902-540-1156	Sequence 1156, App
C 1019	31.6	2.1	601	4	US-09-949-016-191468	Sequence 191468, A	1092	31.6	2.1	17125	4	US-09-902-540-1168	Sequence 1168, App
C 1020	31.6	2.1	601	4	US-09-949-016-191469	Sequence 191469, A	1093	31.6	2.1	19237	4	US-09-949-016-13657	Sequence 13657, A
C 1021	31.6	2.1	601	4	US-09-949-016-191470	Sequence 191470, A	1094	31.6	2.1	19383	4	US-09-949-016-16031	Sequence 16031, A
C 1022	31.6	2.1	601	4	US-09-949-016-191471	Sequence 191471, A	1095	31.6	2.1	19472	4	US-09-949-016-13223	Sequence 13223, A
1023	31.6	2.1	634	1	US-08-451-947-1	Sequence 1, Appl	1096	31.6	2.1	21196	4	US-09-949-016-14670	Sequence 14670, A
1024	31.6	2.1	634	2	US-08-424-826A-1	Sequence 1, Appl	1097	31.6	2.1	27150	4	US-09-949-016-17378	Sequence 17378, A
1025	31.6	2.1	634	3	US-08-928-694-1	Sequence 1, Appl	1098	31.6	2.1	27525	4	US-09-949-016-16835	Sequence 16835, A
1026	31.6	2.1	634	4	US-08-450-842-1	Sequence 1, Appl	1099	31.6	2.1	28862	4	US-09-949-016-16793	Sequence 16793, A
1027	31.6	2.1	634	4	US-08-451-390-1	Sequence 1, Appl	1100	31.6	2.1	30000	4	US-10-007-010-10	Sequence 10, Appl
1028	31.6	2.1	634	5	PCT-US91-06950-1	Sequence 1, Appl	1101	31.6	2.1	30001	1	US-08-125-468-1	Sequence 1, Appl
1029	31.6	2.1	789	4	US-09-902-540-3374	Sequence 3374, Ap	1102	31.6	2.1	30001	2	US-08-474-933-1	Sequence 1, Appl
1030	31.6	2.1	867	4	US-09-482-273-50	Sequence 50, Appl	1103	31.6	2.1	37254	4	US-09-949-016-15973	Sequence 15973, A
C 1031	31.6	2.1	927	4	US-09-252-991A-2499	Sequence 2499, Ap	1104	31.6	2.1	37875	4	US-09-949-016-13782	Sequence 13782, A
C 1032	31.6	2.1	1149	4	US-09-902-540-6250	Sequence 6250, Ap	1105	31.6	2.1	44459	4	US-09-949-016-12711	Sequence 12711, A
C 1033	31.6	2.1	1207	3	US-09-417-882-42	Sequence 42, Appl	1106	31.6	2.1	51967	4	US-09-949-016-16982	Sequence 16982, A
C 1034	31.6	2.1	1207	4	US-09-957-837A-42	Sequence 42, Appl	1107	31.6	2.1	53366	4	US-09-949-016-12500	Sequence 12500, A
C 1035	31.6	2.1	1353	4	US-09-902-540-9159	Sequence 9159, Ap	1108	31.6	2.1	53337	4	US-09-949-016-16082	Sequence 16082, A
1036	31.6	2.1	1393	1	US-07-602-824A-1	Sequence 1, Appl	1109	31.6	2.1	67911	4	US-09-949-016-15976	Sequence 15976, A
1037	31.6	2.1	1393	1	US-07-983-451-1	Sequence 1, Appl	1110	31.6	2.1	76124	4	US-09-949-016-15976	Sequence 15976, A
1038	31.6	2.1	1393	1	US-08-261-577-6	Sequence 6, Appl	1111	31.6	2.1	82494	4	US-09-949-016-16937	Sequence 16937, A
1039	31.6	2.1	1404	1	US-07-796-106-32	Sequence 22, Appl	1112	31.6	2.1	109159	4	US-09-949-016-14169	Sequence 14169, A
C 1040	31.6	2.1	1408	3	US-09-180-109A-5	Sequence 5, Appl	1113	31.6	2.1	109159	4	US-09-949-016-14170	Sequence 14170, A
C 1041	31.6	2.1	1408	3	US-09-180-109A-7	Sequence 7, Appl	1114	31.6	2.1	113042	4	US-09-949-016-12543	Sequence 12543, A
C 1042	31.6	2.1	1501	3	US-09-902-540-271	Sequence 271, App	1115	31.6	2.1	113042	4	US-09-949-016-15246	Sequence 15246, A
C 1043	31.6	2.1	1525	4	US-09-964-895-3	Sequence 3, Appl	1116	31.6	2.1	152914	4	US-09-949-016-15578	Sequence 15578, A
C 1044	31.6	2.1	1571	2	US-08-145-658D-21	Sequence 21, Appl	1117	31.6	2.1	177797	4	US-09-949-016-14125	Sequence 14125, A
C 1045	31.6	2.1	2351	4	US-09-902-540-344	Sequence 344, App	1118	31.6	2.1	220296	4	US-09-949-016-11842	Sequence 11842, A
C 1046	31.6	2.1	2412	4	US-09-489-039A-5571	Sequence 5571, Ap	1119	31.6	2.1	260293	4	US-09-949-016-17037	Sequence 17037, A
1047	31.6	2.1	2538	4	US-09-489-039A-6419	Sequence 6419, Ap	1120	31.6	2.1	260293	4	US-09-949-016-12106	Sequence 12106, A
C 1048	31.6	2.1	2567	4	US-09-902-540-7310	Sequence 7310, Ap	1121	31.6	2.1	317366	4	US-09-949-016-16001	Sequence 16001, A
1049	31.6	2.1	2795	4	US-09-688-188B-25	Sequence 25, Appl	1122	31.6	2.1	336024	4	US-09-949-016-12373	Sequence 12373, A

C1123	31.6	2.1	390416	4	US-09-949-016-16923	Sequence 16923, A	1196	31.4	2.1	119982	4	US-09-949-016-13606	Sequence 13606, A
1154	31.6	2.1	786431	4	US-09-751-389-3	Sequence 3, Appl1	1197	31.4	2.1	325034	4	US-09-949-016-14957	Sequence 14957, A
1125	31.4	2.1	285	4	US-09-902-540-1950	Sequence 1950, Ap	1198	31.4	2.1	389504	4	US-09-949-016-11774	Sequence 11774, A
C1126	31.4	2.1	336	4	US-09-902-540-7416	Sequence 7416, Ap	C1199	31.2	2.1	259	4	US-09-313-294A-3922	Sequence 3922, Ap
C1127	31.4	2.1	358	2	US-08-454-557C-15	Sequence 15, Appl	C1200	31.2	2.1	301	2	US-08-333-766A-23	Sequence 23, Appl
C1128	31.4	2.1	358	2	US-08-340-426D-15	Sequence 15, Appl	1201	31.2	2.1	315	3	US-09-060-756-46	Sequence 46, Appl
C1129	31.4	2.1	358	2	US-08-450-673C-15	Sequence 15, Appl	1202	31.2	2.1	315	4	US-09-670-314-46	Sequence 46, Appl
C1130	31.4	2.1	358	5	PCR-US95-1711A-15	Sequence 15, Appl	C1203	31.2	2.1	315	4	US-09-248-796A-12307	Sequence 12307, A
1131	31.4	2.1	570	4	US-09-266-965-20	Sequence 20, Appl	1204	31.2	2.1	324	3	US-09-008-481A-5	Sequence 5, Appl1
1132	31.4	2.1	601	4	US-09-949-016-29160	Sequence 29160, A	1205	31.2	2.1	324	3	US-09-008-481A-14	Sequence 14, Appl
1133	31.4	2.1	601	4	US-09-949-016-41115	Sequence 41115, A	1206	31.2	2.1	324	3	US-09-309-592-5	Sequence 5, Appl1
C1134	31.4	2.1	601	4	US-09-949-016-77650	Sequence 77650, A	1207	31.2	2.1	324	3	US-09-309-592-5	Sequence 14, Appl
1135	31.4	2.1	831	4	US-09-902-540-4202	Sequence 4202, Ap	C1208	31.2	2.1	342	4	US-09-902-540-4243	Sequence 4243, Ap
C1136	31.4	2.1	894	4	US-09-902-540-6843	Sequence 6843, Ap	C1209	31.2	2.1	399	4	US-09-621-976-6976	Sequence 8976, Ap
C1137	31.4	2.1	1017	4	US-09-252-991A-11927	Sequence 11927, A	C1210	31.2	2.1	420	4	US-09-585-645A-3	Sequence 3, Appl1
C1138	31.4	2.1	1071	2	US-08-997-080-180	Sequence 180, App	1211	31.2	2.1	474	4	US-09-252-991A-8385	Sequence 8385, Ap
C1139	31.4	2.1	1071	2	US-08-997-362-180	Sequence 180, App	C1212	31.2	2.1	504	4	US-09-252-991A-3681	Sequence 3681, Ap
C1140	31.4	2.1	1071	3	US-09-095-885-180	Sequence 180, App	C1213	31.2	2.1	601	4	US-09-949-016-81519	Sequence 81519, A
C1141	31.4	2.1	1071	3	US-09-324-542-180	Sequence 180, App	C1214	31.2	2.1	601	4	US-09-949-016-81629	Sequence 81629, A
C1142	31.4	2.1	1071	3	US-09-205-426-180	Sequence 180, App	C1215	31.2	2.1	601	4	US-09-949-016-85094	Sequence 85094, A
1143	31.4	2.1	1110	4	US-09-252-991A-12079	Sequence 12079, A	C1216	31.2	2.1	601	4	US-09-949-016-85245	Sequence 85245, A
1144	31.4	2.1	1281	4	US-09-620-312D-849	Sequence 3710, App	C1217	31.2	2.1	601	4	US-09-949-016-122719	Sequence 122719, A
1145	31.4	2.1	1305	4	US-09-902-540-3710	Sequence 3710, Ap	C1218	31.2	2.1	601	4	US-09-949-016-165849	Sequence 165849, A
C1146	31.4	2.1	1458	4	US-09-252-991A-12019	Sequence 12019, A	C1220	31.2	2.1	601	4	US-09-949-016-173781	Sequence 173781, A
C1147	31.4	2.1	1502	4	US-09-902-540-6160	Sequence 6160, Ap	C1226	31.2	2.1	601	4	US-09-949-016-185608	Sequence 185608, A
C1148	31.4	2.1	1608	4	US-09-365-247-24	Sequence 301, App	1221	31.2	2.1	601	4	US-09-949-016-407	Sequence 407, App
1149	31.4	2.1	1608	4	US-09-365-247-24	Sequence 24, Appl	1222	31.2	2.1	601	4	US-09-298-731-46	Sequence 46, Appl
C1150	31.4	2.1	1661	4	US-09-436-521A-1	Sequence 1, Appl1	1223	31.2	2.1	913	3	US-09-298-731-46	Sequence 112, App
C1151	31.4	2.1	1675	4	US-09-902-540-302	Sequence 302, App	1224	31.2	2.1	925	4	US-09-461-345-112	Sequence 112, App
C1152	31.4	2.1	1686	4	US-09-724-797-9	Sequence 9, Appl1	1225	31.2	2.1	925	4	US-10-012-542-112	Sequence 112, App
C1153	31.4	2.1	1701	4	US-09-902-540-9608	Sequence 9608, Ap	1226	31.2	2.1	925	4	US-10-115-123-112	Sequence 112, App
C1154	31.4	2.1	1869	4	US-09-489-039A-4200	Sequence 4200, Ap	C1227	31.2	2.1	954	4	US-09-902-540-4253	Sequence 4253, Ap
1155	31.4	2.1	2328	4	US-09-949-016-762	Sequence 762, App	C1228	31.2	2.1	963	4	US-09-902-540-4323	Sequence 4323, Ap
C1156	31.4	2.1	2397	1	US-07-891-942G-11	Sequence 11, Appl	1229	31.2	2.1	1188	4	US-09-902-540-5280	Sequence 9280, Ap
1157	31.4	2.1	2561	4	US-09-616-289-48	Sequence 48, Appl	1230	31.2	2.1	1242	4	US-09-902-540-5329	Sequence 5329, Ap
1158	31.4	2.1	3899	4	US-09-902-540-573	Sequence 573, App	1231	31.2	2.1	1260	1	US-08-029-404-1	Sequence 1, Appl1
1159	31.4	2.1	3934	3	US-09-226-568-18	Sequence 18, Appl	1232	31.2	2.1	1260	3	US-08-459-953A-1	Sequence 1, Appl1
1160	31.4	2.1	3946	1	US-08-077-848A-1	Sequence 1, Appl1	1233	31.2	2.1	1260	4	US-09-393-212-1	Sequence 1, Appl1
1161	31.4	2.1	3946	3	US-09-211-640-1	Sequence 1, Appl1	1234	31.2	2.1	1284	3	US-09-319-648-16	Sequence 16, Appl
1162	31.4	2.1	3946	3	US-09-378-538-1	Sequence 1, Appl1	1235	31.2	2.1	1284	4	US-09-023-655-1182	Sequence 1182, Ap
1163	31.4	2.1	3946	4	US-09-687-260-1	Sequence 1, Appl1	1236	31.2	2.1	1293	1	US-08-924-440-1	Sequence 1, Appl1
C1164	31.4	2.1	3946	5	PCR-US94-03547-1	Sequence 1, Appl1	1237	31.2	2.1	1371	4	US-09-949-016-2236	Sequence 2236, Ap
C1165	31.4	2.1	4852	1	US-07-853-913-3	Sequence 3, Appl1	1238	31.2	2.1	1385	4	US-09-949-016-2373	Sequence 2373, Ap
C1166	31.4	2.1	5245	4	US-09-902-540-714	Sequence 714, App	C1239	31.2	2.1	1385	4	US-08-932-411A-17	Sequence 17, Appl
C1167	31.4	2.1	5649	4	US-09-949-016-14408	Sequence 14408, A	C1240	31.2	2.1	1385	4	US-08-585-645A-30	Sequence 30, Appl
1168	31.4	2.1	6436	4	US-09-600-099-1	Sequence 1, Appl1	C1241	31.2	2.1	1407	4	US-09-902-540-6637	Sequence 6637, Ap
C1170	31.4	2.1	6757	4	US-09-023-655-1087	Sequence 1087, Ap	C1242	31.2	2.1	1412	4	US-09-585-645A-6	Sequence 6, Appl1
C1171	31.4	2.1	12128	4	US-09-949-016-12587	Sequence 12587, A	C1243	31.2	2.1	1442	4	US-09-585-645A-37	Sequence 37, Appl
1172	31.4	2.1	12129	4	US-09-949-016-15713	Sequence 15713, A	1244	31.2	2.1	1446	2	US-08-933-750C-91	Sequence 91, Appl
1173	31.4	2.1	12194	4	US-09-902-540-1091	Sequence 1091, Ap	1245	31.2	2.1	1446	3	US-09-234-613-91	Sequence 91, Appl
C1174	31.4	2.1	12249	4	US-09-266-965-74	Sequence 74, Appl	C1246	31.2	2.1	1458	4	US-09-902-540-3540	Sequence 3540, Ap
C1175	31.4	2.1	12608	4	US-09-949-016-15533	Sequence 15533, A	1247	31.2	2.1	1506	4	US-09-902-540-9624	Sequence 9624, Ap
C1176	31.4	2.1	17807	4	US-09-949-016-12779	Sequence 12779, A	1248	31.2	2.1	1515	4	US-09-252-991A-3746	Sequence 3746, Ap
C1177	31.4	2.1	17864	4	US-09-949-016-15511	Sequence 15511, A	1249	31.2	2.1	1524	4	US-09-795-927-9	Sequence 9, Appl
1178	31.4	2.1	18031	4	US-09-902-540-1180	Sequence 1180, Ap	C1250	31.2	2.1	1587	4	US-09-010-147B-19	Sequence 19, Appl
C1179	31.4	2.1	18331	4	US-09-266-965-96	Sequence 96, Appl	1251	31.2	2.1	1649	2	US-08-845-566-2	Sequence 2, Appl1
C1180	31.4	2.1	21330	4	US-09-902-540-1109	Sequence 1209, App	1252	31.2	2.1	1673	4	US-09-949-016-2544	Sequence 2544, Ap
1186	31.4	2.1	85850	4	US-09-949-016-13424	Sequence 13424, A	C1253	31.2	2.1	1673	4	US-09-949-016-2921	Sequence 2921, Ap
C1187	31.4	2.1	88245	4	US-09-949-016-13835	Sequence 13835, A	1254	31.2	2.1	1673	3	US-09-153-804-10	Sequence 10, Appl
1188	31.4	2.1	94133	4	US-09-949-016-11901	Sequence 11901, A	C1261	31.2	2.1	1724	4	US-09-620-312D-650	Sequence 650, App
C1189	31.4	2.1	94133	4	US-09-949-016-12713	Sequence 12713, A	1262	31.2	2.1	1761	4	US-09-252-991A-8423	Sequence 8423, App
1190	31.4	2.1	94133	4	US-09-949-016-15934	Sequence 15934, A	1263	31.2	2.1	1825	4	US-09-976-594-48	Sequence 673, App
1191	31.4	2.1	94133	4	US-09-949-016-15935	Sequence 15935, A	C1264	31.2	2.1	1859	3	US-09-399-913-30	Sequence 30, Appl
1192	31.4	2.1	94133	4	US-09-949-016-15936	Sequence 15936, A	1265	31.2	2.1	1859	3	US-09-298-731-23	Sequence 23, Appl
C1193	31.4	2.1	94135	4	US-09-949-016-15937	Sequence 15937, A	1266	31.2	2.1	1859	4	US-09-350-614-23	Sequence 23, Appl
C1194	31.4	2.1	105055	4	US-09-949-016-14001	Sequence 14001, A	1267	31.2	2.1	1896	4	US-09-461-325-17	Sequence 37, Appl
1195	31.4	2.1	119981	4	US-09-949-016-11844	Sequence 11844, A	1268	31.2	2.1	1896	4	US-10-012-542-37	Sequence 37, Appl

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c1270	31.2	2.1	1908	4	US-09-252-991A-3727	Sequence 3727, Ap	c1343	31.2	2.1	278866	4	US-09-949-016-13922	Sequence 13922, A
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c1281	31.2	2.1	2207	4	US-09-949-016-5071	Sequence 5071, Ap	c1354	31.2	2.1	304533	4	US-09-949-016-15372	Sequence 15372, A
1282	31.2	2.1	2222	4	US-09-795-927-11	Sequence 11, Appl	c1355	31.2	2.1	312957	4	US-09-949-001-31	Sequence 31, Appl
1283	31.2	2.1	2270	4	US-09-731-030A-10	Sequence 10, Appl	c1356	31.2	2.1	421494	4	US-09-949-016-12805	Sequence 12805, A
1284	31.2	2.1	2341	4	US-09-902-540-395	Sequence 395, App	c1357	31.2	2.1	421494	4	US-09-949-016-14060	Sequence 14060, A
c1285	31.2	2.1	2348	4	US-09-658-688A-3	Sequence 3, Appl1	c1358	31.2	2.1	421494	4	US-09-902-540-6919	Sequence 6919, Ap
c1286	31.2	2.1	2444	4	US-09-482-273-100	Sequence 100, App	c1359	31.2	2.1	251	4	US-09-621-976-14639	Sequence 14639, A
c1287	31.2	2.1	2621	4	US-09-799-451-743	Sequence 743, App	c1360	31	2.1	211	4	US-09-313-294A-1739	Sequence 1739, Ap
1288	31.2	2.1	2712	4	US-09-902-540-4301	Sequence 4301, Ap	c1361	31	2.1	270	2	US-08-332-766A-16	Sequence 16, Appl
c1289	31.2	2.1	2911	3	US-08-981-825-5	Sequence 5, Appl1	c1362	31	2.1	445	4	US-08-332-991A-15507	Sequence 15507, A
c1290	31.2	2.1	2911	3	US-09-480-784-5	Sequence 5, Appl1	c1363	31	2.1	549	4	US-09-792-568-3	Sequence 3, Appl1
c1291	31.2	2.1	3049	4	US-09-300-958A-42	Sequence 42, Appl	c1364	31	2.1	570	4	US-09-501-115-39	Sequence 39, Appl
1292	31.2	2.1	3049	4	US-09-949-016-991	Sequence 991, App	c1365	31	2.1	580	4	US-09-252-991A-15455	Sequence 15455, A
1293	31.2	2.1	3169	4	US-09-620-312D-713	Sequence 713, App	c1366	31	2.1	591	4	US-09-949-016-6784	Sequence 26784, A
c1294	31.2	2.1	3300	4	US-09-482-273-68	Sequence 68, App	c1367	31	2.1	601	4	US-09-949-016-68398	Sequence 58398, A
1295	31.2	2.1	3778	4	US-09-799-451-160	Sequence 160, App	c1368	31	2.1	601	4	US-09-949-016-68399	Sequence 58399, A
c1296	31.2	2.1	3893	4	US-09-799-451-21	Sequence 21, Appl	c1369	31	2.1	601	4	US-09-949-016-68360	Sequence 68360, A
1297	31.2	2.1	5919	4	US-08-875-435B-2	Sequence 9, Appl1	c1370	31	2.1	601	4	US-09-949-016-80104	Sequence 80104, A
1298	31.2	2.1	6043	4	US-09-989-981A-9	Sequence 9, Appl1	c1371	31	2.1	601	4	US-09-949-016-80104	Sequence 80104, A
c1299	31.2	2.1	6507	4	US-09-949-016-15053	Sequence 15053, A	c1372	31	2.1	601	4	US-09-949-016-87648	Sequence 87648, A
c1300	31.2	2.1	7201	4	US-09-902-540-914	Sequence 914, App	c1373	31	2.1	684	4	US-09-949-016-183033	Sequence 183033, A
1301	31.2	2.1	8009	4	US-09-949-016-14978	Sequence 9478, A	c1374	31	2.1	702	4	US-09-902-540-6731	Sequence 6731, Ap
1302	31.2	2.1	9818	4	US-09-902-540-987	Sequence 987, App	c1375	31	2.1	748	3	US-09-902-540-6731	Sequence 6731, Ap
1303	31.2	2.1	10321	4	US-09-949-016-13587	Sequence 13587, A	c1376	31	2.1	748	3	US-08-998-416-434	Sequence 416, App
c1304	31.2	2.1	10717	4	US-09-949-016-11587	Sequence 991, App	c1377	31	2.1	902	4	US-09-949-016-51170	Sequence 5170, App
1305	31.2	2.1	11280	4	US-09-949-016-15203	Sequence 15203, A	c1378	31	2.1	945	3	US-09-268-364-3	Sequence 3, Appl
1306	31.2	2.1	11280	4	US-09-949-016-15204	Sequence 15204, A	c1379	31	2.1	1011	4	US-09-902-540-1143	Sequence 1143, A
1307	31.2	2.1	11585	2	US-08-687-080-105	Sequence 105, App	c1380	31	2.1	1144	4	US-09-640-211A-154	Sequence 154, App
1308	31.2	2.1	12631	4	US-09-902-540-1092	Sequence 1092, App	c1381	31	2.1	1281	4	US-09-620-312D-849	Sequence 849, App
c1309	31.2	2.1	17228	4	US-09-902-540-1170	Sequence 1170, App	c1382	31	2.1	1344	4	US-09-902-540-2519	Sequence 2519, App
1310	31.2	2.1	17896	4	US-09-949-016-11986	Sequence 11986, A	c1383	31	2.1	1353	4	US-09-902-540-7306	Sequence 7306, App
c1311	31.2	2.1	18034	4	US-09-266-965-75	Sequence 75, Appl	c1384	31	2.1	1371	4	US-09-252-991A-13600	Sequence 13600, A
1312	31.2	2.1	18343	4	US-09-949-016-16413	Sequence 16413, A	c1385	31	2.1	1392	4	US-09-252-991A-12449	Sequence 12449, A
1313	31.2	2.1	18471	4	US-09-902-540-1167	Sequence 1167, App	c1386	31	2.1	1407	4	US-09-252-991A-12661	Sequence 12661, A
c1314	31.2	2.1	20347	4	US-09-949-016-16752	Sequence 16752, A	c1387	31	2.1	1479	4	US-09-270-767-10543	Sequence 10543, A
1315	31.2	2.1	20840	4	US-09-949-016-14115	Sequence 14115, A	c1388	31	2.1	1480	4	US-09-501-115-9	Sequence 9, Appl1
c1316	31.2	2.1	22339	4	US-09-949-016-12411	Sequence 12411, A	c1389	31	2.1	2091	4	US-09-252-991A-12312	Sequence 12312, A
1317	31.2	2.1	22339	4	US-09-949-016-16154	Sequence 16154, A	c1390	31	2.1	2112	4	US-09-902-540-539	Sequence 539, App
1318	31.2	2.1	22807	4	US-09-902-540-1314	Sequence 1215, App	c1391	31	2.1	2147	4	US-09-949-016-5245	Sequence 5245, App
c1319	31.2	2.1	25733	4	US-09-902-540-1215	Sequence 1215, App	c1392	31	2.1	2149	4	US-09-949-016-456	Sequence 456, App
1320	31.2	2.1	26510	4	US-09-949-016-1408	Sequence 12408, A	c1393	31	2.1	2186	2	US-08-878-546-8	Sequence 9, Appl1
c1321	31.2	2.1	31300	4	US-09-949-016-15967	Sequence 16967, A	c1394	31	2.1	2208	4	US-09-252-991A-13675	Sequence 13675, A
1322	31.2	2.1	36542	4	US-09-949-016-12149	Sequence 12149, A	c1395	31	2.1	2235	4	US-09-252-991A-12994	Sequence 12994, A
c1323	31.2	2.1	36544	4	US-09-949-016-13434	Sequence 13434, A	c1396	31	2.1	2319	4	US-09-252-991A-15884	Sequence 15884, A
1324	31.2	2.1	40576	4	US-09-949-016-13329	Sequence 12329, A	c1397	31	2.1	2361	4	US-09-252-991A-13870	Sequence 13870, A
c1325	31.2	2.1	40577	4	US-09-949-016-16663	Sequence 16663, A	c1398	31	2.1	2427	4	US-09-252-991A-15395	Sequence 15395, A
1326	31.2	2.1	41318	4	US-09-949-016-16225	Sequence 16225, A	c1399	31	2.1	2628	4	US-09-252-991A-13485	Sequence 13485, A
c1327	31.2	2.1	43353	4	US-09-949-016-15302	Sequence 15302, A	c1400	31	2.1	2862	4	US-09-252-991A-13468	Sequence 13468, A
1328	31.2	2.1	44554	4	US-09-949-016-12043	Sequence 12043, A	c1401	31	2.1	2905	4	US-09-949-016-110	Sequence 410, App
c1329	31.2	2.1	44555	4	US-09-949-016-12043	Sequence 12043, A	c1402	31	2.1	2905	4	US-09-949-016-1249	Sequence 5249, App
1330	31.2	2.1	62908	4	US-09-949-016-17554	Sequence 17554, A	c1403	31	2.1	3000	1	US-08-393-985-3	Sequence 3, Appl1
c1331	31.2	2.1	62908	4	US-09-949-016-11804	Sequence 11804, A	c1404	31	2.1	3070	4	US-09-902-540-593	Sequence 593, App
1332	31.2	2.1	67479	4	US-09-949-016-14555	Sequence 12455, A	c1405	31	2.1	3157	2	US-08-939-002A-1	Sequence 1, Appl1
c1333	31.2	2.1	69813	4	US-09-949-016-13906	Sequence 13906, A	c1406	31	2.1	3171	4	US-09-016-434-1348	Sequence 1348, App
1334	31.2	2.1	69813	4	US-09-949-016-13906	Sequence 13906, A	c1407	31	2.1	3219	4	US-09-895-652A-17	Sequence 17, Appl
c1335	31.2	2.1	69813	4	US-09-949-016-13906	Sequence 13906, A	c1408	31	2.1	3486	4	US-09-252-991A-12477	Sequence 12477, A
1336	31.2	2.1	71119	4	US-09-949-016-15358	Sequence 15358, A	c1409	31	2.1	4201	4	US-09-792-568-7	Sequence 7, Appl1
c1337	31.2	2.1	121982	4	US-09-949-016-12085	Sequence 12085, A	c1410	31	2.1	4998	4	US-09-501-171-5	Sequence 591, App
1338	31.2	2.1	121982	4	US-09-949-016-14105	Sequence 14105, A	c1411	31	2.1	5074	4	US-09-902-540-691	Sequence 691, App
c1339	31.2	2.1	123463	4	US-09-949-016-11078	Sequence 11078, A	c1412	31	2.1	7398	4	US-09-949-016-15901	Sequence 15901, App
1340	31.2	2.1	190078	4	US-09-949-016-12707	Sequence 12707, A	c1413	31	2.1	7610	4	US-09-949-016-5516	Sequence 5516, App
c1341	31.2	2.1	190078	4	US-09-949-016-17026	Sequence 17026, A	c1414	31	2.1	7654	4	US-09-949-016-384	Sequence 384, App

C1415	1415	31	2.1	8578	4	US-09-902-540-871
C1416	1416	31	2.1	8931	4	US-09-902-540-925
C1417	1417	31	2.1	8914	3	US-09-902-540-934-28
C1418	1418	31	2.1	10733	4	US-09-902-540-1021
C1419	1419	31	2.1	11978	4	US-09-902-540-11978
C1420	1420	31	2.1	18228	4	US-09-949-016-11964
C1421	1421	31	2.1	18229	4	US-09-949-016-11965
C1422	1422	31	2.1	18469	4	US-09-902-540-1205
C1423	1423	31	2.1	18538	4	US-09-902-540-1169
C1424	1424	31	2.1	19819	4	US-09-949-016-12129
C1425	1425	31	2.1	19819	4	US-09-949-016-16887
C1426	1426	31	2.1	20634	4	US-09-949-016-16627
C1427	1427	31	2.1	26086	4	US-09-949-016-15955
C1428	1428	31	2.1	26238	4	US-09-949-016-15955
C1429	1429	31	2.1	30350	4	US-10-118-328-3
C1430	1430	31	2.1	31797	4	US-09-949-016-17188
C1431	1431	31	2.1	36542	4	US-09-949-016-12149
C1432	1432	31	2.1	36544	4	US-09-949-016-13434
C1433	1433	31	2.1	38239	4	US-09-949-016-12348
C1434	1434	31	2.1	38232	4	US-09-949-016-13570
C1435	1435	31	2.1	49301	4	US-09-949-016-15126
C1436	1436	31	2.1	71645	4	US-09-949-016-15126
C1437	1437	31	2.1	71651	4	US-09-949-016-11258
C1438	1438	31	2.1	76888	4	US-09-949-016-14201
C1439	1439	31	2.1	165651	4	US-09-949-016-13032
C1440	1440	31	2.1	178883	4	US-09-949-016-12733
C1441	1441	31	2.1	178884	4	US-09-949-016-13039
C1442	1442	31	2.1	250958	4	US-09-949-016-15061
C1443	1443	31	2.1	260247	4	US-09-949-016-13358
C1444	1444	31	2.1	288336	4	US-09-949-016-15600
C1445	1445	31	2.1	312470	4	US-09-949-016-14043
C1446	1446	31	2.1	336024	4	US-09-949-016-12373
C1447	1447	31	2.1	767677	4	US-09-949-016-12147
C1448	1448	31	2.1	767677	4	US-09-949-016-11361
C1449	1449	30.8	2.1	282	4	US-09-949-016-13611
C1450	1450	30.8	2.1	277	3	US-09-907-005-3
C1451	1451	30.8	2.1	277	3	US-09-949-016-12693
C1452	1452	30.8	2.1	279	2	US-08-623-906A-3
C1453	1453	30.8	2.1	286	4	US-09-949-016-12055
C1454	1454	30.8	2.1	447	4	US-09-949-016-1576
C1455	1455	30.8	2.1	477	4	US-09-949-016-1576
C1456	1456	30.8	2.1	537	4	US-09-949-016-15733
C1457	1457	30.8	2.1	601	4	US-09-949-016-148224
C1458	1458	30.8	2.1	601	4	US-09-949-016-148224
C1459	1459	30.8	2.1	601	4	US-09-949-016-15733
C1460	1460	30.8	2.1	601	4	US-09-949-016-15733
C1461	1461	30.8	2.1	601	4	US-09-949-016-15972
C1462	1462	30.8	2.1	601	4	US-09-949-016-16942
C1463	1463	30.8	2.1	601	4	US-09-949-016-120639
C1464	1464	30.8	2.1	601	4	US-09-949-016-124039
C1465	1465	30.8	2.1	601	4	US-09-949-016-158255
C1466	1466	30.8	2.1	601	4	US-09-949-016-158255
C1467	1467	30.8	2.1	601	4	US-09-949-016-158255
C1468	1468	30.8	2.1	601	4	US-09-949-016-15825

[illegible]

CL1488	30.8	2.1	882	4	US-09-252-991A-6694	Sequence 8694, Ap
1489	30.8	2.1	909	4	US-09-252-991A-7471	Sequence 7471, Ap
1490	30.8	2.1	1020	4	US-09-902-540-6405	Sequence 6405, Ap
CL1491	30.8	2.1	1028	4	US-09-902-540-6405	Sequence 6405, Ap
CL1492	30.8	2.1	1028	3	US-08-118-200-1	Sequence 1, Appli
CL1493	30.8	2.1	1028	3	US-08-458-745-1	Sequence 1, Appli
CL1494	30.8	2.1	1035	1	US-08-891-254-8	Sequence 8, Appli
CL1495	30.8	2.1	1035	2	US-08-819-539-8	Sequence 8, Appli
CL1496	30.8	2.1	1035	2	US-09-030-270A-8	Sequence 8, Appli
CL1497	30.8	2.1	1035	3	US-08-984-207-8	Sequence 8, Appli
CL1498	30.8	2.1	1035	3	US-09-013-587-8	Sequence 8, Appli
CL1499	30.8	2.1	1035	4	US-09-086-118-28	Sequence 28, Appli
CL1500	30.8	2.1	1035	4	US-09-431-614-16	Sequence 16, Appli

ALIGNMENTS

RESULT 1

US-09-049-672A-16

Sequence 16, Application US/09049672A

Patent No. 6135941

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

APPLICANT: Lal, Preeti

APPLICANT: Tang, Y. Tom

APPLICANT: Yue, Henry

APPLICANT: Au-Young, Janice

APPLICANT: Corley, Neil C.

APPLICANT: Guegler, Karl J.

APPLICANT: Baughn, Mariah R.

TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/049,672A

FILING DATE: HEREWITH

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Gettione, Michael C

REGISTRATION NUMBER: 39,132

REFERENCE/DOCKET NUMBER: PF-0497 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-855-0555

TELEFAX: 650-845-4166

TELEX:

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 3449 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: BLADNOT04

CLONE: 1320068

US-09-049-672A-16

Query Match

Best Local Similarity

97.3%;

99.7%;

Score 1445.6;

Pred No. 0;

DB 3;

Length 3449;

Matches 1459; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY	7	ACACGACGATAGCCCGAGAGCCCGGACCAAGGCGCTGTGCTCTCTCTCGTCCCTCGGCGCG	66
Db	1	ACACGACGATAGCCCGAGAGCCCGGACCAAGGCGCTGTGCTCTCTCTCGTCCCTCGGCGCG	60
QY	67	TCGCGAAGCCCTGAGCCCGGCGGAGGCCCGCGCTGCGCATGTGCGGCGAGCTCAGCAAC	124
Db	61	TCGCGAAGCCCTGAGCGCCGCGGAGAG-CCCGGCGCTGCGCATGTGCGGCGAGCTCAGCAAC	114
QY	127	AGGTTCCAAAGAGGAGGAGCGCTTCGGCTTGTGCTCAAAAGCCCGGCGAGAGAGAGCGCTGCC	184
Db	120	AGGTTCCAAAGAGGAGGAGCGCTTGGCTTGTCTCAAAAGCCCGGCGAGAGAGAGCGCTGCC	174
QY	187	GAGATCAACCGGAGGATTTCTGTGTGACCAAGAGTCAAGTGAATGAAGAGAACCTTTCAGAA	244
Db	180	GAGATCAACCGGAGGATTTCTGTGTGACCAAGAGTCAAGTGAATGAAGAGAACCTTTCAGAA	234
QY	247	AAGCTCAGAGCTTCAAGAGAAATACATGAGATTGACCTGAACATATGAAGAGGAGATTT	304
Db	240	AAGCTCAGAGCTTCAAGAGAAATACATGAGATTGACCTGAACATATGAAGAGGAGATTT	299
QY	307	GACCTGATGTCTTTAAAGAGATGATGAGAAAGCTGATGTGCCCAAGACCACTTGAG	366
Db	300	GACCTGATGTCTTTAAAGAGATGATGAGAAAGCTGATGTGCCCAAGACCACTTGAG	359
QY	367	ATGAGAGAAATGATCTCAGAGGTGACAGAGAGGGGTGATGACATATATCTTACCGAGAC	426
Db	360	ATGAGAGAAATGATCTCAGAGGTGACAGAGAGGGGTGATGACATATATCTTACCGAGAC	419
QY	427	TTTGTGAACATGATGCTGCGGAGAAACGGTCGGCTGTCTCTCAAGTATGATGATGTGTGA	486
Db	420	TTTGTGAACATGATGCTGCGGAGAAACGGTCGGCTGTCTCTCAAGTATGATGATGTGTGA	479
QY	487	GGAAGAGCCACAGAGAGAGAGCCCGACAGCCAGTTGGCCCCCTTCAAGAGAGACATTTGCT	546
Db	480	GGAAGAGCCACAGAGAGAGAGCCCGACAGCCAGTTGGCCCCCTTCAAGAGAGACATTTGCT	539
QY	547	AGCTTCGCTTGAAGAGAGCCCGCTGACCTCCAGCTTCCACCCGATACCTCCGCGCG	606
Db	540	AGCTTCGCTTGAAGAGAGCCCGCTGACCTCCAGCTTCCACCCGATACCTCCGCGCG	599
QY	607	ATCTTTCGCGCCCTTTCAGACATGTGATCTCTCTCTCTCATATTTGTTGGTCAATGA	666
Db	600	ATCTTTCGCGCCCTTCTTGAACAACATGTGATCTCTCTCTCATATTTGTTGGTCAATGA	659
QY	667	GGGTTGTTGTGTTTTCATCATATGCTTTGTAAAGCACAATATATCTGACCTTAAAGGGG	726
Db	660	GGGTTGTTGTGTTTTCATCATATGCTTTGTAAAGCACAATATATCTGACCTTAAAGGGG	719
QY	727	CTCTGGGTGCGGGAAATCTGAGGCTTTGGGTCCCTCCCTCTCTTCTTCCCTTCCCG	786
Db	720	CTCTGGGTGCGGGAAATCTGAGGCTTTGGGTCCCTCCCTCTCTTCTTCCCTTCCCG	779
QY	787	CTCCCTGTGCAAGAGGGCTGATATCAAAACAAAACCTAGAGGGGCGAGGGCGAGGGCAGG	846
Db	780	CTCCCTGTGCAAGAGGGCTGATATCAAAACAAAACCTAGAGGGGCGAGGGCGAGGGCAGG	839
QY	847	GAGGTTTCCAGCTGTGTCTTCCCTCATTTGAGAAACCAAGCATCTTCATCTTTTCAGAA	906
Db	840	GAGGTTTCCAGCTGTGTCTTCCCTCATTTGAGAAACCAAGCATCTTCATCTTTTCAGAA	899
QY	907	AGTCTCCAAAGCCAGGTTCAAGGCTCACTGACCTGGGTCTGAGAGACCCGAGGCGACTCT	966
Db	900	AGTCTCCAAAGCCAGGTTCAAGGCTCACTGACCTGGGTCTGAGAGAGACCCGAGGCGACTCT	959
QY	967	GAGAAAGCTTTGAGATGAGGACAAAGCTGACGAGGCTTTTCGGGTTTCTTGGACAGTG	1026
Db	960	GAGAAAGCTTTGAGATGAGGACAAAGCTGACGAGGCTTTTCGGGTTTCTTGGACAGTG	1019
QY	1027	CCAGGTTTCCAGGTCCTGCGTGTACCAAGAGACAGGCACTCGGGGCTCCGCTGGCCCA	1086
Db	1020	CCAGGTTTCCAGGTCCTGCGTGTACCAAGAGACAGGCACTCGGGGCTCCGCTGGCCCA	1079

QY	1087	GCTGATCCCACTCATTTCCACACCTCTTCTCATCTCAGTATATGAAAGTGGAAAGGA	1146
Db	1080	GCTGATCCCACTCATTTCCACACCTCTTCTCATCTCAGTATATGAAAGTGGAAAGGA	1139
QY	1147	AGGACTTGGGATTTGGGAGGCCCTTCAAGAAAGTACAGAAAGAAACCTCCAGTCTGCTC	1206
Db	1140	AGGACTTGGGATTTGGGAGGCCCTTCAAGAAAGTACAGAAAGAAACCTCCAGTCTGCTC	1199
QY	1207	TCTGGCCACACCTGTGACGACGCTGAGAGGACAGTGCAGCCCTACTGTCCTTACTCG	1266
Db	1200	TCTGGCCACACCTGTGACGACGCTGAGAGGACAGTGCAGCCCTACTGTCCTTACTCG	1259
QY	1267	GGCAGCAGAGGGCTTTGGAGGACAGAAAGTGAAGCTGGAGTTTGGGGGAAAAGTCACTC	1326
Db	1260	GGCAGCAGAGGGCTTTGGAGGACAGAAAGTGAAGCTGGAGTTTGGGGGAAAAGTCACTC	1319
QY	1327	AGTCTGTTCCACTTTTAAAGGAGGAATCAGAGGGGACCGAGATGGAGAAATGAGAGTA	1386
Db	1320	AGTCTGTTCCACTTTTAAAGGAGGAATCAGAGGGGACCGAGATGGAGAAATGAGAGTA	1379
QY	1387	AAATGCTCAAGGCAAACTCAGCAGCACTGGTAAAGCCAAAGCTGAGAAATCAAGGTTGCT	1446
Db	1380	AAATGCTCAAGGCAAACTCAGCAGCACTGGTAAAGCCAAAGCTGAGAAATCAAGGTTGCT	1439
QY	1447	TGTCGTACCCCAATTCGCTTGAAA	1470
Db	1440	TGTCGTACCCCAATTCGCTTGAAA	1463

RESULT 2
US-09-010-147B-11
Sequence 11, Application US/09010147B
Patent No. 6653445
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: Human Proteins
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC
compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,147B
FILING DATE: 12-No. 6653445-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,205
FILING DATE: 21-JAN-1997
APPLICATION NUMBER: US 60/034,204
FILING DATE: 21-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Jonathan L. Klein
REGISTRATION NUMBER: 41,119
REFERENCE/DOCKET NUMBER: PF553
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 632 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear


```

;
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/792,013
; FILING DATE: Filed Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION/DOCKET NUMBER: 36,749
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 658 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: OVAR1UT01
; CLONE: 815614
;
US-08-792-013-5

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Query Match 12.9%; Score 192.2; DB 3; Length 658;
Best Local Similarity 67.1%; Pred. No. 1.1e-43;
Matches 288; Conservative 0; Mismatches 138; Indels 3; Gaps 1;

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QY 130 TTCCAAGGAGGAGGCGTTGCTGCTCAAGCCCGGAGAGAGAGGCTGCGCGAG 189
DB 114 TTACAGGAGAGAAAGCTTTGAGCTGCTGAGGCCGAGAGAGAGGCTGAGTAG 173
QY 190 ATCAACCGGAGGTTCTGTGTGACCAAGAGTACAGTGTAGAGAACTTCCAGAAAG 249
DB 174 ATCAACAGCAATTCCTAGACGATCCCAATATAGCAGTGTAGAGATCTGCCCTCCAA 233
QY 250 CTCACAGCTTCAAGAGAGTACATGAGATTGACCTGAAACATGAAAGCGAGATTGAC 309
DB 234 CTGGAAGGCTTCAAGAGAAATACATGAGATTGACCTTAATGAAATGCGCATTTGAT 293
QY 310 CTGATGCTTTAAAGAGATGATGAGAGAGGTTGCTGCCCAAGACCCACTGAGATG 369
DB 294 ATCATGTCCTGAAACGAATCTGAGAACTTGAATCCCAAGACTCACTAGAGCTA 353
QY 370 AAGAAGATGATCTCAGAGGTGACAGAGGGGTCACTATATCTTACCGAGCTTT 429
DB 354 AAGAATTAATTGAGAGGTGTCCAGTGGCTCCGGGAGAGGTTCACTGACTTT 413
QY 430 GTGAACATGATGCTGGGGAACGCTGGCTGCTCAAGTTAGTCATGATTTGAAGA 489
DB 414 CTCAGATGATGCTGGGAGAGAGATCTGCCATCTTAAATGATCTGATAGAGAA 473
QY 490 AAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 549
DB 474 AAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 530
QY 550 CTGCCCTGA 558
DB 531 TTGCCCTGA 539

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;
; RESULT 5
; US-09-513-999C-3906
; Sequence 3906, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclet, A.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59, US2, REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 3906
; LENGTH: 658
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 109..624
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 525
; OTHER INFORMATION: n=a, y, c or t
;
US-09-513-999C-3906

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Query Match 12.5%; Score 186; DB 4; Length 658;
Best Local Similarity 66.2%; Pred. No. 6.1e-42;
Matches 284; Conservative 0; Mismatches 141; Indels 4; Gaps 1;

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QY 130 TTCCAAGGAGGAGGCGTTGCTGCTCAAGCCCGGAGAGAGAGGCTGCGCGAG 189
DB 127 TTACAGGAGAGAAAGCTTTGAGCTGCTGAGGCCGAGAGAGAGGCTGAGTAG 186
QY 190 ATCAACCGGAGGTTCTGTGTGACCAAGAGTACAGTGTAGAGAACTTCCAGAAAG 249
DB 187 ATCAACAGCAATTCCTAGACGATCCCAATATAGCAGTGTAGAGATCTGCCCTCCAA 246
QY 250 CTCACAGCTTCAAGAGAGTACATGAGATTGACCTGAAACATGAAAGCGAGATTGAC 309
DB 247 CTGGAAGGCTTCAAGAGAAATACATGAGATTGACCTTAATGAAATGCGCATTTGAT 306
QY 310 CTGATGCTTTAAAGAGATGATGAGAGAGGTTGCTGCCCAAGACCCACTGAGATG 369
DB 307 ATCATGTCCTGAAACGAATCTGAGAACTTGAATCCCAAGACTCACTAGAGCTA 366
QY 370 AAGAAGATGATCTCAGAGGTGACAGAGGGGTCACTATATCTTACCGAGACTTT 429
DB 367 AAGAATTAATTGAGAGGTGTCCAGTGGCTCCGGGAGAGGTTCACTGACTTT 426
QY 430 GTGAACATGATGCTGGGGAACGCTGGCTGCTCAAGTTAGTCATGATTTGAAGA 489
DB 427 CTCAGATGATGCTGGGAGAGAGATCTGCCATCTTAAATGATCTGATAGAGAA 486
QY 490 AAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 549
DB 487 AAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 542
QY 550 CTGCCCTGA 558
DB 543 TTGCCCTGA 551

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RESULT 6
US-09-513-999C-14979
; Sequence 14979, Application US/09513999C
; Patent No. 6783961

GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duciart, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59, US2, REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 14979
LENGTH: 597
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 464
OTHER INFORMATION: n=a, g, c or t
US-09-513-999C-14979

Query Match 12.3%; Score 183.2; DB 4; Length 597;
Best Local Similarity 66.2%; Pred. No. 3.6e-41;
Matches 280; Conservative 0; Mismatches 139; Indels 4; Gaps 1;

QY 136 GAGGAGAAAGCGCTTGGCTGCTCAAGCCCGCAGAGAGAGCGCTGCGGAGATCAAC 195
DB 72 GAGAGAAAAGCTTTCGAGCTGCTGAAGCCCGCAGAGAGAGCGCTGATGATCAAC 131
QY 196 GCGGAGTTCTGTGTGACCAAGATGATGATGAGAGAACTCCGAAAAGCTCA 255
DB 132 AAGCAATTCCTAGACGATCCCAATATAGCAATGATGATGATGATGATGATGATGAT 191
QY 256 GCTTCAAGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 315
DB 192 GCTTCAAGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 251
QY 316 TCTTTAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 375
DB 252 TCCCTGAAACGAAATGCTGAGAACTTGAAGTCCCAAGACTCACTGAGCTAAAGAAA 311
QY 376 ATGATCTGAGAGTGAAG 435
DB 312 TTAATGAGAGAGTGTCCAGTGGCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 371
QY 436 ATGATCTGAGAGAAAGCGCTGCTGCTCAAGTTAGTATGATGATGATGATGATGATGATG 495
DB 372 ATGATCTGAGAGAAAGCGCTGCTGCTCAAGTTAGTATGATGATGATGATGATGATGATG 429
QY 496 AAGCAG 555
DB 430 --CGAG 487
QY 556 TGA 558
DB 488 TGA 490

RESULT 7

US-08-361-441B-4
Sequence 4, Application US/08361441B
Patent No. 6077948
GENERAL INFORMATION:
APPLICANT: Russell, Mary E.
APPLICANT: Ureans, Ulrike
TITLE OF INVENTION: MEDIATORS OF CHRONIC ALLOGRAFT REJECTION
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston

STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/361,441B
FILING DATE: 21-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/171,385
FILING DATE: 21-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Frazer, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05433/014001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 627 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-361-441B-4

Query Match 12.1%; Score 180.4; DB 3; Length 627;
Best Local Similarity 64.8%; Pred. No. 2.2e-40;
Matches 284; Conservative 0; Mismatches 151; Indels 3; Gaps 1;

QY 121 AGCAACAGTCTCAAG 180
DB 80 AGCAAGATTTGAG 139
QY 181 CTGCGCGAGATCAACCGGAGATTTCTGTGTACCAAGATGATGATGATGATGATGATG 240
DB 140 TTGATGGAGATCAACAGCACTTCTGATGATCCCAAGTACAGAGATGATGATGATG 199
QY 241 CCAGAAAAGCTCAGACAGCTTCAAGAGAGATGATGATGATGATGATGATGATGATGATG 300
DB 200 CAGTCCAACTGAG 259
QY 301 GAGATGACCTGATGCTTTAAAGAGATGATGATGATGATGATGATGATGATGATGATG 360
DB 260 GATATGATATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 319
QY 361 CTGAGATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
DB 320 CTGAGCTGAGAGATTAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 379
QY 421 CGAGCTTTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
DB 380 TCTGATTTCTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 439
QY 481 TTTGAG 540
DB 440 TATGAG 496
QY 541 ATTGCTAGCTGCTGCTGA 558
DB 497 ATTCTGAGTTGCCCTAA 514

RESULT 8

US-08-171-385-4
Sequence 4, Application US/08171385
Patent No. 5527884
GENERAL INFORMATION:
APPLICANT: Mary E. Russell

APPLICANT: Unlike Utans
TITLE OF INVENTION: Mediators of Chronic Allograft
NUMBER OF INVENTION: Rejection
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESS: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/171,385
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05433/006001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
FILING DATE:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 651
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-171-385-4
Query Match 12.1%; Score 180.4; DB 1; Length 651;
Best Local Similarity 64.8%; Pred. No. 2.3e-40;
Matches 284; Conservative 0; Mismatches 151; Indels 3; Gaps 1;
QY 121 AGCAACAGGTCCTCAAGAGGAGGAGGCTTCGCTTGTCTCAAGAGGAGGAGGAGGAGG 180
DB 80 ACACAGGATTTGAGAGGAGGAGGAGGAGGCTTTTGTGCACTGCTGAGAGGAGGAGGAGG 139
QY 181 CTGCGCGAGATCAACCGGAGGAGGCTTCTGTGTGACACAGAGTACAGTATGAGAGAACCTT 240
DB 140 TTGAGATGGATCAACAGACATTCCTCGATGATCCCAAGTACAGCAGTATGAGGATCTG 199
QY 241 CCAAGAAAGCTCAACGCTTCAAGAGAGTACATGAGATTTGACCTGAAACAATGAGGC 300
DB 200 CAGTCCAACTGAGAGGCTTCAAGAGAGTACATGAGATTTGATCTGATGAGCAATGGA 259
QY 301 GAGATTGACCTGATGCTTTAAAGAGATGAGAGAGCTTGATGCTCCCAAGAGCCAC 360
DB 260 GATATCGATATATGCTCTTGAAGCAATGCTGAGAGAACTTGAGGCTTCCCAAGACCAT 319
QY 361 CTGAGATGAGAGAGATGATCTCAGAGTGAACAGAGGAGTCACTATATCTTAC 420
DB 320 CTAGAGCTGAAGAAATTAATTGAGAGGTGTCAGAGGCTCCGAGAGAGAGTTCAGATTAC 379
QY 421 CGAGACTTTGTGAACATGATGCTGGGAGAAACGTCGCTGCTCTCAAGTTAATGATGATG 480
DB 380 TCTGACTTTCTCAGAAATGATGCTGGGCAAGAGATCTGCATCTTGAGAAATGATCTGATG 439
QY 481 TTGAG 540
DB 440 TATGAG 496
QY 541 ATTGCTAGCCTGCTGCA 558
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DB 497 ATTCTGAGTTGCCCTAA 514
RESULT 9
US-09-513-999C-10617
Sequence 10617, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.Y.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59,US2,REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 10617
LENGTH: 507
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 443
OTHER INFORMATION: k=g or t
US-09-513-999C-10617
Query Match 8.8%; Score 131.4; DB 4; Length 507;
Best Local Similarity 66.3%; Pred. No. 1.2e-26;
Matches 205; Conservative 0; Mismatches 101; Indels 3; Gaps 1;
QY 250 CTCACAGCTTCAAGAGAGTACATGAGATTTGACCTGAAACAATGAGAGAGATGAC 309
DB 95 CTCCTCCCTCAACCGAGAAATACATGAGATTTGACCTTAAAGAAATGCGGATTTGAT 154
QY 310 CTGATGCTTTTAAAGAGATGATGAGAGAGCTTGCTGCTCCCAAGAGAGAGAGAGATG 369
DB 155 ATCATGTCCTCGAAGACATGCTGAGAGAACTTGAGATCCCAAGAGAGAGAGAGAGAG 214
QY 370 AAGAGATGATCTCAGAGTGAACAGAGGAGTCACTGACATATCTTACCGAGACTTT 429
DB 215 AAGAAATTAATTGAGAGAGTGTCCAGTGGCTCCGAGAGAGAGTCACTACCTGACTTT 274
QY 430 GTGAACATGATGAGGAG 489
DB 275 CTCAGATGATGCTGGGAGAGAGATCTGCTCTTAAAGATGCTGATGATGAGAGAA 334
QY 490 AAAGCCAG 549
DB 335 AAAG 391
QY 550 CTGCGCTGCA 558
DB 392 TTGCGCTGCA 400
RESULT 10
US-08-171-385-1/c
Sequence 1, Application US/08171385
Patent No. 5527884
GENERAL INFORMATION:
APPLICANT: Mary E. Russell
APPLICANT: Unlike Utans
TITLE OF INVENTION: Mediators of Chronic Allograft
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESS: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston

Search completed: March 29, 2005, 03:26:36
Job time : 370 secs

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GenCore version 5.1.6
Run on: March 28, 2005, 23:56:39 ; Search time 869 Seconds
(without alignments)
10116.014 Million cell updates/sec

Title: US-10-015-610A-195
Perfect score: 1485
Sequence: 1 gcggccacacgacgtacgc.....tgaaaaaaaaaaaaaaaaaa 1485
Scoring table: IDENTITY NUC
Gapop 10-0, Gapext 1.0
4390206 segs, 2359870667 residues
Total number of hits satisfying chosen parameters: 8780412
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : N_Geneseq_16dec04:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AA337076	standard;	CDNA;	1485	BP.	
DE	Human PRO1306	(UNQ672)	CDNA	sequence	SEQ ID NO:195.	
PN	WO200012708-A2.					
PD	09-MAR-2000.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 1485;	DB 3;	Length 1485;	
Best Local Similarity		100.0%;	Pred. No. 0;			
RESULT 2						
ID	AA54342	standard;	DNA;	1485	BP.	
DE	DNA encoding	protein of the	invention	#55.		
PN	WO200078961-A1.					
PD	28-DEC-2000.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 1485;	DB 4;	Length 1485;	
Best Local Similarity		100.0%;	Pred. No. 0;			
RESULT 3						
ID	ABK3590	standard;	CDNA;	1485	BP.	
DE	CDNA encoding	human PRO	protein, seq	ID NO 109.		
PN	WO200208288-A2.					
PD	31-JAN-2002.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 1485;	DB 6;	Length 1485;	
Best Local Similarity		100.0%;	Pred. No. 0;			
RESULT 4						
ID	ABL8176	standard;	CDNA;	1485	BP.	
DE	Human PRO1306	CDNA	sequence	SEQ ID NO:209.		
PN	WO200200690-A2.					
PD	03-JAN-2002.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 1485;	DB 6;	Length 1485;	
Best Local Similarity		100.0%;	Pred. No. 0;			
RESULT 5						
ID	AB195665	standard;	CDNA;	1485	BP.	
DE	Human angiotensin	related	CDNA	PRO1306	SEQ ID NO: 209.	
PN	WO200208284-A2.					
PD	31-JAN-2002.					
PA	(GETH) GENENTECH INC.					

PA	(BAKE/)	BAKER K P.
PA	(FERR/)	FERRARA N.
PA	(GERB/)	GERBER H.
PA	(GERR/)	GERRITSEN M E.
PA	(GODD/)	GODDARD A.
PA	(GODO/)	GODOWSKI P J.
PA	(GURN/)	GURNEY A L.
PA	(HILL/)	HILLAN K J.
PA	(MARS/)	MARSTERS S A.
PA	(PANU/)	PAN J.
PA	(PAON/)	PAONT N F.
PA	(STEP/)	STEPHAN J P.
PA	(WATA/)	WATANABE C K.
PA	(WILL/)	WILLIAMS P M.
PA	(WOOD/)	WOOD W I.
Query Match		100.0%;
Best Local Similarity		100.0%;
RESULT 6		
ID	ACA6851	standard;
DE	Novel human	secreted and transmembrane protein
PN	US200308063-A1.	
PD	08-MAY-2003.	
PA	(GETH) GENENTECH INC.	
Query Match		100.0%;
Best Local Similarity		100.0%;
RESULT 7		
ID	ABT44280	standard;
DE	Human PRO1306	CDNA.
PN	US2003050448-A1.	
PD	13-MAR-2003.	
PA	(GETH) GENENTECH INC.	
Query Match		100.0%;
Best Local Similarity		100.0%;
RESULT 8		
ID	ACD68379	standard;
DE	Novel human	secreted and transmembrane protein
PN	US2003073130-A1.	
PD	17-APR-2003.	
PA	(GETH) GENENTECH INC.	
Query Match		100.0%;
Best Local Similarity		100.0%;
RESULT 9		
ID	ABT44563	standard;
DE	Human PRO1306	CDNA.
PN	US2003027988-A1.	
PD	06-FEB-2003.	
PA	(GETH) GENENTECH INC.	
Query Match		100.0%;
Best Local Similarity		100.0%;
RESULT 10		
ID	ACD82230	standard;
DE	Human secreted	/transmembrane polypeptide PRO 1306
PN	US2003044934-A1.	
PD	06-MAR-2003.	
PA	(GETH) GENENTECH INC.	
Query Match		100.0%;
Best Local Similarity		100.0%;
RESULT 11		
ID	ACH04481	standard;
DE	Human CDNA	encoding secreted/transmembrane protein
PN	US2003044841-A1.	
PD	06-MAR-2003.	
PA	(GETH) GENENTECH INC.	
Query Match		100.0%;
Best Local Similarity		100.0%;
RESULT 12		
ID	ACD68025	standard;
DE	Novel human	secreted and transmembrane protein
PN	US2003073129-A1.	
PD	17-APR-2003.	
PA	(GETH) GENENTECH INC.	
Query Match		100.0%;
Best Local Similarity		100.0%;

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RESULT 13
ID ADB13936 standard; cDNA; 1485 BP.
DE Human membrane bound receptor/protein PRO1306 cDNA sequence.
PN US2003065147-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 9; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 14
ID ADB83599 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003073814-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 9; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 15
ID ADB80705 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003088068-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 9; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 16
ID ADB73246 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003096969-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 9; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 17
ID ADB78328 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003092889-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 9; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 18
ID ADB84976 standard; cDNA; 1485 BP.
DE Human PRO polynucleotide #55.
PN US2003073817-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 19
ID ADB78082 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003092886-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 20
ID ADB87148 standard; cDNA; 1485 BP.
DE Human PRO polynucleotide #55.
PN US2003088067-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 21
ID ADB84730 standard; cDNA; 1485 BP.
DE Human PRO polynucleotide #55.
PN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 22
ID ADB83845 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003069397-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 23
ID ADB73000 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 24
ID ADC18064 standard; cDNA; 1485 BP.
DE Human PRO polynucleotide #55.
PN US2003064925-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 25
ID ADC36838 standard; cDNA; 1485 BP.
DE Human PRO polynucleotide #55.
PN US2003088065-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 26
ID ADC21828 standard; cDNA; 1485 BP.
DE Human PRO polynucleotide #55.
PN US2003096969-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 27
ID ADC49859 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003088064-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 28
ID ADC49058 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003088070-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 29
ID ADC49575 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003088071-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 30
ID ADC47436 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003088072-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 31
ID ADC47181 standard; cDNA; 1485 BP.
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DE Novel human secreted and transmembrane protein PRO1306 cDNA.
FN US2003105288-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 32
ID ADD78056 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
FN US2003096972-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 33
ID ADD06291 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
FN US2003073816-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 34
ID ADD10498 standard; cDNA; 1485 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #105.
FN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 35
ID ADDC7810 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
FN US2003088066-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 36
ID ADD11458 standard; cDNA; 1485 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #105.
FN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 37
ID ADD50773 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
FN US2003105291-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 38
ID ADD51019 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
FN US2003105290-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 39
ID ADD70710 standard; cDNA; 1485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1306.
FN US2003099625-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 40
ID ADD39787 standard; cDNA; 1485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1306.

FN US2003083462-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 41
ID ADD70233 standard; cDNA; 1485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1306.
FN US2003054406-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 42
ID ADD37251 standard; cDNA; 1485 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #105.
FN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 43
ID ADD38354 standard; cDNA; 1485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1306.
FN US2003096955-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 44
ID ADD39310 standard; cDNA; 1485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1306.
FN US2003096954-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 45
ID ADD50500 standard; cDNA; 1485 BP.
DE Human PRO polynucleotide #55.
FN US2003096971-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 46
ID ADD50254 standard; cDNA; 1485 BP.
DE Human PRO polynucleotide #55.
FN US2003096970-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 47
ID ADD38833 standard; cDNA; 1485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1306.
FN US2003092061-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 48
ID ADD40264 standard; cDNA; 1485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1306.
FN US2003082627-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 49
ID ADD51265 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
FN US2003105289-A1.

PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 50
ID ADE50485 standard; cDNA; 1485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1306.
PN US2003069179-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 51
ID ADE20097 standard; cDNA; 1485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1306.
PN US2003092883-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 52
ID ADE50008 standard; cDNA; 1485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1306.
PN US2003082626-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 53
ID ADE21566 standard; cDNA; 1485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1306.
PN US2003082628-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 54
ID ADE29991 standard; cDNA; 1485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1306.
PN US2003204053-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 55
ID ADE55884 standard; cDNA; 1485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1306.
PN US2003204054-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 56
ID ADE99388 standard; cDNA; 1485 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1306.
PN US2003065142-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 57
ID ACA66895 standard; cDNA; 1485 BP.
DE cDNA encoding human PRO polypeptide #55.
PN US2003036635-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 58
ID ACD68647 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003045687-A1.
PD 06-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 10; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 59
ID ADC48812 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003092888-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 60
ID ADE20983 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 61
ID ADE05827 standard; cDNA; 1485 BP.
DE Human PRO polynucleotide #55.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 62
ID ADE75056 standard; cDNA; 1485 BP.
DE Human PRO polynucleotide #55.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 63
ID ADE75802 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 64
ID ADE85034 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 65
ID ADE66860 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 66
ID ADE20737 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 67
ID ADE39034 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003096362-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 68
ID ADE05581 standard; cDNA; 1485 BP.
DE Human PRO polynucleotide #55.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 69
ID ADD73566 standard; cDNA; 1485 BP.
DE Human PRO polynucleotide #55.
PN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 70
ID ADD78406 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 71
ID ADE41459 standard; cDNA; 1485 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #105.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 72
ID ADE21229 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 73
ID ADD77344 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 74
ID ADE20491 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 75
ID ADD75556 standard; cDNA; 1485 BP.
DE Human PRO polynucleotide #55.
PN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 76
ID ADD74072 standard; cDNA; 1485 BP.
DE Human PRO polynucleotide #55.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;

Best Local Similarity 100.0%; Pred. No. 0;
RESULT 77
ID ADD74318 standard; cDNA; 1485 BP.
DE Human PRO polynucleotide #55.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 78
ID ADD76048 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 79
ID ADE85540 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003100721-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 80
ID ADE05089 standard; cDNA; 1485 BP.
DE Human PRO polynucleotide #55.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 81
ID ADD75302 standard; cDNA; 1485 BP.
DE Human PRO polynucleotide #55.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 82
ID ADD76846 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 83
ID ADE86614 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 84
ID ADD78082 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 85
ID ADD77590 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 86
ID ADP7836 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 87
ID ADP85294 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 88
ID ADP7826 standard; cDNA; 1485 BP.
DE Human PRO polynucleotide #55.
PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 89
ID ADP74564 standard; cDNA; 1485 BP.
DE Human PRO polynucleotide #55.
PN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 90
ID ADP77092 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 91
ID ADP85786 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 92
ID ADE05335 standard; cDNA; 1485 BP.
DE Human PRO polynucleotide #55.
PN US2003100723-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 93
ID ADP74810 standard; cDNA; 1485 BP.
DE Human PRO polynucleotide #55.
PN US2003100724-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 94
ID ADP86568 standard; cDNA; 1485 BP.
DE Human CDNA encoding secreted/transmembrane protein PRO1306.
PN US2003195347-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 95

ID ADP25879 standard; cDNA; 1485 BP.
DE Human CDNA encoding secreted/transmembrane protein PRO1306.
PN US2003196675-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 96
ID ADP24778 standard; cDNA; 1485 BP.
DE Human CDNA encoding secreted/transmembrane protein PRO1306.
PN US2003198993-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 97
ID ADP29514 standard; cDNA; 1485 BP.
DE Human CDNA encoding secreted/transmembrane protein PRO1306.
PN US2003203401-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 98
ID ADP87045 standard; cDNA; 1485 BP.
DE Human CDNA encoding secreted/transmembrane protein PRO1306.
PN US2003195334-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 99
ID ADG05622 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003096559-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 100
ID ADG27176 standard; cDNA; 1485 BP.
DE Human PRO polynucleotide #55.
PN US2003096962-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 101
ID ADG11239 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003096967-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 102
ID ADG12018 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 103
ID ADP94575 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 cDNA.
PN US2003096964-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 104
ID ADG06671 standard; cDNA; 1485 BP.

DE Human PRO polynucleotide #55.
PN US2003096966-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 105
ID ADH03083 standard; cDNA; 1485 BP.
DE Human CDNA encoding secreted/transmembrane protein PRO1306.
PN US2003216562-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 106
ID ADH04037 standard; cDNA; 1485 BP.
DE Human CDNA encoding secreted/transmembrane protein PRO1306.
PN US2003220471-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 107
ID ADH03560 standard; cDNA; 1485 BP.
DE Human CDNA encoding secreted/transmembrane protein PRO1306.
PN US2003224478-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 108
ID ADH39015 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 CDNA.
PN US2003096965-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 109
ID ADH43642 standard; cDNA; 1485 BP.
DE Human PRO polynucleotide #105.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 110
ID ADG34105 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 CDNA.
PN US2004006306-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 111
ID ADH04514 standard; cDNA; 1485 BP.
DE Human CDNA encoding secreted/transmembrane protein PRO1306.
PN US2004005626-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 112
ID ADI33575 standard; cDNA; 1485 BP.
DE Human PRO polynucleotide #55.
PN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 113
ID ADH69669 standard; cDNA; 1485 BP.
DE Human PRO polynucleotide #55.
PN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 114
ID ADH61515 standard; cDNA; 1485 BP.
DE Human CDNA encoding secreted/transmembrane protein PRO1306.
PN US2004014130-A1.
PD 22-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 115
ID ADI29830 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 CDNA.
PN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 116
ID ADM27227 standard; cDNA; 1485 BP.
DE Novel human secreted and transmembrane protein PRO1306 CDNA.
PN US2004044179-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 117
ID ADK82987 standard; cDNA; 1485 BP.
DE Human PRO polynucleotide #105.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 118
ID ADK66585 standard; cDNA; 1485 BP.
DE Human PRO polynucleotide #55.
PN US2004044180-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 119
ID ADL94714 standard; cDNA; 1485 BP.
DE Human CDNA encoding secreted/transmembrane protein PRO1306.
PN US2004073015-A1.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1485; DB 12; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 120
ID ADH17625 standard; cDNA; 3375 BP.
DE Human CDNA Sequence SEQ ID NO:117244.
PN BE1074617-A2.
PD 07-FEB-2001.
PA (HSEI-) HELIX RES INST.
Query Match 98.5%; Score 1462.4; DB 4; Length 3375;
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 121
ID ABK05007 standard; cDNA; 3385 BP.
DE Human novel polynucleotide #22.
PN WO200274961-A1.
PD 26-SEP-2002.
PA (HSEI-) HYSEQ INC.
Query Match 98.5%; Score 1462.4; DB 8; Length 3385;
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 122
ID ABA93720 standard; cDNA; 3381 BP.
DE Human differentiation/development CDNA clone amy2_1j19.
PN WO200198454-A2.

PD 27-DEC-2001.
PA (GERM-) GERMAN HUMAN GENOME PROJECT.
Query Match 97.8%; Score 1453; DB 6; Length 3381;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 123
ID ACN38972 standard; cDNA; 3362 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA325244, SEQ ID NO:2818.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GERM-) GENENTECH INC.
Query Match 97.4%; Score 1446.6; DB 13; Length 3362;
Best Local Similarity 99.7%; Pred. No. 0;
RESULT 124
ID AAC66521 standard; cDNA; 3449 BP.
DE Human immune system associated protein HISA-3 coding sequence.
PN US6135941-A.
PD 24-OCT-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match 97.3%; Score 1445.6; DB 4; Length 3449;
Best Local Similarity 99.7%; Pred. No. 0;
RESULT 125
ID AAI58050 standard; cDNA; 1731 BP.
DE Human polynucleotide SEQ ID NO 253.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 96.4%; Score 1430.8; DB 4; Length 1731;
Best Local Similarity 99.1%; Pred. No. 0;
RESULT 126
ID AAI59836 standard; cDNA; 1743 BP.
DE Human polynucleotide SEQ ID NO 3825.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 96.4%; Score 1430.8; DB 4; Length 1743;
Best Local Similarity 99.1%; Pred. No. 0;
RESULT 127
ID APT03024 standard; DNA; 3470 BP.
DE Human breast specific coding sequence SEQ ID NO: 29.
PN WO200240672-A2.
PD 23-MAY-2002.
PA (DIAD-) DIADEXUS INC.
Query Match 95.8%; Score 1423.2; DB 6; Length 3470;
Best Local Similarity 99.7%; Pred. No. 0;
RESULT 128
ID ADO80255 standard; cDNA; 3451 BP.
DE Full length human cDNA useful for treating neurological disease Seq 1761.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 92.6%; Score 1374.4; DB 13; Length 3451;
Best Local Similarity 94.9%; Pred. No. 0;
RESULT 129
ID ADR26679 standard; DNA; 1343 BP.
DE Breast cancer prognosis marker #2540.
PN WO2004065545-A2.
PD 05-AUG-2004.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
Query Match 83.2%; Score 1236; DB 13; Length 1343;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 130
ID AAI96212 standard; cDNA; 781 BP.
DE Human neuroblastoma expressed polynucleotide SEQ ID NO 2287.
PN WO200166719-A1.
PD 13-SEP-2001.
PA (CHIB-) CHIBA PREFECTURE.
Query Match 43.4%; Score 644.4; DB 4; Length 781;
Best Local Similarity 97.0%; Pred. No. 5.3e-169;
RESULT 131
ID AAI96213 standard; cDNA; 768 BP.
DE Human neuroblastoma expressed polynucleotide SEQ ID NO 2288.
PN WO200166719-A1.
PD 13-SEP-2001.
PA (CHIB-) CHIBA PREFECTURE.
Query Match 43.0%; Score 638.2; DB 4; Length 768;
Best Local Similarity 93.5%; Pred. No. 2.8e-167;
RESULT 132
ID AAH05908 standard; cDNA; 857 BP.
DE Human cDNA clone (5'-primer) SEQ ID NO:2743.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 41.5%; Score 616; DB 4; Length 857;
Best Local Similarity 92.0%; Pred. No. 4.7e-161;
RESULT 133
ID AAV41919 standard; cDNA; 632 BP.
DE Nucleotide sequence of the cDNA clone AIF-2 (HERGM49).
PN WO9831800-A2.
PD 23-JUL-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 40.6%; Score 602.8; DB 2; Length 632;
Best Local Similarity 99.5%; Pred. No. 1.9e-157;
RESULT 134
ID ACH39813 standard; cDNA; 593 BP.
DE Human foetal brain cDNA #1180.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES I W.
Query Match 32.1%; Score 476.2; DB 9; Length 593;
Best Local Similarity 96.4%; Pred. No. 4.1e-122;
RESULT 135
ID ABL49913 standard; DNA; 453 BP.
DE Intracellular calcium ion transport related DNA sequence SEQ ID NO:33.
PN WO200210371-A1.
PD 07-FEB-2002.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 30.4%; Score 451.4; DB 6; Length 453;
Best Local Similarity 99.8%; Pred. No. 3e-115;
RESULT 136
ID AAV82798 standard; cDNA; 453 BP.
DE cDNA encoding a ATG-1117 (allograft inflammatory factor, AIF3) protein.
PN EP879880-A1.
PD 25-NOV-1998.
PA (SMIK) SMITHLINE BECHAM CORP.
Query Match 30.2%; Score 448.2; DB 2; Length 453;
Best Local Similarity 99.3%; Pred. No. 2.3e-114;
RESULT 137
ID ABX74821 standard; cDNA; 437 BP.
DE Human cDNA sequence #121 down-regulated in CC-RCC patients.
PN WO200279411-A2.
PD 10-OCT-2002.
PA (VAND-) VAN ANDEL INST.
Query Match 23.4%; Score 348; DB 10; Length 437;
Best Local Similarity 94.4%; Pred. No. 2.1e-86;
RESULT 138
ID APT03023 standard; DNA; 393 BP.
DE Human breast specific coding sequence SEQ ID NO: 28.
PN WO200240672-A2.
PD 23-MAY-2002.
PA (DIAD-) DIADEXUS INC.
Query Match 18.7%; Score 278.4; DB 6; Length 393;
Best Local Similarity 99.3%; Pred. No. 5.3e-67;
RESULT 139
ID ABL49912 standard; DNA; 444 BP.
DE Intracellular calcium ion transport related DNA sequence SEQ ID NO:32.
PN WO200210371-A1.
PD 07-FEB-2002.
PA (KYOW) KYOWA HAKKO KOGYO KK.

Query Match 12.9%; Score 192.2; DB 6; Length 444;
Best Local Similarity 67.1%; Pred. No. 6.4e-43;
RESULT 140
ID AAG9369 standard; cDNA; 491 BP.
DE Human allograft inflammatory factor 1 (AIF-1) cDNA.
PN W05517506-A1.
PD 29-JUN-1995.
PA (HARD) HARVARD COLLEGE.
Query Match 12.9%; Score 192.2; DB 2; Length 491;
Best Local Similarity 67.1%; Pred. No. 6.8e-43;
RESULT 141
ID AA65628 standard; cDNA; 491 BP.
DE Human allograft inflammatory factor 1 (AIF-1) encoding cDNA SEQ ID NO:43.
PN US6077948-A.
PD 20-JUN-2000.
PA (HARD) HARVARD COLLEGE.
Query Match 12.9%; Score 192.2; DB 3; Length 491;
Best Local Similarity 67.1%; Pred. No. 6.8e-43;
RESULT 142
ID AAT64809 standard; cDNA; 635 BP.
DE Human RC-9 cDNA useful in proliferative arterial disease diagnosis.
PN W09722880-A1.
PD 26-JUN-1997.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 12.9%; Score 192.2; DB 2; Length 635;
Best Local Similarity 67.1%; Pred. No. 7.7e-43;
RESULT 143
ID AAV82800 standard; cDNA; 635 BP.
DE ATG-750/RC-9 (allograft inflammatory factor-1) cDNA.
PN EP879883-A1.
PD 25-NOV-1998.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 12.9%; Score 192.2; DB 2; Length 635;
Best Local Similarity 67.1%; Pred. No. 7.7e-43;
RESULT 144
ID AAV82802 standard; cDNA; 635 BP.
DE ATG-750/RC-9 (allograft inflammatory factor-1) cDNA.
PN EP879883-A1.
PD 25-NOV-1998.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 12.9%; Score 192.2; DB 2; Length 635;
Best Local Similarity 67.1%; Pred. No. 7.7e-43;
RESULT 145
ID ADA19323 standard; cDNA; 639 BP.
DE Human insulin resistance marker IRM228 (AIP1) cDNA.
PN W020029835-A2.
PD 12-DEC-2002.
PA (CLIN-) CLINGENIX INC.
Query Match 12.9%; Score 192.2; DB 10; Length 639;
Best Local Similarity 67.1%; Pred. No. 7.7e-43;
RESULT 146
ID AAD05035 standard; cDNA; 659 BP.
DE Novel human cytokine-2 (NHC-2) cDNA.
PN US6204021-B1.
PD 20-MAR-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 12.9%; Score 192.2; DB 4; Length 659;
Best Local Similarity 67.1%; Pred. No. 7.9e-43;
RESULT 147
ID ABR15589 standard; cDNA; 659 BP.
DE DNA encoding novel human cytokine-2 (NHC-2), version #2.
PN US200201827-A1.
PD 03-JAN-2002.
PA (INCY-) INCYTE PHARM INC.
Query Match 12.9%; Score 192.2; DB 6; Length 659;
Best Local Similarity 67.1%; Pred. No. 7.9e-43;
RESULT 148
ID ADA67731 standard; DNA; 659 BP.
DE Novel human cytokine 2, NHC-2, DNA #2.
PN US2003096371-A1.
PD 22-MAY-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 12.9%; Score 192.2; DB 9; Length 659;

Best Local Similarity 67.1%; Pred. No. 7.9e-43;
RESULT 149
ID ADQ22610 standard; DNA; 760 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5430.
PN W0200404838-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 12.9%; Score 192.2; DB 12; Length 760;
Best Local Similarity 67.1%; Pred. No. 8.4e-43;
RESULT 150
ID ABK84357 standard; cDNA; 639 BP.
DE Human cDNA differentially expressed in granulocytic cells #928.
PN W0200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 12.9%; Score 191; DB 6; Length 639;
Best Local Similarity 68.7%; Pred. No. 1.7e-42;
RESULT 151
ID ACA89946 standard; cDNA; 639 BP.
DE Gene differentially regulated in cardiovascular disease #67.
PN W02003031650-A2.
PD 17-APR-2003.
PA (FARB) BAYER AG.
Query Match 12.9%; Score 191; DB 8; Length 639;
Best Local Similarity 68.7%; Pred. No. 1.7e-42;
RESULT 152
ID ADR24778 standard; DNA; 639 BP.
DE Breast cancer prognosis marker #639.
PN W02004065545-A2.
PD 05-AUG-2004.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
PA (NECA-) NETHERLANDS CANCER INST.
Query Match 12.9%; Score 191; DB 13; Length 639;
Best Local Similarity 68.7%; Pred. No. 1.7e-42;
RESULT 153
ID ADR52830 standard; DNA; 639 BP.
DE Drug therapy altered expressed gene #181.
PN W02004072265-A2.
PD 26-AUG-2004.
PA (AMHP) WYETH.
PA (BURC/) BURCZYNSKI M.
PA (TWIN/) TWINE N.
PA (DORN/) DORNER A J.
PA (TREP/) TREPICCHIO W L.
Query Match 12.9%; Score 191; DB 13; Length 639;
Best Local Similarity 68.7%; Pred. No. 1.7e-42;
RESULT 154
ID AAH25798 standard; DNA; 441 BP.
DE Human Mpi type Iba1 DNA.
PN JP2001078775-A.
PD 27-MAR-2001.
PA (KOKU-) KOKURITSU SEISHIN SHINKET CENT SOCHO.
PA (IYAK-) IYAKUHIN FUKUSAYO HIGAI KYUSAI KENKYU SH.
PA (MOCH) MOCHIDA PHARM CO LTD.
Query Match 12.7%; Score 189.2; DB 4; Length 441;
Best Local Similarity 66.9%; Pred. No. 4.4e-42;
RESULT 155
ID ABR15587 standard; cDNA; 658 BP.
DE DNA encoding novel human cytokine-2 (NHC-2) version #1.
PN US2002001827-A1.
PD 03-JAN-2002.
PA (INCY-) INCYTE PHARM INC.
Query Match 12.6%; Score 186.8; DB 6; Length 658;
Best Local Similarity 65.2%; Pred. No. 2.5e-41;
RESULT 156
ID AAC03908 standard; cDNA; 658 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 3906.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 12.5%; Score 186; DB 3; Length 658;
Best Local Similarity 66.2%; Pred. No. 4.2e-41;
RESULT 157

ID AAC10904 standard; cDNA; 597 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 14979.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GENSET) GENSET.
Query Match 12.3%; Score 183.2; DB 3; Length 597;
Best Local Similarity 66.2%; Pred. No. 2.4e-40;
RESULT 158
ID AAH25799 standard; DNA; 441 BP.
DE Murine Mpl type Iba1 DNA.
PN JP2001078775-A.
PD 27-MAR-2001.
PA (KOKU-) KOKURITSU SEISHIN SHINKEI CENT SOCHO.
PA (IYAK-) IYAKUHIN FUKUSAYO HIGAI KYUSAI KENKYU SH.
PA (MOCH) MOCHIDA PHARM CO LTD.
Query Match 12.3%; Score 182.2; DB 4; Length 441;
Best Local Similarity 65.3%; Pred. No. 4e-40;
RESULT 159
ID AAG99370 standard; cDNA; 627 BP.
DE Rat allograft inflammatory factor 1 (AIF-1) cDNA.
PN WO9517506-A1.
PD 29-JUN-1995.
PA (HARD) HARVARD COLLEGE.
Query Match 12.3%; Score 182; DB 2; Length 627;
Best Local Similarity 65.1%; Pred. No. 5.4e-40;
RESULT 160
ID ADB58279 standard; DNA; 653 BP.
DE Toxicity-related gene, SEQ ID 3305.
PN WO2003064624-A2.
PD 07-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 12.3%; Score 182; DB 10; Length 653;
Best Local Similarity 65.1%; Pred. No. 5.5e-40;
RESULT 161
ID AAA65591 standard; cDNA; 627 BP.
DE Rat allograft inflammatory factor 1 (AIF-1) encoding cDNA SEQ ID NO:4.
PN US6077948-A.
PD 20-JUN-2000.
PA (HARD) HARVARD COLLEGE.
Query Match 12.1%; Score 180.4; DB 3; Length 627;
Best Local Similarity 64.8%; Pred. No. 1.5e-39;
RESULT 162
ID ADA19322 standard; cDNA; 536 BP.
DE Human insulin resistance marker IM228 (AIF1) EST.
PN WO200298355-A2.
PD 12-DEC-2002.
PA (CLIN-) CLINGENIX INC.
Query Match 12.0%; Score 177.8; DB 10; Length 536;
Best Local Similarity 66.5%; Pred. No. 7.4e-39;
RESULT 163
ID AAT64808 standard; cDNA; 696 BP.
DE Rat RC-9 cDNA useful in proliferative arterial disease diagnosis.
PN WO9722880-A1.
PD 26-JUN-1997.
PA (SMK) SMITHKLINE BEECHAM CORP.
Query Match 11.9%; Score 176; DB 2; Length 696;
Best Local Similarity 65.1%; Pred. No. 2.7e-38;
RESULT 164
ID AAH25804 standard; DNA; 441 BP.
DE Murine Iba1 (EP1-EF1) DNA.
PN JP2001078775-A.
PD 27-MAR-2001.
PA (KOKU-) KOKURITSU SEISHIN SHINKEI CENT SOCHO.
PA (IYAK-) IYAKUHIN FUKUSAYO HIGAI KYUSAI KENKYU SH.
PA (MOCH) MOCHIDA PHARM CO LTD.
Query Match 11.3%; Score 167.8; DB 4; Length 441;
Best Local Similarity 63.2%; Pred. No. 4.2e-36;
RESULT 165
ID AAH25805 standard; DNA; 360 BP.
DE Murine Iba1 (1-120) DNA.
PN JP2001078775-A.
PD 27-MAR-2001.
PA (KOKU-) KOKURITSU SEISHIN SHINKEI CENT SOCHO.

PA (IYAK-) IYAKUHIN FUKUSAYO HIGAI KYUSAI KENKYU SH.
PA (MOCH) MOCHIDA PHARM CO LTD.
Query Match 11.2%; Score 166.8; DB 4; Length 360;
Best Local Similarity 67.6%; Pred. No. 7.1e-36;
RESULT 166
ID AAH25800 standard; DNA; 345 BP.
DE Murine Iba1 (1-115) DNA.
PN JP2001078775-A.
PD 27-MAR-2001.
PA (KOKU-) KOKURITSU SEISHIN SHINKEI CENT SOCHO.
PA (IYAK-) IYAKUHIN FUKUSAYO HIGAI KYUSAI KENKYU SH.
PA (MOCH) MOCHIDA PHARM CO LTD.
Query Match 11.0%; Score 163.8; DB 4; Length 345;
Best Local Similarity 68.1%; Pred. No. 4.8e-35;
RESULT 167
ID AAH25803 standard; DNA; 441 BP.
DE Murine Iba1 (EP2-EF2) DNA.
PN JP2001078775-A.
PD 27-MAR-2001.
PA (KOKU-) KOKURITSU SEISHIN SHINKEI CENT SOCHO.
PA (IYAK-) IYAKUHIN FUKUSAYO HIGAI KYUSAI KENKYU SH.
PA (MOCH) MOCHIDA PHARM CO LTD.
Query Match 10.8%; Score 159.8; DB 4; Length 441;
Best Local Similarity 62.1%; Pred. No. 7.1e-34;
RESULT 168
ID AAH25801 standard; DNA; 354 BP.
DE Murine Iba1 (30-147) DNA.
PN JP2001078775-A.
PD 27-MAR-2001.
PA (KOKU-) KOKURITSU SEISHIN SHINKEI CENT SOCHO.
PA (IYAK-) IYAKUHIN FUKUSAYO HIGAI KYUSAI KENKYU SH.
PA (MOCH) MOCHIDA PHARM CO LTD.
Query Match 9.6%; Score 143.2; DB 4; Length 354;
Best Local Similarity 64.6%; Pred. No. 2.7e-29;
RESULT 169
ID AAC06542 standard; cDNA; 507 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 10617.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GENSET) GENSET.
Query Match 8.8%; Score 131.4; DB 3; Length 507;
Best Local Similarity 66.3%; Pred. No. 6.4e-26;
RESULT 170
ID AAV62799 standard; cDNA; 579 BP.
DE ATG-1100 (allograft inflammatory factor-1gamma) cDNA.
PN EP879882-A1.
PD 25-NOV-1998.
PA (SMK) SMITHKLINE BEECHAM CORP.
Query Match 8.8%; Score 131.4; DB 2; Length 579;
Best Local Similarity 66.3%; Pred. No. 6.9e-26;
RESULT 171
ID AAH25802 standard; DNA; 273 BP.
DE Murine Iba1 (30-120) DNA.
PN JP2001078775-A.
PD 27-MAR-2001.
PA (KOKU-) KOKURITSU SEISHIN SHINKEI CENT SOCHO.
PA (IYAK-) IYAKUHIN FUKUSAYO HIGAI KYUSAI KENKYU SH.
PA (MOCH) MOCHIDA PHARM CO LTD.
Query Match 8.6%; Score 127.8; DB 4; Length 273;
Best Local Similarity 67.4%; Pred. No. 4.8e-25;
RESULT 172
ID ADA67729 standard; DNA; 639 BP.
DE Novel human cytokine 2, NHC-2, DNA #1.
PN US2003096371-A1.
PD 22-MAY-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 8.5%; Score 126.4; DB 9; Length 639;
Best Local Similarity 65.2%; Pred. No. 1.8e-24;
RESULT 173
ID AAT64807 standard; DNA; 1678 BP.
DE Rat RC-9 gene useful in proliferative arterial disease diagnosis.
PN WO9722880-A1.
PD 26-JUN-1997.

PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 8.4%; Score 124; DB 2; Length 1678;
Best Local Similarity 64.8%; Pred. No. 1.4e-23;
RESULT 174
ID AA190746 standard; cDNA; 351 BP.
DE Human polynucleotide SEQ ID NO 10806.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 8.3%; Score 123.2; DB 4; Length 351;
Best Local Similarity 62.8%; Pred. No. 1e-23;
RESULT 175
ID ACH42742 standard; cDNA; 379 BP.
DE Human foetal kidney cDNA #276.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 7.9%; Score 117.8; DB 9; Length 379;
Best Local Similarity 66.2%; Pred. No. 3.5e-22;
RESULT 176
ID AAT64806 standard; DNA; 424 BP.
DE Rat RC-9 DNA useful in proliferative arterial disease diagnosis.
PN WO9722880-A1.
PD 26-JUN-1997.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 7.9%; Score 117.8; DB 2; Length 424;
Best Local Similarity 64.6%; Pred. No. 3.7e-22;
RESULT 177
ID ADP2830 standard; DNA; 424 BP.
DE Renal toxin progression gene marker #1419.
PN WO2004048598-A2.
PD 10-JUN-2004.
PA (GENE-) GENE LOGIC INC.
Query Match 7.9%; Score 117.8; DB 12; Length 424;
Best Local Similarity 64.6%; Pred. No. 3.7e-22;
RESULT 178
ID AB149899 standard; DNA; 117 BP.
DE Intracellular calcium ion transport related DNA sequence SEQ ID NO:14.
PN WO200210371-A1.
PD 07-FEB-2002.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 7.9%; Score 117; DB 6; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.2e-22;
RESULT 179
ID AAV82801 standard; cDNA; 631 BP.
DE ATG-1120 (allograft inflammatory factor-1-delta) cDNA.
PN EP979883-A1.
PD 25-NOV-1998.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 7.7%; Score 114.2; DB 2; Length 631;
Best Local Similarity 59.7%; Pred. No. 4.5e-21;
RESULT 180
ID AB149900 standard; DNA; 117 BP.
DE Intracellular calcium ion transport related DNA sequence SEQ ID NO:15.
PN WO200210371-A1.
PD 07-FEB-2002.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 7.0%; Score 104.2; DB 6; Length 117;
Best Local Similarity 93.2%; Pred. No. 1.2e-18;
RESULT 181
ID AAQ9371 standard; cDNA; 331 BP.
DE Rat allograft inflammatory factor 1 (AIF-1) partial cDNA sequence.
PN WO9517506-A1.
PD 29-JUN-1995.
PA (HARD) HARVARD COLLEGE.
Query Match 6.4%; Score 94.8; DB 2; Length 331;
Best Local Similarity 63.7%; Pred. No. 8.5e-16;
RESULT 182
ID AA65588 standard; cDNA; 331 BP.

DE Rat allograft inflammatory factor 1 (AIF-1) cDNA sequence SEQ ID NO:1.
PN US607948-A.
PD 20-JUN-2000.
PA (HARD) HARVARD COLLEGE.
Query Match 6.4%; Score 94.8; DB 3; Length 331;
Best Local Similarity 63.7%; Pred. No. 8.5e-16;
RESULT 183
ID AB149901 standard; DNA; 117 BP.
DE Intracellular calcium ion transport related DNA sequence SEQ ID NO:16.
PN WO200210371-A1.
PD 07-FEB-2002.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 6.0%; Score 88.8; DB 6; Length 117;
Best Local Similarity 85.3%; Pred. No. 2.4e-14;
RESULT 184
ID ADP10331 standard; DNA; 1363 BP.
DE Reference mRNA sequences for marker probe #8.
PN WO2004042346-A2.
PD 21-MAY-2004.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match 5.3%; Score 79.4; DB 12; Length 1363;
Best Local Similarity 68.3%; Pred. No. 3.4e-11;
RESULT 185
ID ADP10462 standard; DNA; 1363 BP.
DE Reference mRNA sequences for marker probe #139.
PN WO2004042346-A2.
PD 21-MAY-2004.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match 5.3%; Score 79.4; DB 12; Length 1363;
Best Local Similarity 68.3%; Pred. No. 3.4e-11;
RESULT 186
ID ADQ84989 standard; cDNA; 1363 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #1803.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 5.3%; Score 79.4; DB 12; Length 1363;
Best Local Similarity 68.3%; Pred. No. 3.4e-11;
RESULT 187
ID ADQ83815 standard; cDNA; 1363 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #629.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 5.3%; Score 79.4; DB 12; Length 1363;
Best Local Similarity 68.3%; Pred. No. 3.4e-11;
RESULT 188
ID ADR25232 standard; DNA; 1363 BP.
DE Breast cancer prognosis marker #1093.
PN WO2004065545-A2.
PD 05-AUG-2004.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
PA (NECA-) NETHERLANDS CANCER INST.
Query Match 5.3%; Score 79.4; DB 13; Length 1363;
Best Local Similarity 68.3%; Pred. No. 3.4e-11;
RESULT 189
ID ABK84756 standard; cDNA; 81800 BP.
DE Human cDNA differentially expressed in granulocytic cells #1327.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 5.3%; Score 79.4; DB 6; Length 81800;
Best Local Similarity 68.3%; Pred. No. 2.6e-10;
RESULT 190
ID AAX89526 standard; cDNA; 1235 BP.
DE Nucleotide sequence of Interferon Responsive Transcript-1.
PN WO9934814-A1.
PD 15-JUL-1999.
PA (UTEM) UNIV TEMPLE.

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Query Match          5.1%; Score 76.2; DB 2; Length 1235;
Best Local Similarity 67.1%; Pred. No. 2.5e-10;
RESULT 191
ID ADQ18012 standard; DNA; 325 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 829.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match          4.9%; Score 73.4; DB 12; Length 325;
Best Local Similarity 69.3%; Pred. No. 7.9e-10;
RESULT 192
ID AAH08134 standard; cDNA; 646 BP.
DE Human cDNA clone (5'-primer) SEQ ID NO:4969.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match          4.7%; Score 69.2; DB 4; Length 646;
Best Local Similarity 60.4%; Pred. No. 1.7e-08;
RESULT 193
ID AAH18153 standard; cDNA; 1876 BP.
DE Human cDNA sequence SEQ ID NO:18038.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match          4.6%; Score 68.8; DB 4; Length 1876;
Best Local Similarity 59.9%; Pred. No. 3.6e-08;
RESULT 194
ID ABZ11562 standard; cDNA; 1897 BP.
DE Human polynucleotide SEQ ID NO 444.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match          4.6%; Score 68.8; DB 6; Length 1897;
Best Local Similarity 59.9%; Pred. No. 3.7e-08;
RESULT 195
ID ADM44080 standard; cDNA; 1897 BP.
DE Novel human arginine-rich protein cDNA #444.
PN US2004053250-A1.
PD 18-MAR-2004.
PA (TANG/) TANG Y T.
PA (XUEA/) XUE A.
PA (DRMA/) DRMANAC R T.
Query Match          4.6%; Score 68.8; DB 12; Length 1897;
Best Local Similarity 59.9%; Pred. No. 3.7e-08;
RESULT 196
ID ACN37848 standard; cDNA; 1898 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA324241, SEQ ID NO:1000.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH-) GENENTECH INC.
Query Match          4.6%; Score 68.8; DB 13; Length 1898;
Best Local Similarity 59.9%; Pred. No. 3.7e-08;
RESULT 197
ID ABA04457 standard; cDNA; 1923 BP.
DE Human PP3051 protein encoding cDNA SEQ ID NO:19/21.
PN CN13131316-A.
PD 19-SEP-2001.
PA (SHAN-) SHANGHAI INST ONCOLOGY
Query Match          4.6%; Score 68.8; DB 6; Length 1923;
Best Local Similarity 59.9%; Pred. No. 3.7e-08;
RESULT 198
ID AD347517 standard; cDNA; 1924 BP.
DE Human cDNA upregulated in dendritic cells SEQ ID NO 217.
PN US2003134283-A1.
PD 17-JUL-2003.
PA (PETE/) PETERSON D P.
PA (PEAR/) PEARSON C I.
PA (COCK/) COCKS B G.
Query Match          4.6%; Score 68.8; DB 10; Length 1924;
Best Local Similarity 59.9%; Pred. No. 3.7e-08;
RESULT 199
ID ABA04454 standard; cDNA; 1562 BP.
DE Human PPI187 protein encoding cDNA SEQ ID NO:10/12.
CN13131316-A.
PD 19-SEP-2001.
PA (SHAN-) SHANGHAI INST ONCOLOGY.
Query Match          4.5%; Score 66.4; DB 6; Length 1562;
Best Local Similarity 62.8%; Pred. No. 1.6e-07;
RESULT 200
ID AAV1920 standard; cDNA; 582 BP.
DE Nucleotide sequence of the cDNA clone AIF-3 (HNGBH45).
PN WO9831800-A2.
PD 23-JUL-1998.
PA (HOMA-) HUMAN GENOME SCI INC.
PA (AUCC-) AUCKLAND UNISERVICES LTD.
Query Match          4.3%; Score 64.2; DB 2; Length 582;
Best Local Similarity 59.7%; Pred. No. 3.9e-07;
RESULT 201
ID ABK43437 standard; cDNA; 717 BP.
DE DNA encoding novel central nervous system protein #17.
PN WO200155318-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match          4.3%; Score 64.2; DB 4; Length 717;
Best Local Similarity 59.7%; Pred. No. 4.3e-07;
RESULT 202
ID AD153824 standard; cDNA; 717 BP.
DE cDNA encoding novel human protein seq id 27.
PN US2004018969-A1.
PD 29-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match          4.3%; Score 64.2; DB 12; Length 717;
Best Local Similarity 59.7%; Pred. No. 4.3e-07;
RESULT 203
ID ADK51980 standard; cDNA; 2277 BP.
DE Human atopic dermatitis/psoriasis-associated cDNA #13.
PN WO2004016785-A1.
PD 26-FEB-2004.
PA (GENO-) GENOX RES INC.
PA (UYJU-) UNIV JUJENDENO.
Query Match          4.3%; Score 64.2; DB 12; Length 2277;
Best Local Similarity 59.7%; Pred. No. 7.7e-07;
RESULT 204
ID ACN37282 standard; cDNA; 2277 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA323749, SEQ ID NO:62.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH-) GENENTECH INC.
Query Match          4.3%; Score 64.2; DB 13; Length 2277;
Best Local Similarity 59.7%; Pred. No. 7.7e-07;
RESULT 205
ID ADE54054 standard; cDNA; 2369 BP.
DE Human prostate cancer cDNA #401.
PN US2003190640-A1.
PD 09-OCT-2003.
PA (FARI/) FARIS M.
PA (PEAR/) PEARSON C I.
Query Match          4.3%; Score 64.2; DB 10; Length 2369;
Best Local Similarity 59.7%; Pred. No. 7.9e-07;
RESULT 206
ID ACC79092 standard; cDNA; 2490 BP.
DE Human secreted protein SECP-67 encoding cDNA SEQ ID NO:147.
PN WO2003016506-A2.
PD 27-FEB-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match          4.3%; Score 64.2; DB 10; Length 2490;
Best Local Similarity 59.7%; Pred. No. 8.1e-07;
RESULT 207
ID AD130758 standard; cDNA; 1358 BP.
DE Human cDNA #84.
PN US6607879-B1.
PD 19-AUG-2003.
PA (INCY-) INCYTE CORP.
Query Match          4.3%; Score 63.2; DB 11; Length 1358;
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Best Local Similarity 59.1%; Pred. No. 1.1e-06;
RESULT 208
ID AAI63901 standard; cDNA; 505 BP.
DE Human polynucleotide seq ID NO 109.
PN WO200155308-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCT INC.
Query Match 4.2%; Score 63; DB 4; Length 505;
Best Local Similarity 60.0%; Pred. No. 7.9e-07;
RESULT 209
ID AAS31615 standard; cDNA; 505 BP.
DE cDNA encoding novel human calcium-binding protein #39.
PN WO200155304-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCT INC.
Query Match 4.2%; Score 63; DB 4; Length 505;
Best Local Similarity 60.0%; Pred. No. 7.9e-07;
RESULT 210
ID ABR43760 standard; cDNA; 505 BP.
DE DNA encoding novel central nervous system protein #340.
PN WO200155318-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCT INC.
Query Match 4.2%; Score 63; DB 4; Length 505;
Best Local Similarity 60.0%; Pred. No. 7.9e-07;
RESULT 211
ID AD154147 standard; cDNA; 505 BP.
DE cDNA encoding novel human protein seq id 350.
PN US2004018969-A1.
PD 29-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 4.2%; Score 63; DB 12; Length 505;
Best Local Similarity 60.0%; Pred. No. 7.9e-07;
RESULT 212
ID ADM24452 standard; cDNA; 505 BP.
DE Human PRO polynucleotide #99.
PN US2004014039-A1.
PD 22-JAN-2004.
PA (HUMA-) HUMAN GENOME SCT INC.
Query Match 4.2%; Score 63; DB 12; Length 505;
Best Local Similarity 60.0%; Pred. No. 7.9e-07;
RESULT 213
ID ABL49896 standard; DNA; 117 BP.
DE Intracellular calcium ion transport related DNA sequence SEQ ID NO:11.
PN WO200210371-A1.
PD 07-FEB-2002.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 4.2%; Score 62.6; DB 6; Length 117;
Best Local Similarity 70.9%; Pred. No. 4.9e-07;
RESULT 214
ID ABL30333 standard; DNA; 1000 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 42472.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.1%; Score 60.4; DB 4; Length 1000;
Best Local Similarity 53.4%; Pred. No. 5.9e-06;
RESULT 215
ID ABL49697 standard; DNA; 117 BP.
DE Intracellular calcium ion transport related DNA sequence SEQ ID NO:12.
PN WO200210371-A1.
PD 07-FEB-2002.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 4.0%; Score 59.4; DB 6; Length 117;
Best Local Similarity 69.2%; Pred. No. 3.9e-06;
RESULT 216
ID ABL49898 standard; DNA; 117 BP.
DE Intracellular calcium ion transport related DNA sequence SEQ ID NO:13.
PN WO200210371-A1.
PD 07-FEB-2002.
PA (KYOW) KYOWA HAKKO KOGYO KK.

Query Match 3.9%; Score 57.8; DB 6; Length 117;
Best Local Similarity 68.4%; Pred. No. 1.1e-05;
RESULT 217
ID ABL30332 standard; DNA; 10902 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 42469.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.8%; Score 56; DB 4; Length 10902;
Best Local Similarity 57.4%; Pred. No. 0.00033;
RESULT 218
ID AAC26771 standard; cDNA; 55 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 30846.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GENST) GENSET.
Query Match 3.7%; Score 54.6; DB 3; Length 55;
Best Local Similarity 98.2%; Pred. No. 5.8e-05;
RESULT 219
ID AAI21783 standard; DNA; 186 BP.
DE Probe #11716 for gene expression analysis in human cervical cell sample.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 3.7%; Score 54.4; DB 4; Length 186;
Best Local Similarity 72.9%; Pred. No. 0.00012;
RESULT 220
ID ABA66854 standard; DNA; 186 BP.
DE Human foetal liver single exon nucleic acid probe #15159.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 3.7%; Score 54.4; DB 4; Length 186;
Best Local Similarity 72.9%; Pred. No. 0.00012;
RESULT 221
ID AAI47066 standard; DNA; 186 BP.
DE Probe #15752 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 3.7%; Score 54.4; DB 4; Length 186;
Best Local Similarity 72.9%; Pred. No. 0.00012;
RESULT 222
ID ABA48939 standard; DNA; 186 BP.
DE Human breast cell single exon nucleic acid probe #7634.
PN WO200157271-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 3.7%; Score 54.4; DB 4; Length 186;
Best Local Similarity 72.9%; Pred. No. 0.00012;
RESULT 223
ID ABA33923 standard; DNA; 186 BP.
DE Probe #12389 for gene expression analysis in human heart cell sample.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 3.7%; Score 54.4; DB 4; Length 186;
Best Local Similarity 72.9%; Pred. No. 0.00012;
RESULT 224
ID AAK41013 standard; DNA; 186 BP.
DE Human bone marrow expressed single exon probe SEQ ID NO: 15570.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 3.7%; Score 54.4; DB 4; Length 186;
Best Local Similarity 72.9%; Pred. No. 0.00012;
RESULT 225
ID AAK15290 standard; DNA; 186 BP.
DE Human brain expressed single exon probe SEQ ID NO: 15281.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 3.7%; Score 54.4; DB 4; Length 186;
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Best Local Similarity 72.9%; Pred. No. 0.00012;
RESULT 226
ID ABS40605 standard; DNA; 186 BP.
DE Human liver single exon probe, SEQ ID No 15595.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 3.7%; Score 54.4; DB 4; Length 186;
Best Local Similarity 72.9%; Pred. No. 0.00012;
RESULT 227
ID AA107468 standard; DNA; 186 BP.
DE Probe #7459 used to measure gene expression in human breast sample.
PN WO200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 3.7%; Score 54.4; DB 5; Length 186;
Best Local Similarity 72.9%; Pred. No. 0.00012;
RESULT 228
ID ABS14985 standard; DNA; 186 BP.
DE Human genome-derived single exon probe ORF from lung SEQ ID No 14976.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 3.7%; Score 54.4; DB 6; Length 186;
Best Local Similarity 72.9%; Pred. No. 0.00012;
RESULT 229
ID AA112595 standard; DNA; 500 BP.
DE Probe #2528 for gene expression analysis in human cervical cell sample.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 3.7%; Score 54.4; DB 4; Length 500;
Best Local Similarity 72.9%; Pred. No. 0.0002;
RESULT 230
ID ABA54292 standard; DNA; 500 BP.
DE Human foetal liver single exon nucleic acid probe #2597.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 3.7%; Score 54.4; DB 4; Length 500;
Best Local Similarity 72.9%; Pred. No. 0.0002;
RESULT 231
ID AA133943 standard; DNA; 500 BP.
DE Probe #2629 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 3.7%; Score 54.4; DB 4; Length 500;
Best Local Similarity 72.9%; Pred. No. 0.0002;
RESULT 232
ID ABA43836 standard; DNA; 500 BP.
DE Human breast cell single exon nucleic acid probe #2531.
PN WO200157271-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 3.7%; Score 54.4; DB 4; Length 500;
Best Local Similarity 72.9%; Pred. No. 0.0002;
RESULT 233
ID ABA24049 standard; DNA; 500 BP.
DE Probe #2515 for gene expression analysis in human heart cell sample.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 3.7%; Score 54.4; DB 4; Length 500;
Best Local Similarity 72.9%; Pred. No. 0.0002;
RESULT 234
ID AAK8012 standard; DNA; 500 BP.
DE Human bone marrow expressed single exon probe SEQ ID NO: 2569.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 3.7%; Score 54.4; DB 4; Length 500;
Best Local Similarity 72.9%; Pred. No. 0.0002;
RESULT 235
ID AAK02576 standard; DNA; 500 BP.
DE Human brain expressed single exon probe SEQ ID NO: 2567.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 3.7%; Score 54.4; DB 4; Length 500;
Best Local Similarity 72.9%; Pred. No. 0.0002;
RESULT 236
ID ABS27607 standard; DNA; 500 BP.
DE Human liver single exon probe, SEQ ID No 2597.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 3.7%; Score 54.4; DB 4; Length 500;
Best Local Similarity 72.9%; Pred. No. 0.0002;
RESULT 237
ID AA102500 standard; DNA; 500 BP.
DE Probe #2491 used to measure gene expression in human breast sample.
PN WO200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 3.7%; Score 54.4; DB 5; Length 500;
Best Local Similarity 72.9%; Pred. No. 0.0002;
RESULT 238
ID ABS02484 standard; DNA; 500 BP.
DE Human genome-derived single exon probe from lung SEQ ID No 2475.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 3.7%; Score 54.4; DB 6; Length 500;
Best Local Similarity 72.9%; Pred. No. 0.0002;
RESULT 239
ID AB132566 standard; DNA; 6907 BP.
DE Human immune system associated gene SEQ ID NO: 539.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIC-) EPIDEMIOLOGICS AG.
Query Match 3.6%; Score 54.2; DB 6; Length 6907;
Best Local Similarity 56.4%; Pred. No. 0.00083;
RESULT 240
ID ADC75907 standard; DNA; 638 BP.
DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 831.
PN WO2003020905-A2.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
Query Match 3.5%; Score 51.8; DB 10; Length 638;
Best Local Similarity 50.6%; Pred. No. 0.0012;
RESULT 241
ID ADC77192 standard; DNA; 654 BP.
DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 2121.
PN WO2003020905-A2.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
Query Match 3.5%; Score 51.8; DB 10; Length 654;
Best Local Similarity 50.6%; Pred. No. 0.0012;
RESULT 242
ID ADC76478 standard; DNA; 654 BP.
DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 1747.
PN WO2003020905-A2.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
Query Match 3.5%; Score 51.8; DB 10; Length 654;
Best Local Similarity 50.6%; Pred. No. 0.0012;
RESULT 243
ID ADK57002 standard; DNA; 654 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #4385.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
Query Match 3.5%; Score 51.8; DB 10; Length 654;
Best Local Similarity 50.6%; Pred. No. 0.0012;
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RESULT 244
ID ADK55204 standard; DNA; 654 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #2587.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
PA (DOWC) DOW AGROSCIENCES LLC.
Query Match 3.5%; Score 51.8; DB 10; Length 654;
Best Local Similarity 50.6%; Pred. No. 0.0012;
RESULT 245
ID ADC76480 standard; DNA; 620 BP.
DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 1749.
PN WO2003020905-A2.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
Query Match 3.3%; Score 49.6; DB 10; Length 620;
Best Local Similarity 50.0%; Pred. No. 0.0048;
RESULT 246
ID ADC77196 standard; DNA; 620 BP.
DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 2125.
PN WO2003020905-A2.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
Query Match 3.3%; Score 49.6; DB 10; Length 620;
Best Local Similarity 50.0%; Pred. No. 0.0048;
RESULT 247
ID ADK59086 standard; DNA; 620 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #6469.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
PA (DOWC) DOW AGROSCIENCES LLC.
Query Match 3.3%; Score 49.6; DB 10; Length 620;
Best Local Similarity 50.0%; Pred. No. 0.0048;
RESULT 248
ID ADK57006 standard; DNA; 620 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #4389.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
PA (DOWC) DOW AGROSCIENCES LLC.
Query Match 3.3%; Score 49.6; DB 10; Length 620;
Best Local Similarity 50.0%; Pred. No. 0.0048;
RESULT 249
ID ADK55190 standard; DNA; 622 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #2573.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
PA (DOWC) DOW AGROSCIENCES LLC.
Query Match 3.3%; Score 49.6; DB 10; Length 622;
Best Local Similarity 50.0%; Pred. No. 0.0048;
RESULT 250
ID ADK58040 standard; DNA; 691 BP.
DE Toxicity-related gene, SEQ ID 3066.
PN WO2003064624-A2.
PD 07-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 3.3%; Score 49.2; DB 10; Length 691;
Best Local Similarity 50.4%; Pred. No. 0.0066;
RESULT 251
ID ADK52516 standard; DNA; 691 BP.
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3058.
PN WO2003065993-A2.
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 3.3%; Score 49.2; DB 10; Length 691;
Best Local Similarity 50.4%; Pred. No. 0.0066;
RESULT 252
ID ADA71938 standard; DNA; 2000 BP.
DE Rice gene, SEQ ID 5263.
PN WO2003000898-A1.
PD 03-JAN-2003.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 3.3%; Score 49.2; DB 8; Length 2000;
Best Local Similarity 9.4%; Pred. No. 0.011;
RESULT 253
ID ACA26827 standard; DNA; 2451 BP.
DE Prokaryotic essential gene #8484.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 3.1%; Score 46.4; DB 8; Length 2451;
Best Local Similarity 46.8%; Pred. No. 0.074;
RESULT 254
ID ADJ42629 standard; cDNA; 768 BP.
DE Plant cDNA #3629.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MUG/) MUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICE D.
PA (ZHU/) ZHU T.
Query Match 3.1%; Score 46; DB 12; Length 768;
Best Local Similarity 50.9%; Pred. No. 0.054;
RESULT 255
ID AAC01147 standard; cDNA; 452 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 1145.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 3.1%; Score 45.6; DB 3; Length 452;
Best Local Similarity 51.5%; Pred. No. 0.054;
RESULT 256
ID ADL07540 standard; cDNA; 498 BP.
DE Human His-tagged Troponin C, TnC, cDNA.
PN CN1412312-A.
PD 23-APR-2003.
PA (CHON-) CHONGQING KANGRWEI PHARM IND CO LTD.
Query Match 3.1%; Score 45.6; DB 12; Length 498;
Best Local Similarity 51.5%; Pred. No. 0.056;
RESULT 257
ID AAC03907 standard; cDNA; 547 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 3905.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 3.1%; Score 45.6; DB 3; Length 547;
Best Local Similarity 51.5%; Pred. No. 0.059;
RESULT 258
ID ADQ23762 standard; DNA; 1001 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6582.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.1%; Score 45.6; DB 12; Length 1001;
Best Local Similarity 51.5%; Pred. No. 0.08;
RESULT 259
ID ADA71938 standard; DNA; 2000 BP.
DE Rice gene, SEQ ID 5263.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 3.1%; Score 45.4; DB 8; Length 2000;
Best Local Similarity 9.9%; Pred. No. 0.13;
RESULT 260
ID ADA58445 standard; cDNA; 303 BP.
DE Maize sucrose synthase EST #89.
PN US2003135870-A1.

PD 17-JUL-2003.
PA (CHEIT/) CHEIKH N.
PA (FISH/) FISHER D. K.
PA (LIUJ/) LIU J.
Query Match 3.0%; Score 45.2; DB 9; Length 303;
Best Local Similarity 54.6%; Pred. No. 0.057;
RESULT 261
ID AD858316 standard; DNA; 1112 BP.
DE Toxicity-related gene, SEQ ID 3342.
PN WO2003064624-A2.
PD 07-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 3.0%; Score 45; DB 10; Length 1112;
Best Local Similarity 49.8%; Pred. No. 0.12;
RESULT 262
ID AB711999 standard; DNA; 1112 BP.
DE Toxicity modelling related rat gene SEQ ID No 1701.
PN WO200295000-A2.
PD 28-NOV-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 3.0%; Score 45; DB 10; Length 1112;
Best Local Similarity 49.8%; Pred. No. 0.12;
RESULT 263
ID ADP72640 standard; DNA; 1112 BP.
DE Renal toxin progression gene marker #1229.
PN WO2004048598-A2.
PD 10-JUN-2004.
PA (GENE-) GENE LOGIC INC.
Query Match 3.0%; Score 45; DB 12; Length 1112;
Best Local Similarity 49.8%; Pred. No. 0.12;
RESULT 264
ID AAH48729 standard; cDNA; 3372 BP.
DE Human HCN2 cDNA.
PN WO200159153-A2.
PD 16-AUG-2001.
PA (AVET) AVENTIS PHARMA DEUT GMBH.
Query Match 3.0%; Score 44.6; DB 4; Length 3372;
Best Local Similarity 57.6%; Pred. No. 0.28;
RESULT 265
ID ADQ83419 standard; cDNA; 3372 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #233.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GERTH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 3.0%; Score 44.6; DB 13; Length 3372;
Best Local Similarity 57.6%; Pred. No. 0.28;
RESULT 266
ID AAH98302 standard; cDNA; 3431 BP.
DE Human EST-derived coding sequence SEQ ID NO: 159.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.0%; Score 44.6; DB 4; Length 3431;
Best Local Similarity 57.6%; Pred. No. 0.28;
RESULT 267
ID AAD29756 standard; DNA; 3459 BP.
DE Human hyperpolarisation-activated cyclic nucleotide-gated channel 2 DNA.
PN WO200202630-A2.
PD 10-JAN-2002.
PA (SMIX) SMTHTLINE BEECHAM PLC.
Query Match 3.0%; Score 44.6; DB 6; Length 3459;
Best Local Similarity 57.6%; Pred. No. 0.28;
RESULT 268
ID ADA9154 standard; DNA; 447 BP.
DE Maize gene conferring disease resistance in plants.
PN WO2003000906-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 3.0%; Score 44.4; DB 9; Length 447;
Best Local Similarity 50.5%; Pred. No. 0.12;
RESULT 269

ID ADA49026 standard; DNA; 787 BP.
DE Wheat gene conferring disease resistance in plants.
PN WO2003000906-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 3.0%; Score 44.4; DB 9; Length 787;
Best Local Similarity 50.5%; Pred. No. 0.15;
RESULT 270
ID AD111958 standard; DNA; 787 BP.
DE Wheat cDNA modulated by post-transcriptional gene silencing seqid 594.
PN US200313588-A1.
PD 17-JUL-2003.
PA (ZHUT/) ZHU T.
PA (WANG/) WANG X.
PA (CHANG/) CHANG H.
PA (BRIG/) BRIGGS S. P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S. A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (MOUG/) MUGHAMER T.
PA (PROV/) PROVART N.
PA (RICK/) RICE D.
Query Match 3.0%; Score 44.4; DB 11; Length 787;
Best Local Similarity 50.5%; Pred. No. 0.15;
RESULT 271
ID ADJ42631 standard; cDNA; 787 BP.
DE Plant cDNA #3631.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MUGHAMER T.
PA (BRIG/) BRIGGS S. P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S. A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICE D.
PA (ZHUT/) ZHU T.
Query Match 3.0%; Score 44.4; DB 12; Length 787;
Best Local Similarity 50.5%; Pred. No. 0.15;
RESULT 272
ID ADJ42636 standard; cDNA; 802 BP.
DE Plant cDNA #3636.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MUGHAMER T.
PA (BRIG/) BRIGGS S. P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S. A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICE D.
PA (ZHUT/) ZHU T.
Query Match 3.0%; Score 44.4; DB 12; Length 802;
Best Local Similarity 50.5%; Pred. No. 0.15;
RESULT 273
ID ADJ42639 standard; cDNA; 841 BP.
DE Plant cDNA #3639.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MUGHAMER T.
PA (BRIG/) BRIGGS S. P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S. A.

PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVAT N.
PA (RICK/) RICE D.
PA (ZHUT/) ZHU T.
Query Match 3.0%; Score 44.4; DB 12; Length 844;
Best Local Similarity 50.5%; Pred. No. 0.16;
RESULT 274
ID AAC40960 standard; DNA; 490 BP.
DE Zee mays DNA fragment SEQ ID NO: 30145.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 3.0%; Score 44; DB 3; Length 490;
Best Local Similarity 50.0%; Pred. No. 0.16;
RESULT 275
ID ABB83907 standard; DNA; 1251 BP.
DE Calcium sensor G85 encoding sequence.
PN EP1209167-A1.
PD 29-MAY-2002.
PA (OKAZ-) OKAZAKI NAT RES INST.
Query Match 3.0%; Score 44; DB 6; Length 1251;
Best Local Similarity 49.2%; Pred. No. 0.25;
RESULT 276
ID ADJ67515 standard; DNA; 1527 BP.
DE Human ovarian specific gene SEQ ID NO:229.
PN WO2004013311-A2.
PD 12-FEB-2004.
PA (DIAD-) DIADEXUS INC.
Query Match 3.0%; Score 44; DB 12; Length 1527;
Best Local Similarity 58.3%; Pred. No. 0.27;
RESULT 277
ID ADJ67300 standard; DNA; 1527 BP.
DE Human ovarian specific gene SEQ ID NO:14.
PN WO2004013311-A2.
PD 12-FEB-2004.
PA (DIAD-) DIADEXUS INC.
Query Match 3.0%; Score 44; DB 12; Length 1527;
Best Local Similarity 58.3%; Pred. No. 0.27;
RESULT 278
ID ABB63767 standard; cDNA; 2175 BP.
DE Human cDNA differentially expressed in granulocytic cells #338.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 3.0%; Score 44; DB 6; Length 2175;
Best Local Similarity 49.2%; Pred. No. 0.33;
RESULT 279
ID ABB64770 standard; DNA; 2190 BP.
DE Human calmodulin 2 gene.
PN WO200285308-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
Query Match 3.0%; Score 44; DB 10; Length 2190;
Best Local Similarity 49.2%; Pred. No. 0.33;
RESULT 280
ID ABB21000 standard; DNA; 2190 BP.
DE Human calmodulin 2 DNA.
PN WO200285309-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
Query Match 3.0%; Score 44; DB 11; Length 2190;
Best Local Similarity 49.2%; Pred. No. 0.33;
RESULT 281
ID ABB60285 standard; cDNA; 2190 BP.
DE Human calmodulin 2 encoding cDNA.
PN WO2004039955-A2.
PD 13-MAY-2004.
PA (RIGE-) RIGEL PHARM INC.
Query Match 3.0%; Score 44; DB 13; Length 2190;
Best Local Similarity 49.2%; Pred. No. 0.33;
RESULT 282
ID ABB44950 standard; cDNA; 2247 BP.
DE cDNA encoding novel human secretory protein, Seq ID No 31.

PN WO200166689-A2.
PD 13-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.0%; Score 44; DB 5; Length 2247;
Best Local Similarity 49.2%; Pred. No. 0.33;
RESULT 283
ID ADQ84750 standard; cDNA; 2363 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #1564.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH-) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 3.0%; Score 44; DB 12; Length 2363;
Best Local Similarity 49.2%; Pred. No. 0.34;
RESULT 284
ID ADQ86930 standard; cDNA; 2363 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #3805.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH-) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 3.0%; Score 44; DB 13; Length 2363;
Best Local Similarity 49.2%; Pred. No. 0.34;
RESULT 285
ID ADA58674 standard; cDNA; 255 BP.
DE Maize sucrose synthase EST #318.
PN US2003135870-A1.
PD 17-JUL-2003.
PA (CHEI/) CHEIKH N.
PA (FISH/) FISHER D K.
PA (LIU/) LIU J.
Query Match 2.9%; Score 43.8; DB 9; Length 255;
Best Local Similarity 54.4%; Pred. No. 0.13;
RESULT 286
ID ABB63305 standard; DNA; 1161 BP.
DE Breast cancer related gene sequence SEQ ID NO:1642.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 2.9%; Score 43.6; DB 6; Length 1161;
Best Local Similarity 52.8%; Pred. No. 0.31;
RESULT 287
ID AAX90997 standard; DNA; 1173 BP.
DE Human centrin-2 gene (Hcen-2).
PN WO9951186-A2.
PD 14-OCT-1999.
PA (MILL-) MILLENNIUM PHARM INC.
PA (REGC) UNIV CALIFORNIA.
Query Match 2.9%; Score 43.6; DB 2; Length 1173;
Best Local Similarity 52.8%; Pred. No. 0.31;
RESULT 288
ID AAX90998 standard; DNA; 6710 BP.
DE Human centrin-2 genomic sequence (Hcen-2).
PN WO9951186-A2.
PD 14-OCT-1999.
PA (MILL-) MILLENNIUM PHARM INC.
PA (REGC) UNIV CALIFORNIA.
Query Match 2.9%; Score 43.6; DB 2; Length 6710;
Best Local Similarity 52.8%; Pred. No. 0.74;
RESULT 289
ID ADT66612 standard; cDNA; 1084 BP.
DE Rat calmodulin cDNA.
PN WO2004070383-A2.
PD 19-AUG-2004.
PA (CHEP) GRUNENTHAL GMBH.
Query Match 2.9%; Score 43.4; DB 13; Length 1084;
Best Local Similarity 49.3%; Pred. No. 0.34;
RESULT 290
ID AAC55847 standard; DNA; 2466 BP.
DE Mitomycin biosynthetic gene cluster related alpha amy1ase orf20.
PN WO200053737-A2.

PD 14-SEP-2000.
PA (MINU) UNIV MINNESOTA.
PA (SHER) SHERMAN D H.
PA (MAOY) MAO Y.
PA (VARO) VAROGLU M.
PA (HEMW) HE M.
PA (SHEL) SHELTON P C.
Query Match 2.9%; Score 43.4; DB 3; Length 2466;
Best Local Similarity 52.5%; Pred. No. 0.51;
RESULT 291
ID ADE10328 standard; DNA; 2466 BP.
DE S. lavendulae gene for orf20.
PN US2003134398-A1.
PD 17-JUL-2003.
PA (SHER) SHERMAN D H.
PA (MAOY) MAO Y.
PA (VARO) VAROGLU M.
PA (HEMW) HE M.
PA (SHEL) SHELTON P.
Query Match 2.9%; Score 43.4; DB 10; Length 2466;
Best Local Similarity 52.5%; Pred. No. 0.51;
RESULT 292
ID AAC5841 standard; DNA; 18034 BP.
DE Complete Mitomycin ORF 11-22 nucleotide sequence.
PN WO20053737-A2.
PD 14-SEP-2000.
PA (MINU) UNIV MINNESOTA.
PA (SHER) SHERMAN D H.
PA (MAOY) MAO Y.
PA (VARO) VAROGLU M.
PA (HEMW) HE M.
PA (SHEL) SHELTON P C.
Query Match 2.9%; Score 43.4; DB 3; Length 18034;
Best Local Similarity 52.5%; Pred. No. 1.4;
RESULT 293
ID ADE10260 standard; DNA; 18034 BP.
DE S. lavendulae mitomycin C gene cluster for ORFs 11-22.
PN US2003134398-A1.
PD 17-JUL-2003.
PA (SHER) SHERMAN D H.
PA (MAOY) MAO Y.
PA (VARO) VAROGLU M.
PA (HEMW) HE M.
PA (SHEL) SHELTON P.
Query Match 2.9%; Score 43.4; DB 10; Length 18034;
Best Local Similarity 52.5%; Pred. No. 1.4;
RESULT 294
ID ADA58464 standard; cDNA; 294 BP.
DE Maize sucrose synthase EST #108.
PN US2003135870-A1.
PD 17-JUL-2003.
PA (CHEI) CHEIKH N.
PA (FISH) FISHER D K.
PA (LIUJ) LIU J.
Query Match 2.9%; Score 43.2; DB 9; Length 294;
Best Local Similarity 54.9%; Pred. No. 0.2;
RESULT 295
ID ABA83905 standard; cDNA; 447 BP.
DE Rat calmodulin encoding sequence.
PN EP1209167-A1.
PD 29-MAY-2002.
PA (OKAZ) OKAZAKI NAT RES INST.
Query Match 2.9%; Score 43.2; DB 6; Length 447;
Best Local Similarity 50.5%; Pred. No. 0.25;
RESULT 296
ID ADO21558 standard; DNA; 450 BP.
DE Calmodulin mutant Y99F/Y138F-encoding DNA, SEQ ID NO:5.
PN WO2004046179-A1.
PD 03-JUN-2004.
PA (CNSJ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.
Query Match 2.9%; Score 43.2; DB 12; Length 450;
Best Local Similarity 50.5%; Pred. No. 0.25;
RESULT 297

ID ADO21554 standard; DNA; 450 BP.
DE Calmodulin mutant Y99F-encoding DNA, SEQ ID NO:1.
PN WO2004046179-A1.
PD 03-JUN-2004.
PA (CNSJ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.
Query Match 2.9%; Score 43.2; DB 12; Length 450;
Best Local Similarity 50.5%; Pred. No. 0.25;
RESULT 298
ID ADO21556 standard; DNA; 450 BP.
DE Calmodulin mutant Y138F-encoding DNA, SEQ ID NO:3.
PN WO2004046179-A1.
PD 03-JUN-2004.
PA (CNSJ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.
Query Match 2.9%; Score 43.2; DB 12; Length 450;
Best Local Similarity 50.5%; Pred. No. 0.25;
RESULT 299
ID AAC03638 standard; cDNA; 564 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 3836.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 2.9%; Score 43.2; DB 3; Length 564;
Best Local Similarity 49.1%; Pred. No. 0.28;
RESULT 300
ID ADF60791 standard; DNA; 1182 BP.
DE BCC DNA #SEQ ID 13.
PN WO2003076466-A1.
PD 18-SEP-2003.
PA (NEUR) NEUROGENEX CO LTD.
Query Match 2.9%; Score 43.2; DB 10; Length 1182;
Best Local Similarity 50.5%; Pred. No. 0.4;
RESULT 301
ID AAD45852 standard; cDNA; 2908 BP.
DE Corn sucrose synthase (Sue1) cDNA.
PN WO200267662-A1.
PD 06-SEP-2002.
PA (PION) PIONEER HI-BRED INT INC.
Query Match 2.9%; Score 43.2; DB 6; Length 2908;
Best Local Similarity 54.4%; Pred. No. 0.63;
RESULT 302
ID ADA58522 standard; cDNA; 285 BP.
DE Maize sucrose synthase EST #166.
PN US2003135870-A1.
PD 17-JUL-2003.
PA (CHEI) CHEIKH N.
PA (FISH) FISHER D K.
PA (LIUJ) LIU J.
Query Match 2.9%; Score 43; DB 9; Length 285;
Best Local Similarity 54.8%; Pred. No. 0.23;
RESULT 303
ID AAA1581 standard; DNA; 378 BP.
DE Plant microsatellite marker #542.
PN WO9967421-A1.
PD 29-DEC-1999.
PA (GENE) GENESIS RES & DEV CORP LTD.
PA (FLET) FLETCHER CHALLENGE FOREST LTD.
Query Match 2.9%; Score 43; DB 3; Length 378;
Best Local Similarity 48.9%; Pred. No. 0.26;
RESULT 304
ID AAA1434 standard; DNA; 450 BP.
DE Plant microsatellite marker #395.
PN WO9967421-A1.
PD 29-DEC-1999.
PA (GENE) GENESIS RES & DEV CORP LTD.
PA (FLET) FLETCHER CHALLENGE FOREST LTD.
Query Match 2.9%; Score 43; DB 3; Length 450;
Best Local Similarity 48.9%; Pred. No. 0.26;
RESULT 305
ID AAA1901 standard; DNA; 495 BP.
DE Plant microsatellite marker #862.
PN WO9967421-A1.
PD 29-DEC-1999.
PA (GENE) GENESIS RES & DEV CORP LTD.

PA	(FLET-) FLETCHER CHALLENGE FOREST LTD.
Query Match	2.9%; Score 43; DB 3; Length 495;
Best Local Similarity	48.9%; Pred. No. 0.3;
RESULT 306	
ID	ADJ42635 standard; cDNA; 820 BP.
DE	Plant cDNA #3635.
PN	US2004016025-A1.
PD	22-JAN-2004.
PA	(BUDW/) BUDWORTH P.
PA	(MOUG/) MOUGHAMER T.
PA	(BRIG/) BRIGGS S P.
PA	(COOP/) COOPER B.
PA	(GLAZ/) GLAZEBROOK J.
PA	(GOF/) GOF S A.
PA	(KATA/) KATAGIRI F.
PA	(KEEP/) KEEPS J.
PA	(PROV/) PROVART N.
PA	(RICK/) RICHE D.
PA	(ZHUT/) ZHU T.
Query Match	2.9%; Score 42.8; DB 12; Length 820;
Best Local Similarity	50.0%; Pred. No. 0.44;
RESULT 307	
ID	ADA58468 standard; cDNA; 306 BP.
DE	MaiZe sucrOSE synthase EST #112.
PN	US2003135870-A1.
PD	17-JUL-2003.
PA	(CHEI/) CHEIGH N.
PA	(FISH/) FISHER D K.
PA	(LIU/) LIU J.
Query Match	2.9%; Score 42.6; DB 9; Length 306;
Best Local Similarity	54.9%; Pred. No. 0.3;
RESULT 308	
ID	ADA58455 standard; cDNA; 313 BP.
DE	MaiZe sucrOSE synthase EST #99.
PN	US2003135870-A1.
PD	17-JUL-2003.
PA	(CHEI/) CHEIGH N.
PA	(FISH/) FISHER D K.
PA	(LIU/) LIU J.
Query Match	2.9%; Score 42.6; DB 9; Length 313;
Best Local Similarity	54.9%; Pred. No. 0.31;
RESULT 309	
ID	ADC71780 standard; DNA; 624 BP.
DE	DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 2109.
PN	WO2003020905-A2.
PD	13-MAR-2003.
PA	(DOMC) DOM CHEM CO.
Query Match	2.9%; Score 42.6; DB 10; Length 624;
Best Local Similarity	50.7%; Pred. No. 0.43;
RESULT 310	
ID	ADC75909 standard; DNA; 624 BP.
DE	DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 833.
PN	WO2003020905-A2.
PD	13-MAR-2003.
PA	(DOMC) DOM CHEM CO.
Query Match	2.9%; Score 42.6; DB 10; Length 624;
Best Local Similarity	50.7%; Pred. No. 0.43;
RESULT 311	
ID	ADK59089 standard; DNA; 624 BP.
DE	Plant DNA sequence which confers altered metabolic characteristic #6472.
PN	WO2003020936-A1.
PD	13-MAR-2003.
PA	(DOMC) DOM CHEM CO.
PA	(DOMC) DOM AGROSCIENCES LLC.
Query Match	2.9%; Score 42.6; DB 10; Length 624;
Best Local Similarity	50.7%; Pred. No. 0.43;
RESULT 312	
ID	ADK56990 standard; DNA; 624 BP.
DE	Plant DNA sequence which confers altered metabolic characteristic #4373.
PN	WO2003020936-A1.
PD	13-MAR-2003.
PA	(DOMC) DOM CHEM CO.
PA	(DOMC) DOM AGROSCIENCES LLC.

Query Match	2.8%;	Score 42.6;	DB 10;	Length 624;
Best Local Similarity	50.7%;	Pred. No. 0.43;		
RESULT 313				
ID AD097470 standard; DNA; 28516 BP.				
DE Mouse cancer associated sequence MD09-001, SEQ ID 447.				
PN WO2004060304-A2.				
PD 22-JUL-2004.				
PA (SNAR-) SAGRES DISCOVERY INC.				
Query Match	2.8%;	Score 42;	DB 12;	Length 28516;
Best Local Similarity	47.7%;	Pred. No. 4.3;		
RESULT 314				
ID ADK55193 standard; DNA; 674 BP.				
DE Plant DNA sequence which confers altered metabolic characteristic #576				
PN WO2003020936-A1.				
PD 13-MAR-2003.				
PA (DMWC) DOW CHEM CO.				
DE Mouse cancer associated sequence MD09-001, SEQ ID 447.				
PN WO2004060304-A2.				
PD 22-JUL-2004.				
PA (SNAR-) SAGRES DISCOVERY INC.				
Query Match	2.8%;	Score 41.8;	DB 10;	Length 674;
Best Local Similarity	48.2%;	Pred. No. 0.75;		
RESULT 315				
ID ADCT5903 standard; DNA; 695 BP.				
DE DNA homologous to phytopathogen resistance-related CDNA - SEQ ID 827.				
PN WO2003020905-A2.				
PD 13-MAR-2003.				
PA (DMWC) DOW CHEM CO.				
Query Match	2.8%;	Score 41.8;	DB 10;	Length 695;
Best Local Similarity	48.2%;	Pred. No. 0.76;		
RESULT 316				
ID ADCT7187 standard; DNA; 695 BP.				
DE DNA homologous to phytopathogen resistance-related CDNA - SEQ ID 2116.				
PN WO2003020905-A2.				
PD 13-MAR-2003.				
PA (DMWC) DOW CHEM CO.				
Query Match	2.8%;	Score 41.8;	DB 10;	Length 695;
Best Local Similarity	48.2%;	Pred. No. 0.76;		
RESULT 317				
ID ADKS6997 standard; DNA; 695 BP.				
DE Plant DNA sequence which confers altered metabolic characteristic #4380				
PN WO2003020936-A1.				
PD 13-MAR-2003.				
PA (DMWC) DOW CHEM CO.				
DE Mouse cancer associated sequence MD09-001, SEQ ID 447.				
PN WO2004060304-A2.				
PD 22-JUL-2004.				
PA (SNAR-) SAGRES DISCOVERY INC.				
Query Match	2.8%;	Score 41.8;	DB 10;	Length 695;
Best Local Similarity	48.2%;	Pred. No. 0.76;		
RESULT 318				
ID ADKS9090 standard; DNA; 695 BP.				
DE Plant DNA sequence which confers altered metabolic characteristic #4773				
PN WO2003020936-A1.				
PD 13-MAR-2003.				
PA (DMWC) DOW CHEM CO.				
DE Mouse cancer associated sequence MD09-001, SEQ ID 447.				
PN WO2004060304-A2.				
PD 22-JUL-2004.				
PA (SNAR-) SAGRES DISCOVERY INC.				
Query Match	2.8%;	Score 41.8;	DB 10;	Length 695;
Best Local Similarity	48.2%;	Pred. No. 0.76;		
RESULT 319				
ID AB199274 standard; cDNA; 1361 BP.				
DE Mouse ischaemic condition related CDNA sequence SEQ ID NO:111.				
PN WO200188188-A2.				
PD 22-NOV-2001.				
PA (UTNT-) UNIV NIHON SCHOOL JURIDICAL PERSON.				
Query Match	2.8%;	Score 41.8;	DB 6;	Length 1361;
Best Local Similarity	48.9%;	Pred. No. 1.1;		
RESULT 320				
ID ADP66614 standard; cDNA; 1361 BP.				
DE Murine calmodulin cDNA.				
PN WO2004070383-A2.				
PD 19-AUG-2004.				
PA (CHEF) GRUENENTHAL GMBH.				
Query Match	2.8%;	Score 41.8;	DB 13;	Length 1361;
Best Local Similarity	48.9%;	Pred. No. 1.1;		
RESULT 321				
ID AAH74541 standard; cDNA; 905 BP.				
DE Nucleotide sequence of a chitobiosidase polypeptide.				
PN WO200146387-A1.				

PD 28-JUN-2001.
PA (CORR) CORNELL RES FOUND INC.
Query Match 2.8%; Score 41.4; DB 4; Length 905;
Best Local Similarity 52.6%; Pred. No. 1.1;
RESULT 322
ID ADA49171 standard; DNA; 447 BP.
DE Maize gene conferring disease resistance in plants.
PN WO200300906-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.8%; Score 41.2; DB 9; Length 447;
Best Local Similarity 51.1%; Pred. No. 0.9;
RESULT 323
ID ADJ12052 standard; DNA; 447 BP.
DE Maize cDNA modulated by post-transcriptional gene silencing SeqID 688.
PN US2003135888-A1.
PD 17-JUL-2003.
PA (ZHUT/) ZHU T.
PA (WANG/) WANG X.
PA (CHANG/) CHANG H.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOLF/) GOLF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (MOUG/) MOUGHAMER T.
PA (PROV/) PROVART N.
PA (RICK/) RIQUE D.
Query Match 2.8%; Score 41.2; DB 11; Length 447;
Best Local Similarity 51.1%; Pred. No. 0.9;
RESULT 324
ID ADJ42640 standard; cDNA; 727 BP.
DE Plant cDNA #3640.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDM/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOLF/) GOLF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RIQUE D.
PA (ZHUT/) ZHU T.
Query Match 2.8%; Score 41.2; DB 12; Length 727;
Best Local Similarity 51.1%; Pred. No. 1.1;
RESULT 325
ID ADQ97220 standard; DNA; 52640 BP.
DE Mouse cancer associated sequence MD08-015, SEQ ID 196.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.8%; Score 41.2; DB 12; Length 52640;
Best Local Similarity 57.9%; Pred. No. 9.7;
RESULT 326
ID ADC76479 standard; DNA; 521 BP.
DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 1748.
PN WO2003020905-A2.
PD 13-MAR-2003.
PA (DOMC) DOW CHEM CO.
Query Match 2.8%; Score 41; DB 10; Length 521;
Best Local Similarity 48.5%; Pred. No. 1.1;
RESULT 327
ID ADC77193 standard; DNA; 521 BP.
DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 2122.
PN WO2003020905-A2.
PD 13-MAR-2003.
PA (DOMC) DOW CHEM CO.
Query Match 2.8%; Score 41; DB 10; Length 521;
Best Local Similarity 48.5%; Pred. No. 1.1;

RESULT 328
ID ADK57003 standard; DNA; 521 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #4386.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOMC) DOW CHEM CO.
PA (DOMC) DOW AGROSCIENCES LLC.
Query Match 2.8%; Score 41; DB 10; Length 521;
Best Local Similarity 48.5%; Pred. No. 1.1;
RESULT 329
ID ADK55199 standard; DNA; 521 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #2582.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOMC) DOW CHEM CO.
PA (DOMC) DOW AGROSCIENCES LLC.
Query Match 2.8%; Score 41; DB 10; Length 521;
Best Local Similarity 48.5%; Pred. No. 1.1;
RESULT 330
ID ABZ51912 standard; cDNA; 936 BP.
DE Aspergillus oryzae polynucleotide SEQ ID NO 1025.
PN WO200279476-A1.
PD 10-OCT-2002.
PA (NAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (NARE-) NAT RES INST BREWING.
PA (NORO) NAT FOOD RES INST MIN AGRIC.
Query Match 2.8%; Score 41; DB 8; Length 936;
Best Local Similarity 49.3%; Pred. No. 1.5;
RESULT 331
ID AAC43155 standard; DNA; 975 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 38229.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 2.8%; Score 41; DB 3; Length 975;
Best Local Similarity 48.9%; Pred. No. 1.5;
RESULT 332
ID ABZ14388 standard; DNA; 975 BP.
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 2193.
PN WO200216655-A2.
PD 28-FEB-2002.
PA (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.8%; Score 41; DB 6; Length 975;
Best Local Similarity 48.9%; Pred. No. 1.5;
RESULT 333
ID ABZ42072 standard; cDNA; 975 BP.
DE Arabidopsis thaliana gene #56 modulated by PTGS.
PN WO200281695-A2.
PD 17-OCT-2002.
PA (FRIE-) FRIEDRICH KIESCHER INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.8%; Score 41; DB 8; Length 975;
Best Local Similarity 48.9%; Pred. No. 1.5;
RESULT 334
ID ADA68266 standard; DNA; 975 BP.
DE Arabidopsis thaliana gene, SEQ ID 847.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.8%; Score 41; DB 8; Length 975;
Best Local Similarity 48.9%; Pred. No. 1.5;
RESULT 335
ID AAF14569 standard; cDNA; 1129 BP.
DE Aspergillus oryzae EST SEQ ID NO:7092.
PN WO200056762-A2.
PD 28-SEP-2000.
PA (NOVO) NOVO NORDISK BIOTECH INC.
PA (NOVO) NOVO NORDISK AS.
Query Match 2.8%; Score 41; DB 3; Length 1129;
Best Local Similarity 49.3%; Pred. No. 1.6;
RESULT 336
ID ADJ67514 standard; DNA; 1457 BP.
DE Human ovarian specific gene SEQ ID NO:228.

PN WO2004013311-A2.
 PD 12-FEB-2004.
 PA (DIAD-) DIADEXUS INC.
 Query Match 2.7%; Score 40.8; DB 12; Length 1457;
 Best Local Similarity 56.8%; Pred. No. 2.1;
 RESULT 337
 ID ADQ67299 standard; DNA; 1457 BP.
 DE Human ovarian specific gene SEQ ID NO:13.
 PN WO2004013311-A2.
 PD 12-FEB-2004.
 PA (DIAD-) DIADEXUS INC.
 Query Match 2.7%; Score 40.8; DB 12; Length 1457;
 Best Local Similarity 56.8%; Pred. No. 2.1;
 RESULT 338
 ID AAQ04331 standard; cDNA; 447 BP.
 DE Recombinant calmodulin gene.
 PN JP02092286-A.
 PD 03-APR-1990.
 PA (KIRI) KIRIN BREWERY KK.
 Query Match 2.7%; Score 40.6; DB 2; Length 447;
 Best Local Similarity 49.8%; Pred. No. 1.3;
 RESULT 339
 ID AAQ04334 standard; DNA; 504 BP.
 DE Plasmid pOCAL7 contg. gene for calmodulin.
 PN JP02092286-A.
 PD 03-APR-1990.
 PA (KIRI) KIRIN BREWERY KK.
 Query Match 2.7%; Score 40.6; DB 2; Length 504;
 Best Local Similarity 49.8%; Pred. No. 1.4;
 RESULT 340
 ID ADQ6431 standard; cDNA; 560 BP.
 DE Cotton cDNA sequence, SEQ ID 4912.
 PN US2004181830-A1.
 PD 16-SEP-2004.
 PA (KOVA) KOVALIC D K.
 PA (ZHOV) ZHOV Y.
 PA (CMOY) CMO Y.
 Query Match 2.7%; Score 40.6; DB 13; Length 560;
 Best Local Similarity 49.3%; Pred. No. 1.5;
 RESULT 341
 ID ADJ41936 standard; cDNA; 724 BP.
 DE Plant cDNA #2936.
 PN US2004016025-A1.
 PD 22-JAN-2004.
 PA (BUDW) BUDWORTH P.
 PA (MOUG) MOUGHAMER T.
 PA (BRIG) BRIGGS S P.
 PA (COOP) COOPER B.
 PA (GLAZ) GLAZEBROOK J.
 PA (GOFF) GOFF S A.
 PA (KATA) KATAGIRI F.
 PA (KREP) KREPS J.
 PA (PROV) PROVART N.
 PA (RICK) RICKES D.
 PA (ZHUT) ZHU T.
 Query Match 2.7%; Score 40.6; DB 12; Length 724;
 Best Local Similarity 49.3%; Pred. No. 1.7;
 RESULT 342
 ID ABD33266 standard; DNA; 166407 BP.
 DE Murine cancer-associated (CA) gene MD07-046.
 PN WO2004058146-A2.
 PD 15-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 2.7%; Score 40.6; DB 13; Length 166407;
 Best Local Similarity 52.0%; Pred. No. 25;
 RESULT 343
 ID ABN74463 standard; cDNA; 974 BP.
 DE Bovine embryonic germ (EG) cell cDNA EST #514.
 PN WO200194550-A2.
 PD 13-DEC-2001.
 PA (INFI-) INFIGEN INC.
 Query Match 2.7%; Score 40.4; DB 6; Length 974;
 Best Local Similarity 41.2%; Pred. No. 2.2;
 RESULT 344
 ID ABN74464 standard; cDNA; 974 BP.
 DE Bovine embryonic germ (EG) cell cDNA EST #515.
 PN WO200194550-A2.
 PD 13-DEC-2001.
 PA (INFI-) INFIGEN INC.
 Query Match 2.7%; Score 40.4; DB 6; Length 974;
 Best Local Similarity 41.2%; Pred. No. 2.2;
 RESULT 345
 ID ADM02510 standard; cDNA; 2240 BP.
 DE Human cDNA of the invention SEQ ID NO:1195.
 PN EP1347046-A1.
 PD 24-SEP-2003.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 2.7%; Score 40.4; DB 11; Length 2240;
 Best Local Similarity 63.3%; Pred. No. 3.4;
 RESULT 346
 ID ADQ63828 standard; cDNA; 2284 BP.
 DE Novel human cDNA sequence #989.
 PN EP1440981-A2.
 PD 28-JUL-2004.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 2.7%; Score 40.4; DB 12; Length 2284;
 Best Local Similarity 63.3%; Pred. No. 3.4;
 RESULT 347
 ID AAQ04332 standard; DNA; 654 BP.
 DE Plasmid pRCM1 and gene for construction of calmodulin expression vector.
 PN JP02092286-A.
 PD 03-APR-1990.
 PA (KIRI) KIRIN BREWERY KK.
 Query Match 2.7%; Score 40.2; DB 2; Length 654;
 Best Local Similarity 48.5%; Pred. No. 2.1;
 RESULT 348
 ID ABK63445 standard; cDNA; 654 BP.
 DE Rat sequence differentially expressed in response to a hepatotoxin #1352.
 PN WO200210453-A2.
 PD 07-FEB-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match 2.7%; Score 40.2; DB 6; Length 654;
 Best Local Similarity 48.5%; Pred. No. 2.1;
 RESULT 349
 ID ACA43874 standard; DNA; 2394 BP.
 DE Prokaryotic essential gene #25531.
 PN WO20027183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 2.7%; Score 40.2; DB 8; Length 2394;
 Best Local Similarity 47.8%; Pred. No. 4;
 RESULT 350
 ID ADQ22652 standard; DNA; 3446 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5472.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 2.7%; Score 40.2; DB 12; Length 3446;
 Best Local Similarity 54.4%; Pred. No. 4.7;
 RESULT 351
 ID ADB58685 standard; DNA; 3513 BP.
 DE Toxicity-related gene, SEQ ID 3711.
 PN WO2003064624-A2.
 PD 07-AUG-2003.
 PA (GENE-) GENE LOGIC INC.
 Query Match 2.7%; Score 40.2; DB 10; Length 3513;
 Best Local Similarity 48.5%; Pred. No. 4.8;
 RESULT 352
 ID ADB53373 standard; DNA; 3513 BP.
 DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3915.
 PN WO2003065893-A2.
 PD 14-AUG-2003.
 PA (GENE-) GENE LOGIC INC.
 Query Match 2.7%; Score 40.2; DB 10; Length 3513;
 Best Local Similarity 48.5%; Pred. No. 4.8;
 RESULT 353

ID ABR42260 standard; DNA; 3513 BP.
DE Toxicity modelling related rat gene SEQ ID No 1962.
PN WO200295000-A2.
PD 28-NOV-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 2.7%; Score 40.2; DB 10; Length 3513;
Best Local Similarity 48.5%; Pred. No. 4.8;
RESULT 354
ID ADP72764 standard; DNA; 3513 BP.
DE Renal toxin progression gene marker #1353.
PN WO2004048598-A2.
PD 10-JUN-2004.
PA (GENE-) GENE LOGIC INC.
Query Match 2.7%; Score 40.2; DB 12; Length 3513;
Best Local Similarity 48.5%; Pred. No. 4.8;
RESULT 355
ID ABR16482 standard; DNA; 693 BP.
DE Human intracellular signalling protein coding sequence - SEQ ID No 35.
PN WO2002101008-A2.
PD 19-DEC-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 2.7%; Score 40; DB 10; Length 693;
Best Local Similarity 47.3%; Pred. No. 2.4;
RESULT 356
ID ABR55208 standard; cDNA; 1278 BP.
DE Calcium sensitive circularly permuted EYFP (cpeyfp), #1, cDNA.
PN EP138982-A1.
PD 11-SEP-2002.
PA (RIKE) RIKEN KK.
Query Match 2.7%; Score 40; DB 6; Length 1278;
Best Local Similarity 46.4%; Pred. No. 3.3;
RESULT 357
ID ABA16487 standard; DNA; 6058 BP.
DE Human nervous system related polynucleotide SEQ ID NO 8818.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUNA-) HUMAN GENOME SCI INC.
Query Match 2.7%; Score 40; DB 5; Length 6058;
Best Local Similarity 53.1%; Pred. No. 7.1;
RESULT 358
ID ADA58565 standard; cDNA; 289 BP.
DE Maize sucrose synthase EST #209.
PN US2003135870-A1.
PD 17-JUN-2003.
PA (CHEI/) CHEIKH N.
PA (FISH/) FISHER D K.
PA (LIU/) LIU J.
Query Match 2.7%; Score 39.8; DB 9; Length 289;
Best Local Similarity 57.7%; Pred. No. 1.8;
RESULT 359
ID ADA58555 standard; cDNA; 329 BP.
DE Maize sucrose synthase EST #199.
PN US2003135870-A1.
PD 17-JUN-2003.
PA (CHEI/) CHEIKH N.
PA (FISH/) FISHER D K.
PA (LIU/) LIU J.
Query Match 2.7%; Score 39.8; DB 9; Length 329;
Best Local Similarity 53.5%; Pred. No. 1.9;
RESULT 360
ID AAA1443 standard; DNA; 350 BP.
DE Plant microsatellite marker #404.
PN WO9967421-A1.
PD 29-DEC-1999.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FOREST LTD.
Query Match 2.7%; Score 39.8; DB 3; Length 350;
Best Local Similarity 48.1%; Pred. No. 2;
RESULT 361
ID ADC77194 standard; DNA; 631 BP.
DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 2123.
PN WO2003020905-A2.
PD 13-MAR-2003.

PA (DOMC) DOW CHEM CO.
Query Match 2.7%; Score 39.8; DB 10; Length 631;
Best Local Similarity 50.3%; Pred. No. 2.6;
RESULT 362
ID ADK59087 standard; DNA; 631 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #6470.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOMC) DOW CHEM CO.
PA (DOMC) DOW AGROSCIENCES LLC.
Query Match 2.7%; Score 39.8; DB 10; Length 631;
Best Local Similarity 50.3%; Pred. No. 2.6;
RESULT 363
ID ADK57004 standard; DNA; 631 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #4387.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOMC) DOW CHEM CO.
PA (DOMC) DOW AGROSCIENCES LLC.
Query Match 2.7%; Score 39.8; DB 10; Length 631;
Best Local Similarity 50.3%; Pred. No. 2.6;
RESULT 364
ID AAC10892 standard; cDNA; 681 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 14967.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GSEI) GENSET.
Query Match 2.7%; Score 39.8; DB 3; Length 681;
Best Local Similarity 49.8%; Pred. No. 2.7;
RESULT 365
ID ADA68724 standard; DNA; 798 BP.
DE Rice gene, SEQ ID 2047.
PN WO200300898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.7%; Score 39.8; DB 8; Length 798;
Best Local Similarity 50.3%; Pred. No. 3;
RESULT 366
ID ADB58320 standard; DNA; 1139 BP.
DE Toxicity-related gene, SEQ ID 3346.
PN WO2003064624-A2.
PD 07-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 2.7%; Score 39.8; DB 10; Length 1139;
Best Local Similarity 48.9%; Pred. No. 3.5;
RESULT 367
ID ADB52875 standard; DNA; 1139 BP.
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3417.
PN WO2003065993-A2.
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 2.7%; Score 39.8; DB 10; Length 1139;
Best Local Similarity 48.9%; Pred. No. 3.5;
RESULT 368
ID ABR42002 standard; DNA; 1139 BP.
DE Toxicity modelling related rat gene SEQ ID No 1704.
PN WO200295000-A2.
PD 28-NOV-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 2.7%; Score 39.8; DB 10; Length 1139;
Best Local Similarity 48.9%; Pred. No. 3.5;
RESULT 369
ID ADA69683 standard; DNA; 1248 BP.
DE Rice gene, SEQ ID 3006.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.7%; Score 39.8; DB 8; Length 1248;
Best Local Similarity 50.3%; Pred. No. 3.7;
RESULT 370
ID ADS55071 standard; cDNA; 1890 BP.
DE Bacterial polynucleotide #7058.
PN US2003233675-A1.

PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 2.7%; Score 39.8; DB 13; Length 1890;
RESULT 371
ID ADS49559 standard; cDNA; 1929 BP.
DE Bacterial polynucleotide #4302.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 2.7%; Score 39.8; DB 13; Length 1929;
RESULT 372
ID ABR99819 standard; cDNA; 6512 BP.
DE Mouse ischaemic condition related cDNA sequence SEQ ID NO:932.
PN WO200188188-A2.
PD 22-NOV-2001.
PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
Query Match
Best Local Similarity 2.7%; Score 39.8; DB 6; Length 6512;
RESULT 373
ID AAN80188 standard; DNA; 462 BP.
DE DNA encoding biosynthetic multifunctional protein.
PN MO8809344-A.
PD 01-DEC-1988.
PA (CREA-) CREATIVE BIOMOLECULES INC.
Query Match
Best Local Similarity 2.7%; Score 39.6; DB 1; Length 462;
RESULT 374
ID ADJ42634 standard; cDNA; 541 BP.
DE Plant cDNA #3634.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOLF/) GOLF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICHE D.
PA (ZHUT/) ZHU T.
Query Match
Best Local Similarity 2.7%; Score 39.6; DB 12; Length 541;
RESULT 375
ID ADA48926 standard; DNA; 709 BP.
DE Wheat gene conferring disease resistance in plants.
PN WO200300906-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match
Best Local Similarity 2.7%; Score 39.6; DB 9; Length 709;
RESULT 376
ID ADJ41937 standard; cDNA; 709 BP.
DE Plant cDNA #2937.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOLF/) GOLF S A.

PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICHE D.
PA (ZHUT/) ZHU T.
Query Match
Best Local Similarity 2.7%; Score 39.6; DB 12; Length 709;
RESULT 377
ID ABR120145 standard; DNA; 739 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 11908.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 2.7%; Score 39.6; DB 4; Length 739;
RESULT 378
ID ABL14119 standard; cDNA; 995 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 36839.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 2.7%; Score 39.6; DB 4; Length 995;
RESULT 379
ID ADR46441 standard; DNA; 1011 BP.
DE Batley caltractin-like protein coding sequence SEQ ID NO: 7.
PN WO2004070035-A2.
PD 19-AUG-2004.
PA (SUNG-) SUNGENE GMBH & CO KGAA.
Query Match
Best Local Similarity 2.7%; Score 39.6; DB 13; Length 1011;
RESULT 380
ID ABR20141 standard; DNA; 1049 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 11896.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 2.7%; Score 39.6; DB 4; Length 1049;
RESULT 381
ID ADA69549 standard; DNA; 1434 BP.
DE Rice gene, SEQ ID 2872.
PN WO200300898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match
Best Local Similarity 2.7%; Score 39.6; DB 8; Length 1434;
RESULT 382
ID ABR80332 standard; DNA; 3001 BP.
DE Human chemically modified disease associated gene SEQ ID NO 349.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 2.7%; Score 39.6; DB 6; Length 3001;
RESULT 383
ID ABR28440 standard; DNA; 6120 BP.
DE DNA transcripction associated complementary genomic DNA #157.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 2.7%; Score 39.6; DB 6; Length 6120;
RESULT 384
ID ABR80303 standard; DNA; 6120 BP.
DE Human chemically modified disease associated gene SEQ ID NO 320.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 2.7%; Score 39.6; DB 6; Length 6120;
RESULT 385
ID ADQ97180 standard; DNA; 118063 BP.

DE Mouse cancer associated sequence MD08-011, SEQ ID 156.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.7%; Score 39.6; DB 12; Length 118063;
Best Local Similarity 50.5%; Pred. No. 40;
RESULT 386
ID AD035602 standard; DNA; 1125 BP.
PN WO2004046310-A2.
PD 03-JUN-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 2.7%; Score 39.4; DB 12; Length 1125;
Best Local Similarity 50.3%; Pred. No. 4.5;
RESULT 387
ID AB195566 standard; cDNA; 3396 BP.
DE Mouse ischemic condition related cDNA sequence SEQ ID NO:569.
PN WO20018188-A2.
PD 22-NOV-2001.
PA (UYMI-) UYMI NIHON SCHOOL JURIDICAL PERSON.
Query Match 2.7%; Score 39.4; DB 6; Length 3396;
Best Local Similarity 45.8%; Pred. No. 7.9;
RESULT 388
ID ADC85485 standard; DNA; 20448 BP.
DE Mouse Calm2 genomic sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.7%; Score 39.4; DB 10; Length 20448;
Best Local Similarity 48.4%; Pred. No. 19;
RESULT 389
ID ADA03005 standard; DNA; 20450 BP.
DE Mouse Calm2 carcinoma associated gene, SEQ ID NO:1523.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.7%; Score 39.4; DB 9; Length 20450;
Best Local Similarity 48.4%; Pred. No. 19;
RESULT 390
ID ADB72743 standard; DNA; 20450 BP.
DE Mouse Calm2 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.7%; Score 39.4; DB 10; Length 20450;
Best Local Similarity 48.4%; Pred. No. 19;
RESULT 391
ID ADM74600 standard; DNA; 20450 BP.
DE Murine carcinoma associated (CA) nucleic acid #136.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR/) MORRIS D W.
PA (ENGEL/) ENGELHARD E K.
Query Match 2.7%; Score 39.4; DB 12; Length 20450;
Best Local Similarity 48.4%; Pred. No. 19;
RESULT 392
ID AAC50296 standard; DNA; 514 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 64306.
PN EP1033405-A2.
PD 06-SEP-2000.
PA
Query Match 2.6%; Score 39.2; DB 3; Length 514;
Best Local Similarity 55.0%; Pred. No. 3.5;
RESULT 393
ID ADA70926 standard; DNA; 1146 BP.
DE Rice gene, SEQ ID 4249.
PN WO200300898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.6%; Score 39.2; DB 8; Length 1146;
Best Local Similarity 50.0%; Pred. No. 5.2;
RESULT 394
ID AD040264 standard; cDNA; 1308 BP.
DE Plant cDNA #1264.

PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUTG/) MOUTHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATRA/) KATAGIRI F.
PA (KEEP/) KEEPS J.
PA (PROV/) PROVART N.
PA (RICK/) RIQUE D.
PA (ZHUT/) ZHU T.
Query Match 2.6%; Score 39.2; DB 12; Length 1308;
Best Local Similarity 44.0%; Pred. No. 5.6;
RESULT 395
ID ACN44588 standard; DNA; 33454 BP.
DE Mouse genomic sequence mCG22056.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.6%; Score 39.2; DB 11; Length 33454;
Best Local Similarity 64.1%; Pred. No. 28;
RESULT 396
ID AAK82012 standard; DNA; 49561 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36824.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 39.2; DB 4; Length 49561;
Best Local Similarity 53.2%; Pred. No. 34;
RESULT 397
ID ACH16715 standard; cDNA; 402 BP.
DE Human adult heart cDNA #1029.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 2.6%; Score 39; DB 9; Length 402;
Best Local Similarity 51.4%; Pred. No. 3.5;
RESULT 398
ID ACH18454 standard; cDNA; 451 BP.
DE Human adult heart cDNA #2768.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 2.6%; Score 39; DB 9; Length 451;
Best Local Similarity 51.4%; Pred. No. 3.7;
RESULT 399
ID AAV04232 standard; cDNA; 495 BP.
DE Human cardiac troponin C cDNA.
PN WO9739132-A1.
PD 23-OCT-1997.
PA (UYMI-) UYMI MIAMI.
Query Match 2.6%; Score 39; DB 2; Length 495;
Best Local Similarity 51.4%; Pred. No. 3.9;
RESULT 400
ID ADT02425 standard; cDNA; 744 BP.
DE cDNA encoding Troponin I N-term-troponin C.
PN US6475785-B1.
PD 05-NOV-2002.
PA (SPEC-) SPECTRAL DIAGNOSTICS INC.
Query Match 2.6%; Score 39; DB 5; Length 744;
Best Local Similarity 51.4%; Pred. No. 4.8;
RESULT 401
ID ADT02427 standard; cDNA; 795 BP.

DE cDNA encoding Troponin I N-term-linker-troponin C.
PN US6475785-B1.
PD 05-NOV-2002.
PA (SPEC-) SPECTRAL DIAGNOSTICS INC.
Query Match 2.6%; Score 39; DB 5; Length 795;
Best Local Similarity 51.4%; Pred. No. 4.9;
RESULT 402
ID AC103848 standard; cDNA; 844 BP.
DE Human cDNA differentially expressed in lung cancer #53.
PN US2003065157-A1.
PD 03-APR-2003.
PA (LASE/) LASEK A W.
Query Match 2.6%; Score 39; DB 9; Length 844;
Best Local Similarity 51.4%; Pred. No. 5.1;
RESULT 403
ID ADE77154 standard; cDNA; 846 BP.
DE Human cDNA differentially expressed in a liver disorder #237.
PN US2003108871-A1.
PD 12-JUN-2003.
PA (KASE/) KASER M R.
Query Match 2.6%; Score 39; DB 12; Length 846;
Best Local Similarity 51.4%; Pred. No. 5.1;
RESULT 404
ID ADG14210 standard; cDNA; 1116 BP.
DE Human cDNA encoding troponin I.
PN US2003176655-A1.
PD 18-SEP-2003.
PA (SHIO/) SHI O.
PA (SONG/) SONG Q.
Query Match 2.6%; Score 39; DB 10; Length 1116;
Best Local Similarity 51.4%; Pred. No. 5.8;
RESULT 405
ID AAV04225 standard; cDNA; 1119 BP.
DE DNA encoding cardiac troponin I/cardiac troponin C fusion.
PN WO97393132-A1.
PD 23-OCT-1997.
PA (UMI-) UNIV MIAMI.
Query Match 2.6%; Score 39; DB 2; Length 1119;
Best Local Similarity 51.4%; Pred. No. 5.9;
RESULT 406
ID ADE77155 standard; cDNA; 1158 BP.
DE Human cDNA differentially expressed in a liver disorder #238.
PN US2003108871-A1.
PD 12-JUN-2003.
PA (KASE/) KASER M R.
Query Match 2.6%; Score 39; DB 12; Length 1158;
Best Local Similarity 51.4%; Pred. No. 6;
RESULT 407
ID AAX78382 standard; DNA; 1173 BP.
DE Human cardiac troponin I and troponin C DNA.
PN WO9931235-A1.
PD 24-JUN-1999.
PA (SPEC-) SPECTRAL DIAGNOSTICS INC.
Query Match 2.6%; Score 39; DB 2; Length 1173;
Best Local Similarity 51.4%; Pred. No. 6;
RESULT 408
ID ADG14205 standard; cDNA; 1173 BP.
DE Human cDNA encoding Troponin I-troponin C fusion protein.
PN US2003176655-A1.
PD 18-SEP-2003.
PA (SHIO/) SHI O.
PA (SONG/) SONG Q.
Query Match 2.6%; Score 39; DB 10; Length 1173;
Best Local Similarity 51.4%; Pred. No. 6;
RESULT 409
ID ADG23279 standard; DNA; 1225 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6099.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.6%; Score 39; DB 12; Length 1225;
Best Local Similarity 54.5%; Pred. No. 6.1;
RESULT 410

ID ABX62996 standard; cDNA; 1248 BP.
DE Human activated T cell cDNA #112.
PN US2002137077-A1.
PD 26-SEP-2002.
PA (HOPK/) HOPKINS C M.
PA (PETE/) PETERSON D P.
PA (COCK/) COCKS B G.
PA (HAWK/) HAWKINS P R.
Query Match 2.6%; Score 39; DB 8; Length 1248;
Best Local Similarity 51.4%; Pred. No. 6.2;
RESULT 411
ID ABS55209 standard; cDNA; 1284 BP.
DE Calcium sensitive circularly permuted EYFP (cEYFP), #2, cDNA.
PN EP1238982-A1.
PD 11-SEP-2002.
PA (RIKE/) RIKEN KK.
Query Match 2.6%; Score 39; DB 6; Length 1284;
Best Local Similarity 48.8%; Pred. No. 6.3;
RESULT 412
ID AAV58275 standard; cDNA; 1929 BP.
DE Fluorescent calmodulin-based calcium indicator cameleon-2 cDNA.
PN WO9840477-A1.
PD 17-SEP-1998.
PA (REGC) UNIV CALIFORNIA.
Query Match 2.6%; Score 39; DB 2; Length 1929;
Best Local Similarity 48.8%; Pred. No. 7.7;
RESULT 413
ID AAV58277 standard; cDNA; 1929 BP.
DE Fluorescent calmodulin-based calcium indicator cameleon-3 cDNA.
PN WO9840477-A1.
PD 17-SEP-1998.
PA (REGC) UNIV CALIFORNIA.
Query Match 2.6%; Score 39; DB 2; Length 1929;
Best Local Similarity 48.8%; Pred. No. 7.7;
RESULT 414
ID AAV58276 standard; cDNA; 1958 BP.
DE Fluorescent calmodulin-based calcium indicator cameleon-2nu cDNA.
PN WO9840477-A1.
PD 17-SEP-1998.
PA (REGC) UNIV CALIFORNIA.
Query Match 2.6%; Score 39; DB 2; Length 1958;
Best Local Similarity 48.8%; Pred. No. 7.7;
RESULT 415
ID AAV58278 standard; cDNA; 1971 BP.
DE Fluorescent calmodulin-based calcium indicator cameleon-3er cDNA.
PN WO9840477-A1.
PD 17-SEP-1998.
PA (REGC) UNIV CALIFORNIA.
Query Match 2.6%; Score 39; DB 2; Length 1971;
Best Local Similarity 48.8%; Pred. No. 7.8;
RESULT 416
ID ABI32789 standard; DNA; 6171 BP.
DE Human immune system associated gene SEQ ID NO: 762.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIC-) EPIGENOMICS AG.
Query Match 2.6%; Score 39; DB 6; Length 6171;
Best Local Similarity 55.6%; Pred. No. 14;
RESULT 417
ID ADP74816 standard; DNA; 137560 BP.
DE Parapoxvirus ovis genome DNA sequence Seg1.
Query Match 2.6%; Score 39; DB 12; Length 137560;
Best Local Similarity 50.3%; Pred. No. 64;
RESULT 418
ID AAA31857 standard; DNA; 278 BP.
DE Plant microsatellite marker #818.
PN WO9967421-A1.
PD 29-DEC-1999.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FOREST LTD.
Query Match 2.6%; Score 38.9; DB 3; Length 278;
Best Local Similarity 47.9%; Pred. No. 3.3;
RESULT 419

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ID ABR42401 standard; DNA; 1008 BP.
DE Toxicity modelling related rat gene SEQ ID No 2103.
PN WO20025000-A2.
PD 28-NOV-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 2.6%; Score 38.8; DB 10; Length 1008;
Best Local Similarity 48.4%; Pred. No. 6.3;
RESULT 420
ID ADP72800 standard; DNA; 1008 BP.
DE Renal toxin progression gene marker #1389.
PN WO2004048598-A2.
PD 10-JUN-2004.
PA (GENE-) GENE LOGIC INC.
Query Match 2.6%; Score 38.8; DB 12; Length 1008;
Best Local Similarity 48.4%; Pred. No. 6.3;
RESULT 421
ID ADA69781 standard; DNA; 1650 BP.
DE Rice gene, SEQ ID 3104.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.6%; Score 38.8; DB 8; Length 1650;
Best Local Similarity 50.0%; Pred. No. 8.1;
RESULT 422
ID ACH89551 standard; DNA; 455 BP.
DE Human genome derived single exon probe #22746.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 2.6%; Score 38.6; DB 12; Length 455;
Best Local Similarity 52.1%; Pred. No. 4.8;
RESULT 423
ID ADD3310 standard; DNA; 500 BP.
DE Mouse mitochondrial DNA sequence SEQ ID NO:1081.
PN WO2003020220-A2.
PD 13-MAR-2003.
PA (UYEM-) UNIV EMORY.
Query Match 2.6%; Score 38.6; DB 10; Length 500;
Best Local Similarity 48.0%; Pred. No. 5.1;
RESULT 424
ID AAF93577 standard; cDNA; 773 BP.
DE Lung carcinoma cDNA encoding SRT protein SEQ ID 398.
PN WO200107611-A2.
PD 01-FEB-2001.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 5; Length 773;
Best Local Similarity 58.1%; Pred. No. 6.3;
RESULT 425
ID AD63193 standard; DNA; 1275 BP.
DE Human zygote arrest 1 (Zarl) DNA sequence #2.
PN WO2003091400-A2.
PD 06-NOV-2003.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (AMHP) WYETH.
Query Match 2.6%; Score 38.6; DB 10; Length 1275;
Best Local Similarity 54.6%; Pred. No. 8.1;
RESULT 426
ID ADM99174 standard; DNA; 1293 BP.
DE Bacterial source DNA encoding a protease SegID 57.
PN WO2004033668-A2.
PD 22-APR-2004.
PA (DIVE-) DIVERSA CORP.
Query Match 2.6%; Score 38.6; DB 12; Length 1293;
Best Local Similarity 48.8%; Pred. No. 8.1;
RESULT 427
ID ADA10931 standard; cDNA; 2107 BP.
DE Human cDNA differentially expressed in colon cancer #34.
PN US2002160382-A1.
PD 31-OCT-2002.
PA (LASE/) LASEK A W.
PA (JONE/) JONES D A.
Query Match 2.6%; Score 38.6; DB 9; Length 2107;
Best Local Similarity 52.1%; Pred. No. 10;
RESULT 428
ID ADP13299 standard; DNA; 2110 BP.
DE Renal cell carcinoma differentially expressed gene #35.
PN WO2004048933-A2.
PD 10-JUN-2004.
PA (AMHP) WYETH.
PA (TWIN/) TWINE N C.
PA (BURC/) BURCZYNSKI M E.
PA (TREP/) TREPICCHIO W L.
PA (DORN/) DORNER A.
PA (STOV/) STOVER J A.
PA (SLON/) SLONI D K.
Query Match 2.6%; Score 38.6; DB 12; Length 2110;
Best Local Similarity 52.1%; Pred. No. 10;
RESULT 429
ID ADR25985 standard; DNA; 2110 BP.
DE Breast cancer prognosis marker #1846.
PN WO2004065545-A2.
PD 05-AUG-2004.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
PA (NECA-) NETHERLANDS CANCER INST.
Query Match 2.6%; Score 38.6; DB 13; Length 2110;
Best Local Similarity 52.1%; Pred. No. 10;
RESULT 430
ID ADF28533 standard; cDNA; 2885 BP.
DE Human scavenger receptor-like cDNA - SED ID 443.
PN WO2003048326-A2.
PD 12-JUN-2003.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 38.6; DB 10; Length 2885;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 431
ID ADS09939 standard; DNA; 2885 BP.
DE Human therapeutic DNA - SEQ ID 176.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NIVE-) NIVELO INC.
Query Match 2.6%; Score 38.6; DB 13; Length 2885;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 432
ID ABR70004 standard; DNA; 2945 BP.
DE cDNA encoding human Pro peptide #44.
PN WO200224888-A2.
PD 28-MAR-2002.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 6; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 433
ID ADA01355 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US2003068779-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 9; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 434
ID ADA43784 standard; cDNA; 2945 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO28700.
PN US2003064474-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 9; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 435
ID ADA43552 standard; cDNA; 2945 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO28700.
PN US2003073196-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 9; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
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RESULT 436
ID ADA01227 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US2003068782-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 9; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 437
ID ADA01111 standard; cDNA; 2945 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO28700.
PN US2003068780-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 9; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 438
ID ADA43668 standard; cDNA; 2945 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO28700.
PN US2003073190-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 9; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 439
ID ADA06930 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US2003068781-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 9; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 440
ID ADA08418 standard; cDNA; 2945 BP.
DE Novel human secreted and transmembrane protein PRO28700 cDNA.
PN US2003068783-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 9; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 441
ID ADB99711 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide SEQ ID 87.
PN US2003082728-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 9; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 442
ID ADB86994 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US2003082726-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 9; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 443
ID ADB66149 standard; cDNA; 2945 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO28700.
PN US2003082729-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 9; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 444
ID ADB99827 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide SEQ ID 87.
PN US2003073192-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 10; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 445
ID ADB99482 standard; cDNA; 2945 BP.
DE Novel human secreted and transmembrane protein PRO28700 cDNA.
PN US2003082731-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 10; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 446
ID ADB66033 standard; cDNA; 2945 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO28700.
PN US2003082732-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 10; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 447
ID ADC23431 standard; cDNA; 2945 BP.
DE Human cDNA clone (SeqID 87) encoding the transmembrane PRO protein.
PN US2003073193-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 10; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 448
ID ADC26124 standard; cDNA; 2945 BP.
DE Human PRO28700 cDNA.
PN US2003073194-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 10; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 449
ID ADE04951 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US2003068778-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 10; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 450
ID ADE11257 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US2003073191-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 10; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 451
ID ADB8188 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US2003082733-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 10; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 452
ID ADD95483 standard; cDNA; 2945 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO28700.
PN US2003064473-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 10; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 453
ID ADE06413 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US2003073195-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 10; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 454
ID ADE38188 standard; cDNA; 2945 BP.
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DE Human PRO polynucleotide #44.
PN US2003119120-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 10; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 455
ID ADDB8304 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US2003073189-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 10; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 456
ID ADJ90885 standard; cDNA; 2945 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO28700.
PN US2003073188-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 10; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 457
ID ADF99440 standard; cDNA; 2945 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO28700.
PN US2003078401-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 10; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 458
ID ADG06533 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US2003077742-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 10; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 459
ID ADG05484 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US2003077741-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 10; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 460
ID ADG82485 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US2003077744-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 10; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 461
ID ADEB1738 standard; cDNA; 2945 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO28700.
PN US2003104560-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 12; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 462
ID ADEB1854 standard; cDNA; 2945 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO28700.
PN US2003104561-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 12; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 463
ID ADEB7712 standard; cDNA; 2945 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO28700.

PN US2003104564-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 12; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 464
ID ADEB37596 standard; cDNA; 2945 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO28700.
PN US2003104565-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 12; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 465
ID ADP95367 standard; cDNA; 2945 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO28700.
PN US2003138901-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 12; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 466
ID ADEB38067 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US2003104566-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 12; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 467
ID ADEB76156 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US2003124665-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 12; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 468
ID ADEB9479 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US2003119117-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 12; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 469
ID ADEB04283 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US200309364-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 12; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 470
ID ADEB39880 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US2003138896-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 12; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 471
ID ADEB19745 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US2003138903-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 2.6%; Score 38.6; DB 12; Length 2945;
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 472
ID ADEB77323 standard; cDNA; 2945 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO28700.
PN US2003124666-A1.

PD 03-JUN-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 38.6; DB 12; Length 2945;
Query Match
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 473
ID ADE65431 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US2003119116-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 38.6; DB 12; Length 2945;
Query Match
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 474
ID ADE76040 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US2003124663-A1.
PD 03-JUN-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 38.6; DB 12; Length 2945;
Query Match
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 475
ID ADE37951 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US2003119119-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 38.6; DB 12; Length 2945;
Query Match
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 476
ID ADE64561 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US2003119114-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 38.6; DB 12; Length 2945;
Query Match
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 477
ID ADE38896 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US2003096363-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 38.6; DB 12; Length 2945;
Query Match
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 478
ID ADE51970 standard; cDNA; 2945 BP.
DE Human cDNA encoding secreted/cranmembrane polypeptide PRO28700.
PN US2003104562-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 38.6; DB 12; Length 2945;
Query Match
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 479
ID ADD91001 standard; cDNA; 2945 BP.
DE Human cDNA encoding secreted/cranmembrane polypeptide PRO28700.
PN US2003138902-A1.
PD 24-JUN-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 38.6; DB 12; Length 2945;
Query Match
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 480
ID ADE38780 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US200310896-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 38.6; DB 12; Length 2945;
Query Match
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 481
ID ADE37480 standard; cDNA; 2945 BP.
DE Human cDNA encoding secreted/cranmembrane polypeptide PRO28700.
PN US2003104563-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 38.6; DB 12; Length 2945;
Query Match
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 482
ID ADE06297 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US2003138898-A1.
PD 24-JUN-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 38.6; DB 12; Length 2945;
Query Match
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 483
ID ADD90156 standard; cDNA; 2945 BP.
DE Human cDNA encoding secreted/cranmembrane polypeptide PRO28700.
PN US2003138804-A1.
PD 24-JUN-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 38.6; DB 12; Length 2945;
Query Match
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 484
ID ADE38664 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US2003119086-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 38.6; DB 12; Length 2945;
Query Match
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 485
ID ADE39595 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US2003119118-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 38.6; DB 12; Length 2945;
Query Match
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 486
ID ADD89200 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US2003138897-A1.
PD 24-JUN-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 38.6; DB 12; Length 2945;
Query Match
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 487
ID ADD88967 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US2003138899-A1.
PD 24-JUN-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 38.6; DB 12; Length 2945;
Query Match
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 488
ID ADE19861 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US2003138900-A1.
PD 24-JUN-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 38.6; DB 12; Length 2945;
Query Match
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 489
ID ADE77439 standard; cDNA; 2945 BP.
DE Human cDNA encoding secreted/cranmembrane polypeptide PRO28700.
PN US2003124667-A1.
PD 03-JUN-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 38.6; DB 12; Length 2945;
Query Match
Best Local Similarity 58.1%; Pred. No. 12;
RESULT 490
ID ADE65315 standard; cDNA; 2945 BP.
DE Human PRO polynucleotide #44.
PN US2003119113-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC. 2.6%; Score 38.6; DB 12; Length 2945;
Query Match
Best Local Similarity 58.1%; Pred. No. 12;

Query Match	2.6%;	Score 38.6;	DB 12;	Length 2945;
Best Local Similarity	58.1%;	Pred. No. 12;		
RESULT 491				
ID ADH39363 standard; cDNA; 2945 BP.				
DE Human PRO polynucleotide #44.				
PN US200311915-A1.				
PD 26-JUN-2003.				
PA (GETH) GENENTECH INC.				
Query Match	2.6%;	Score 38.6;	DB 12;	Length 2945;
Best Local Similarity	58.1%;	Pred. No. 12;		
RESULT 492				
ID ADH38548 standard; cDNA; 2945 BP.				
DE Human cDNA encoding secreted/transmembrane polypeptide PRO28700				
PN US2003104559-A1.				
PD 05-JUN-2003.				
PA (GETH) GENENTECH INC.				
Query Match	2.6%;	Score 38.6;	DB 12;	Length 2945;
Best Local Similarity	58.1%;	Pred. No. 12;		
RESULT 493				
ID ADH1101 standard; cDNA; 2945 BP.				
DE Human cDNA encoding secreted/transmembrane polypeptide PRO28700				
PN US2003170809-A1.				
PD 11-SEP-2003.				
PA (GETH) GENENTECH INC.				
Query Match	2.6%;	Score 38.6;	DB 12;	Length 2945;
Best Local Similarity	58.1%;	Pred. No. 12;		
RESULT 494				
ID ADG10985 standard; cDNA; 2945 BP.				
DE Human cDNA encoding secreted/transmembrane polypeptide PRO28700				
PN US200307743-A1.				
PD 24-APR-2003.				
PA (GETH) GENENTECH INC.				
Query Match	2.6%;	Score 38.6;	DB 12;	Length 2945;
Best Local Similarity	58.1%;	Pred. No. 12;		
RESULT 495				
ID ADH31513 standard; cDNA; 2945 BP.				
DE Human PRO polynucleotide #44.				
PN US2003119139-A1.				
PD 26-JUN-2003.				
PA (GETH) GENENTECH INC.				
Query Match	2.6%;	Score 38.6;	DB 12;	Length 2945;
Best Local Similarity	58.1%;	Pred. No. 12;		
RESULT 496				
ID ADH38761 standard; cDNA; 2945 BP.				
DE Human cDNA encoding secreted/transmembrane polypeptide PRO28700.				
PN US2003119140-A1.				
PD 26-JUN-2003.				
PA (GETH) GENENTECH INC.				
Query Match	2.6%;	Score 38.6;	DB 12;	Length 2945;
Best Local Similarity	58.1%;	Pred. No. 12;		
RESULT 497				
ID ADH29396 standard; cDNA; 2945 BP.				
DE Human cDNA encoding secreted/transmembrane polypeptide PRO28700				
PN US2003119137-A1.				
PD 26-JUN-2003.				
PA (GETH) GENENTECH INC.				
Query Match	2.6%;	Score 38.6;	DB 12;	Length 2945;
Best Local Similarity	58.1%;	Pred. No. 12;		
RESULT 498				
ID ADH3569 standard; cDNA; 2945 BP.				
DE Human cDNA encoding secreted/transmembrane polypeptide PRO28700.				
PN US2003119143-A1.				
PD 26-JUN-2003.				
PA (GETH) GENENTECH INC.				
Query Match	2.6%;	Score 38.6;	DB 12;	Length 2945;
Best Local Similarity	58.1%;	Pred. No. 12;		
RESULT 499				
ID ADH27029 standard; cDNA; 2945 BP.				
DE Human cDNA encoding secreted/transmembrane polypeptide PRO28700.				
PN US2003119135-A1.				
PD 26-JUN-2003.				
PA (GETH) GENENTECH INC.				
Query Match	2.6%;	Score 38.6;	DB 12;	Length 2945;
Best Local Similarity	58.1%;	Pred. No. 12;		
RESULT 500				
ID ADH27029 standard; cDNA; 2945 BP.				
DE Human cDNA encoding secreted/transmembrane polypeptide PRO28700.				
PN US2003119135-A1.				
PD 26-JUN-2003.				
PA (GETH) GENENTECH INC.				
Query Match	2.6%;	Score 38.6;	DB 12;	Length 2945;
Best Local Similarity	58.1%;	Pred. No. 12;		
RESULT 501				
ID ADH27029 standard; cDNA; 2945 BP.				
DE Human cDNA encoding secreted/transmembrane polypeptide PRO28700.				
PN US2003119135-A1.				
PD 26-JUN-2003.				
PA (GETH) GENENTECH INC.				
Query Match	2.6%;	Score 38.6;	DB 12;	Length 2945;
Best Local Similarity	58.1%;	Pred. No. 12;		
RESULT 502				
ID ADH27029 standard; cDNA; 2945 BP.				
DE Human cDNA encoding secreted/transmembrane polypeptide PRO28700.				
PN US2003119135-A1.				
PD 26-JUN-2003.				
PA (GETH) GENENTECH INC.				
Query Match	2.6%;	Score 38.6;	DB 12;	Length 2945;
Best Local Similarity	58.1%;	Pred. No. 12;		
RESULT 503				
ID ADH27029 standard; cDNA; 2945 BP.				
DE Human cDNA encoding secreted/transmembrane polypeptide PRO28700.				
PN US2003119135-A1.				
PD 26-JUN-2003.				

Best Local Similarity	58.1%;	Pred. No. 12;
RESULT 500		
ID	ADH38297 standard; cDNA; 2945 BP.	
DE	Novel human secreted and transmembrane protein PRO28700 cDNA.	
PN	US2003119124-A1.	
PD	26-JUN-2003.	
PA	(GENE) GENENTECH INC.	
Query Match	2.6%;	Score 38.6; DB 12; Length 2945;
Best Local Similarity	58.1%;	Pred. No. 12;
RESULT 501		
ID	ADH26913 standard; cDNA; 2945 BP.	
DE	Human cDNA encoding secreted/transmembrane polypeptide PRO28700	
PN	US2003119134-A1.	
PD	26-JUN-2003.	
PA	(GENE) GENENTECH INC.	
Query Match	2.6%;	Score 38.6; DB 12; Length 2945;
Best Local Similarity	58.1%;	Pred. No. 12;
RESULT 502		
ID	ADH38181 standard; cDNA; 2945 BP.	
DE	Novel human secreted and transmembrane protein PRO28700 cDNA.	
PN	US2003119123-A1.	
PD	26-JUN-2003.	
PA	(GENE) GENENTECH INC.	
Query Match	2.6%;	Score 38.6; DB 12; Length 2945;
Best Local Similarity	58.1%;	Pred. No. 12;
RESULT 503		
ID	ADH38877 standard; cDNA; 2945 BP.	
DE	Human cDNA encoding secreted/transmembrane polypeptide PRO28700	
PN	US2003119141-A1.	
PD	26-JUN-2003.	
PA	(GENE) GENENTECH INC.	
Query Match	2.6%;	Score 38.6; DB 12; Length 2945;
Best Local Similarity	58.1%;	Pred. No. 12;
RESULT 504		
ID	ADH23815 standard; cDNA; 2945 BP.	
DE	Human cDNA encoding secreted/transmembrane polypeptide PRO28700	
PN	US2003119142-A1.	
PD	26-JUN-2003.	
PA	(GENE) GENENTECH INC.	
Query Match	2.6%;	Score 38.6; DB 12; Length 2945;
Best Local Similarity	58.1%;	Pred. No. 12;
RESULT 505		
ID	ADH40190 standard; cDNA; 2945 BP.	
DE	Human PRO28700 cDNA.	
PN	US2003119132-A1.	
PD	26-JUN-2003.	
PA	(GENE) GENENTECH INC.	
Query Match	2.6%;	Score 38.6; DB 12; Length 2945;
Best Local Similarity	58.1%;	Pred. No. 12;
RESULT 506		
ID	ADH40075 standard; cDNA; 2945 BP.	
DE	Human PRO28700 cDNA.	
PN	US2003119133-A1.	
PD	26-JUN-2003.	
PA	(GENE) GENENTECH INC.	
Query Match	2.6%;	Score 38.6; DB 12; Length 2945;
Best Local Similarity	58.1%;	Pred. No. 12;
RESULT 507		
ID	ADH31397 standard; cDNA; 2945 BP.	
DE	Human PRO polynucleotide #44.	
PN	US2003119138-A1.	
PD	26-JUN-2003.	
PA	(GENE) GENENTECH INC.	
Query Match	2.6%;	Score 38.6; DB 12; Length 2945;
Best Local Similarity	58.1%;	Pred. No. 12;
RESULT 508		
ID	ADH29275 standard; cDNA; 2945 BP.	
DE	Human cDNA encoding secreted/transmembrane polypeptide PRO28700.	
PN	US2003119136-A1.	
PD	26-JUN-2003.	
PA	(GENE) GENENTECH INC.	
Query Match	2.6%;	Score 38.6; DB 12; Length 2945;
Best Local Similarity	58.1%;	Pred. No. 12;
RESULT 509		
ID	ADH29275 standard; cDNA; 2945 BP.	
DE	Human cDNA encoding secreted/transmembrane polypeptide PRO28700.	
PN	US2003119136-A1.	
PD	26-JUN-2003.	
PA	(GENE) GENENTECH INC.	
Query Match	2.6%;	Score 38.6; DB 12; Length 2945;
Best Local Similarity	58.1%;	Pred. No. 12;

RESULT 509	ID	ADH49490	standard; cDNA; 2945 BP.	
	DE	Novel human secreted and transmembrane protein PRO28700 cDNA.		
	FN	US2003119127-A1.		
	PD	26-JUN-2003.		
	PA	(GETH) GENENTECH INC.		
	Query Match		2.6%; Score 38.6; DB 12; Length 2945;	
	Best Local Similarity		58.1%; Pred. No. 12;	
RESULT 510	ID	ADH1954	standard; cDNA; 2945 BP.	
	DE	Novel human secreted and transmembrane protein PRO28700 cDNA.		
	FN	US2003119125-A1.		
	PD	26-JUN-2003.		
	PA	(GETH) GENENTECH INC.		
	Query Match		2.6%; Score 38.6; DB 12; Length 2945;	
	Best Local Similarity		58.1%; Pred. No. 12;	
RESULT 511	ID	ADH49809	standard; cDNA; 2945 BP.	
	DE	Novel human secreted and transmembrane protein PRO28700 cDNA.		
	FN	US2003119128-A1.		
	PD	26-JUN-2003.		
	PA	(GETH) GENENTECH INC.		
	Query Match		2.6%; Score 38.6; DB 12; Length 2945;	
	Best Local Similarity		58.1%; Pred. No. 12;	
RESULT 512	ID	ADH52410	standard; cDNA; 2945 BP.	
	DE	Novel human secreted and transmembrane protein PRO28700 cDNA.		
	FN	US2003119130-A1.		
	PD	26-JUN-2003.		
	PA	(GETH) GENENTECH INC.		
	Query Match		2.6%; Score 38.6; DB 12; Length 2945;	
	Best Local Similarity		58.1%; Pred. No. 12;	
RESULT 513	ID	ADH52526	standard; cDNA; 2945 BP.	
	DE	Novel human secreted and transmembrane protein PRO28700 cDNA.		
	FN	US2003119129-A1.		
	PD	26-JUN-2003.		
	PA	(GETH) GENENTECH INC.		
	Query Match		2.6%; Score 38.6; DB 12; Length 2945;	
	Best Local Similarity		58.1%; Pred. No. 12;	
RESULT 514	ID	ADH58523	standard; cDNA; 2945 BP.	
	DE	Novel human secreted and transmembrane protein PRO28700 cDNA.		
	FN	US2003119121-A1.		
	PD	26-JUN-2003.		
	PA	(GETH) GENENTECH INC.		
	Query Match		2.6%; Score 38.6; DB 12; Length 2945;	
	Best Local Similarity		58.1%; Pred. No. 12;	
RESULT 515	ID	ADH51838	standard; cDNA; 2945 BP.	
	DE	Novel human secreted and transmembrane protein PRO28700 cDNA.		
	FN	US2003119126-A1.		
	PD	26-JUN-2003.		
	PA	(GETH) GENENTECH INC.		
	Query Match		2.6%; Score 38.6; DB 12; Length 2945;	
	Best Local Similarity		58.1%; Pred. No. 12;	
RESULT 516	ID	ADH58399	standard; cDNA; 2945 BP.	
	DE	Novel human secreted and transmembrane protein PRO28700 cDNA.		
	FN	US2003119131-A1.		
	PD	26-JUN-2003.		
	PA	(GETH) GENENTECH INC.		
	Query Match		2.6%; Score 38.6; DB 12; Length 2945;	
	Best Local Similarity		58.1%; Pred. No. 12;	
RESULT 517	ID	AD113596	standard; cDNA; 2945 BP.	
	DE	Novel human secreted and transmembrane protein PRO28700 cDNA.		
	FN	US2003119131-A1.		
	PD	26-JUN-2003.		
	PA	(GETH) GENENTECH INC.		
	Query Match		2.6%; Score 38.6; DB 12; Length 2945;	
	Best Local Similarity		58.1%; Pred. No. 12;	
RESULT 518	ID	AD113596	standard; cDNA; 2945 BP.	
	DE	Novel human secreted and transmembrane protein PRO28700 cDNA.		
	FN	US2003119131-A1.		
	PD	26-JUN-2003.		
	PA	(GETH) GENENTECH INC.		
	Query Match		2.6%; Score 38.6; DB 12; Length 2945;	
	Best Local Similarity		58.1%; Pred. No. 12;	
RESULT 519	ID	AD113596	standard; cDNA; 2945 BP.	
	DE	Novel human secreted and transmembrane protein PRO28700 cDNA.		
	FN	US2003119131-A1.		
	PD	26-JUN-2003.		
	PA	(GETH) GENENTECH INC.		
	Query Match		2.6%; Score 38.6; DB 12; Length 2945;	
	Best Local Similarity		58.1%; Pred. No. 12;	
RESULT 520	ID	AD113596	standard; cDNA; 2945 BP.	
	DE	Novel human secreted and transmembrane protein PRO28700 cDNA.		
	FN	US2003119131-A1.		
	PD	26-JUN-2003.		
	PA	(GETH) GENENTECH INC.		
	Query Match		2.6%; Score 38.6; DB 12; Length 2945;	
	Best Local Similarity		58.1%; Pred. No. 12;	
RESULT 521	ID	AD113596	standard; cDNA; 2945 BP.	
	DE	Novel human secreted and transmembrane protein PRO28700 cDNA.		
	FN	US2003119131-A1.		
	PD	26-JUN-2003.		
	PA	(GETH) GENENTECH INC.		
	Query Match		2.6%; Score 38.6; DB 12; Length 2945;	
	Best Local Similarity		58.1%; Pred. No. 12;	
RESULT 522	ID	AD113596	standard; cDNA; 2945 BP.	
	DE	Novel human secreted and transmembrane protein PRO28700 cDNA.		
	FN	US2003119131-A1.		
	PD	26-JUN-2003.		
	PA	(GETH) GENENTECH INC.		
	Query Match	</		

ID	ADK00852 standard; cDNA; 2945 BP.	2.6%;	Score 38.6;	DB 12;	Length 2945;
DE	Human PRO polynucleotide #44.				
FN	US2003186373-A1.				
PD	02-OCT-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		2.6%;	Score 38.6;	DB 12;	Length 2945;
Best Local Similarity		58.1%;	Pred. No. 12;		
RESULT 519					
ID	ADL08593 standard; cDNA; 2945 BP.	2.6%;	Score 38.6;	DB 12;	Length 2945;
DE	Human cDNA encoding secreted/transmembrane polypeptide PRO28700.				
FN	US2003186372-A1.				
PD	02-OCT-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		2.6%;	Score 38.6;	DB 12;	Length 2945;
Best Local Similarity		58.1%;	Pred. No. 12;		
RESULT 520					
ID	ADM12925 standard; cDNA; 2945 BP.	2.6%;	Score 38.6;	DB 12;	Length 2945;
DE	PRO28700 encoding sequence.				
FN	WO2004024077-A2.				
PD	25-MAR-2004.				
PA	(GETH) GENENTECH INC.				
Query Match		2.6%;	Score 38.6;	DB 12;	Length 2945;
Best Local Similarity		58.1%;	Pred. No. 12;		
RESULT 521					
ID	ADN05760 standard; cDNA; 2945 BP.	2.6%;	Score 38.6;	DB 12;	Length 2945;
DE	Antipsoariatic cDNA sequence #1111.				
FN	WO2004028479-A2.				
PD	08-APR-2004.				
PA	(GETH) GENENTECH INC.				
Query Match		2.6%;	Score 38.6;	DB 12;	Length 2945;
Best Local Similarity		58.1%;	Pred. No. 12;		
RESULT 522					
ID	ADH82045 standard; DNA; 3608 BP.	2.6%;	Score 38.6;	DB 13;	Length 3608;
DE	Human cancer-associated protein coding sequence #3.				
FN	WO2004035789-A1.				
PD	29-APR-2004.				
PA	(GIDS) LG LIFE SCI LTD.				
Query Match		2.6%;	Score 38.6;	DB 13;	Length 3608;
Best Local Similarity		58.1%;	Pred. No. 14;		
RESULT 523					
ID	ADJ63304 standard; DNA; 6002 BP.	2.6%;	Score 38.6;	DB 10;	Length 6002;
DE	Human zygote arrest 1 (Zarl) DNA sequence #3.				
FN	WO2003091400-A2.				
PD	06-NOV-2003.				
PA	(BAYU) BAYLOR COLLEGE MEDICINE.				
PA	(AMHP) WYETH.				
Query Match		2.6%;	Score 38.6;	DB 10;	Length 6002;
Best Local Similarity		54.4%;	Pred. No. 17;		
RESULT 524					
ID	ACN45200 standard; DNA; 95982 BP.	2.6%;	Score 38.6;	DB 11;	Length 95982;
DE	Mouse genomic sequence MCG9440.				
FN	WO2003073826-A2.				
PD	12-SEP-2003.				
PA	(SAGR-) SAGRES DISCOVERY.				
Query Match		2.6%;	Score 38.6;	DB 11;	Length 95982;
Best Local Similarity		53.7%;	Pred. No. 69;		
RESULT 525					
ID	AAC23266 standard; cDNA; 214 BP.	2.6%;	Score 38.4;	DB 3;	Length 214;
DE	Human secreted protein 5' EST, SEQ ID NO: 27341.				
FN	EP1033401-A2.				
PD	06-SEP-2000.				
PA	(GBST) GENSET.				
Query Match		2.6%;	Score 38.4;	DB 3;	Length 214;
Best Local Similarity		54.5%;	Pred. No. 3.8;		
RESULT 526					
ID	ADA58703 standard; cDNA; 233 BP.	2.6%;	Score 38.4;	DB 9;	Length 233;
DE	Maize sucrose synthase EST #347.				
FN	US2003135870-A1.				
PD	17-JUL-2003.				
PA	(CHEI/) CHEIKH N.				
PA	(FISH/) FISHER D K.				
PA	(LIU/) LIU J.				

Best Local Similarity 52.5%; Pred. No. 3.9;
RESULT 527
ID ADA58629 standard; cDNA; 257 BP.
DE Maize sucrose synthase EST #273.
PN US2003135870-A1.
PD 17-JUL-2003
PA (CHEI//) CHEIKH N.
PA (FISH//) FISHER D K.
PA (LITU//) LITU J.
Query Match 2.6%; Score 38.4; DB 9; Length 257;
Best Local Similarity 53.3%; Pred. No. 4.1;
RESULT 528
ID ADA58619 standard; cDNA; 269 BP.
DE Maize sucrose synthase EST #263.
PN US2003135870-A1.
PD 17-JUL-2003.
PA (CHEI//) CHEIKH N.
PA (FISH//) FISHER D K.
PA (LITU//) LITU J.
Query Match 2.6%; Score 38.4; DB 9; Length 268;
Best Local Similarity 52.5%; Pred. No. 4.2;
RESULT 529
ID ADA58535 standard; cDNA; 274 BP.
DE Maize sucrose synthase EST #179.
PN US2003135870-A1.
PD 17-JUL-2003.
PA (CHEI//) CHEIKH N.
PA (FISH//) FISHER D K.
PA (LITU//) LITU J.
Query Match 2.6%; Score 38.4; DB 9; Length 274;
Best Local Similarity 52.5%; Pred. No. 4.3;
RESULT 530
ID ADA58492 standard; cDNA; 286 BP.
DE Maize sucrose synthase EST #136.
PN US2003135870-A1.
PD 17-JUL-2003.
PA (CHEI//) CHEIKH N.
PA (FISH//) FISHER D K.
PA (LITU//) LITU J.
Query Match 2.6%; Score 38.4; DB 9; Length 286;
Best Local Similarity 52.5%; Pred. No. 4.4;
RESULT 531
ID ADA58422 standard; cDNA; 306 BP.
DE Maize sucrose synthase EST #66.
PN US2003135870-A1.
PD 17-JUL-2003.
PA (CHEI//) CHEIKH N.
PA (FISH//) FISHER D K.
PA (LITU//) LITU J.
Query Match 2.6%; Score 38.4; DB 9; Length 306;
Best Local Similarity 52.5%; Pred. No. 4.5;
RESULT 532
ID ADA58410 standard; cDNA; 316 BP.
DE Maize sucrose synthase EST #54.
PN US2003135870-A1.
PD 17-JUL-2003
PA (CHEI//) CHEIKH N.
PA (FISH//) FISHER D K.
PA (LITU//) LITU J.
Query Match 2.6%; Score 38.4; DB 9; Length 316;
Best Local Similarity 52.5%; Pred. No. 4.6;
RESULT 533
ID ADA58904 standard; cDNA; 360 BP.
DE Maize sucrose synthase EST #548.
PN US2003135870-A1.
PD 17-JUL-2003.
PA (CHEI//) CHEIKH N.
PA (FISH//) FISHER D K.
PA (LITU//) LITU J.
Query Match 2.6%; Score 38.4; DB 9; Length 360;
Best Local Similarity 52.5%; Pred. No. 4.9;
RESULT 534
ID ADA58895 standard; cDNA; 383 BP.

DE Maize sucrose synthase EST #539.
PN US2003135870-A1.
PD 17-JUL-2003.
PA (CHEI//) CHEIKH N.
PA (FISH//) FISHER D K.
PA (LITU//) LITU J.
Query Match 2.6%; Score 38.4; DB 9; Length 383;
Best Local Similarity 52.5%; Pred. No. 5.1;
RESULT 535
ID AD041964 standard; cDNA; 392 BP.
DE Plant cDNA #2964.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW//) BUDMORTH P.
PA (MOUTG//) MOUTHAMER T.
PA (BRIG//) BRIGGS S P.
PA (COOP//) COOPER B.
PA (GLAZ//) GLAZEBROOK J.
PA (GOLF//) GOLF S A.
PA (KATA//) KATAGIRI F.
PA (KREP//) KREPS J.
PA (PROV//) PROVART N.
PA (RICK//) RICE D.
PA (ZHUT//) ZHU T.
Query Match 2.6%; Score 38.4; DB 12; Length 392;
Best Local Similarity 44.8%; Pred. No. 5.1;
RESULT 536
ID ADA58909 standard; cDNA; 413 BP.
DE Maize sucrose synthase EST #553.
PN US2003135870-A1.
PD 17-JUL-2003.
PA (CHEI//) CHEIKH N.
PA (FISH//) FISHER D K.
PA (LITU//) LITU J.
Query Match 2.6%; Score 38.4; DB 9; Length 413;
Best Local Similarity 52.5%; Pred. No. 5.2;
RESULT 537
ID ADA58875 standard; cDNA; 425 BP.
DE Maize sucrose synthase EST #519.
PN US2003135870-A1.
PD 17-JUL-2003.
PA (CHEI//) CHEIKH N.
PA (FISH//) FISHER D K.
PA (LITU//) LITU J.
Query Match 2.6%; Score 38.4; DB 9; Length 425;
Best Local Similarity 52.5%; Pred. No. 5.3;
RESULT 538
ID ADA58893 standard; cDNA; 433 BP.
DE Maize sucrose synthase EST #537.
PN US2003135870-A1.
PD 17-JUL-2003.
PA (CHEI//) CHEIKH N.
PA (FISH//) FISHER D K.
PA (LITU//) LITU J.
Query Match 2.6%; Score 38.4; DB 9; Length 433;
Best Local Similarity 52.5%; Pred. No. 5.4;
RESULT 539
ID ABR95419 standard; DNA; 442 BP.
DE Gene #1917 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 2.6%; Score 38.4; DB 6; Length 442;
Best Local Similarity 52.9%; Pred. No. 5.4;
RESULT 540
ID ADA03007 standard; cDNA; 450 BP.
DE Mouse Calm2 carcinoma associated coding sequence, SEQ ID NO.1525.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.6%; Score 38.4; DB 9; Length 450;
Best Local Similarity 49.0%; Pred. No. 5.5;
RESULT 541

ID ADB72745 standard; cDNA, 450 BP.
DE Mouse Calm2 cDNA.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.6%; Score 38.4; DB 10; Length 450;
Best Local Similarity 49.0%; Pred. No. 5.5;
RESULT 542
ID ADC85487 standard; DNA, 450 BP.
DE Mouse Calm2 coding sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.6%; Score 38.4; DB 10; Length 450;
Best Local Similarity 49.0%; Pred. No. 5.5;
RESULT 543
ID ADM74602 standard; DNA, 450 BP.
DE Murine carcinoma associated (CA) nucleic acid #138.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR/) MORRIS D W.
PA (ENGEL/) ENGELHARD E K.
Query Match 2.6%; Score 38.4; DB 12; Length 450;
Best Local Similarity 49.0%; Pred. No. 5.5;
RESULT 544
ID ADA58866 standard; cDNA, 469 BP.
DE Maize sucrose synthase EST #510.
PN US2003135870-A1.
PD 17-JUL-2003.
PA (CHEI/) CHEIKH N.
PA (FISH/) FISHER D K.
PA (LIUJ/) LIU J.
Query Match 2.6%; Score 38.4; DB 9; Length 469;
Best Local Similarity 52.5%; Pred. No. 5.8;
RESULT 545
ID ADA58877 standard; cDNA, 512 BP.
DE Maize sucrose synthase EST #521.
PN US2003135870-A1.
PD 17-JUL-2003.
PA (CHEI/) CHEIKH N.
PA (FISH/) FISHER D K.
PA (LIUJ/) LIU J.
Query Match 2.6%; Score 38.4; DB 9; Length 512;
Best Local Similarity 52.5%; Pred. No. 5.8;
RESULT 546
ID ABO55780 standard; cDNA, 591 BP.
DE Human ovarian antigen HOPKG47 cDNA, SEQ ID NO:1660.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 38.4; DB 6; Length 591;
Best Local Similarity 49.3%; Pred. No. 6.3;
RESULT 547
ID ADC77182 standard; DNA, 595 BP.
DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 2111.
PN WO2003020905-A2.
PD 13-MAR-2003.
PA (DOMC) DOM CHEM CO.
Query Match 2.6%; Score 38.4; DB 10; Length 595;
Best Local Similarity 48.6%; Pred. No. 6.3;
RESULT 548
ID ADC75913 standard; DNA, 595 BP.
DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 837.
PN WO2003020905-A2.
PD 13-MAR-2003.
PA (DOMC) DOM CHEM CO.
Query Match 2.6%; Score 38.4; DB 10; Length 595;
Best Local Similarity 48.6%; Pred. No. 6.3;
RESULT 549
ID ADK56992 standard; DNA, 595 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #4375.
PN WO2003020936-A1.
PD 13-MAR-2003.

PA (DOMC) DOM CHEM CO.
Query Match 2.6%; Score 38.4; DB 10; Length 595;
Best Local Similarity 48.6%; Pred. No. 6.3;
RESULT 550
ID ADK55191 standard; DNA, 595 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #2574.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOMC) DOM CHEM CO.
PA (DOMC) DOM AGROSCIENCES, LLC.
Query Match 2.6%; Score 38.4; DB 10; Length 595;
Best Local Similarity 48.6%; Pred. No. 6.3;
RESULT 551
ID AAA27845 standard; cDNA, 916 BP.
DE Soybean calmodulin-5 cDNA.
PN EP1018553-A1.
PD 12-JUL-2000.
PA (KOKU-) KOREA KUMHO PETROCHEMICAL CO LTD.
Query Match 2.6%; Score 38.4; DB 3; Length 916;
Best Local Similarity 47.8%; Pred. No. 7.8;
RESULT 552
ID ABA16489 standard; DNA, 3375 BP.
DE Human nervous system related polynucleotide SEQ ID NO 8820.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 38.4; DB 5; Length 3375;
Best Local Similarity 52.5%; Pred. No. 15;
RESULT 553
ID ADC10129 standard; DNA, 5053 BP.
DE Human NOVX polypeptide coding sequence SEQ ID NO: 149.
PN WO2003000842-A2.
PD 03-JAN-2003.
PA (CURA-) CURAGEN CORP.
Query Match 2.6%; Score 38.4; DB 10; Length 5053;
Best Local Similarity 44.3%; Pred. No. 18;
RESULT 554
ID ABA16488 standard; DNA, 6072 BP.
DE Human nervous system related polynucleotide SEQ ID NO 8819.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.6%; Score 38.4; DB 5; Length 6072;
Best Local Similarity 52.5%; Pred. No. 20;
RESULT 555
ID ACN45034 standard; DNA, 99588 BP.
DE Human genomic sequence hCG1640838.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.6%; Score 38.4; DB 11; Length 99588;
Best Local Similarity 56.2%; Pred. No. 80;
RESULT 556
ID ACN44740 standard; DNA, 101241 BP.
DE Mouse genomic sequence MCG3043.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.6%; Score 38.4; DB 11; Length 101241;
Best Local Similarity 42.1%; Pred. No. 81;
RESULT 557
ID ADA58523 standard; cDNA, 281 BP.
DE Maize sucrose synthase EST #167.
PN US2003135870-A1.
PD 17-JUL-2003.
PA (CHEI/) CHEIKH N.
PA (FISH/) FISHER D K.
PA (LIUJ/) LIU J.
Query Match 2.6%; Score 38.2; DB 9; Length 281;
Best Local Similarity 56.9%; Pred. No. 4.9;
RESULT 558
ID ADA58496 standard; cDNA, 288 BP.

DE Maize sucrose synthase EST #140.
PN US200335870-A1.
PD 17-JUL-2003.
PA (CHEI/) CHEIKH N.
PA (FISH/) FISHER D K.
PA (LIU/) LIU J.
Query Match
Best Local Similarity 2.6%; Score 38.2; DB 9; Length 288;
56.9%; Pred. No. 5;
RESULT 559
ID ADA58458 standard; cDNA; 307 BP.
DE Maize sucrose synthase EST #102.
PN US200335870-A1.
PD 17-JUL-2003.
PA (CHEI/) CHEIKH N.
PA (FISH/) FISHER D K.
PA (LIU/) LIU J.
Query Match
Best Local Similarity 2.6%; Score 38.2; DB 9; Length 307;
56.9%; Pred. No. 5.1;
RESULT 560
ID AAC41022 standard; DNA; 388 BP.
DE Zea mays DNA fragment SEQ ID NO: 30368.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 2.6%; Score 38.2; DB 3; Length 388;
47.3%; Pred. No. 5.8;
RESULT 561
ID ACH87297 standard; DNA; 603 BP.
DE Human genome derived single exon probe #20492.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENR/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match
Best Local Similarity 2.6%; Score 38.2; DB 12; Length 603;
49.8%; Pred. No. 7.2;
RESULT 562
ID ADBQ7673 standard; DNA; 747 BP.
DE Novel coding sequence (useful for identifying genetic disorders) #739.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 2.6%; Score 38.2; DB 10; Length 747;
49.8%; Pred. No. 8;
RESULT 563
ID ADJ42633 standard; cDNA; 800 BP.
DE Plant cDNA #3633.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICKS D.
PA (ZHUT/) ZHU T.
Query Match
Best Local Similarity 2.6%; Score 38.2; DB 12; Length 800;
48.8%; Pred. No. 8.3;
RESULT 564
ID AAO9367 standard; DNA; 1793 BP.
DE S. lividans protease P5-10 gene.
PN WO9517512-A2.
PD 29-JUN-1995.
PA (CANG-) CANGENE CORP.
Query Match
Best Local Similarity 2.6%; Score 38.2; DB 2; Length 1793;
48.8%; Pred. No. 12;
RESULT 565
ID ADS49594 standard; cDNA; 2313 BP.
DE Bacterial polynucleotide #4337.
PN US200333675-A1.

PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 2.6%; Score 38.2; DB 13; Length 2313;
47.0%; Pred. No. 14;
RESULT 566
ID ADS55105 standard; cDNA; 2313 BP.
DE Bacterial polynucleotide #7092.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 2.6%; Score 38.2; DB 13; Length 2313;
47.0%; Pred. No. 14;
RESULT 567
ID ACA23764 standard; DNA; 2421 BP.
DE Prokaryotic essential gene #5421.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 2.6%; Score 38.2; DB 8; Length 2421;
47.0%; Pred. No. 14;
RESULT 568
ID ACA25075 standard; DNA; 2421 BP.
DE Prokaryotic essential gene #6732.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 2.6%; Score 38.2; DB 8; Length 2421;
47.0%; Pred. No. 14;
RESULT 569
ID ABV77934 standard; DNA; 3250 BP.
DE Hypoxia-induced protein coding sequence #48.
PN WO200246465-A2.
PD 13-JUN-2002.
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
Query Match
Best Local Similarity 2.6%; Score 38.2; DB 6; Length 3250;
49.8%; Pred. No. 17;
RESULT 570
ID ADJ44797 standard; cDNA; 3250 BP.
DE Human src biomarker polynucleotide SEQ ID NO:191.
PN WO2003062395-A2.
PD 31-JUL-2003.
PA (BRIM-) BRISTOL-MYERS SQUIBB CO.
Query Match
Best Local Similarity 2.6%; Score 38.2; DB 10; Length 3250;
49.8%; Pred. No. 17;
RESULT 571
ID ADN04316 standard; cDNA; 3250 BP.
DE Antiproliferative cDNA sequence #358.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH-) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 38.2; DB 12; Length 3250;
49.8%; Pred. No. 17;
RESULT 572
ID ADP24081 standard; cDNA; 3250 BP.
DE PRO polypeptide encoding cDNA SEQ ID NO:1259.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH-) GENENTECH INC.
Query Match
Best Local Similarity 2.6%; Score 38.2; DB 13; Length 3250;
49.8%; Pred. No. 17;
RESULT 573
ID ADK14120 standard; cDNA; 4139 BP.
DE Human autoimmune disorder gene #24.
PN US2003228617-A1.
PD 11-DEC-2003.

PA (UYVA-) UNIV VANDERBILT.
Query Match 2.6%; Score 38.2; DB 12; Length 4139;
Best Local Similarity 49.8%; Pred. No. 19;
RESULT 574
ID AD809821 standard; DNA; 4323 BP.
DE Novel DNA-related contig nucleotide sequence #543.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 38.2; DB 10; Length 4323;
Best Local Similarity 49.8%; Pred. No. 19;
RESULT 575
ID ADP25280 standard; cDNA; 5019 BP.
DE PRO polypeptide encoding cDNA SEQ ID NO:2458.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH-) GENENTECH INC.
Query Match 2.6%; Score 38.2; DB 13; Length 5019;
Best Local Similarity 49.8%; Pred. No. 21;
RESULT 576
ID AAH73300 standard; cDNA; 5552 BP.
DE Human cervical cancer marker nucleic acid 4574.
PN WO200142467-A2.
PD 14-JUN-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.6%; Score 38.2; DB 4; Length 5552;
Best Local Similarity 49.8%; Pred. No. 22;
RESULT 577
ID ADU63176 standard; DNA; 7405 BP.
DE Human zygote arrest 1 (Zari) DNA sequence #1.
PN WO2003091400-A2.
PD 06-NOV-2003.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
Query Match 2.6%; Score 38.2; DB 10; Length 7405;
Best Local Similarity 53.9%; Pred. No. 25;
RESULT 578
ID ACN44936 standard; DNA; 50460 BP.
DE Mouse genomic sequence mCG5738.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.6%; Score 38.2; DB 11; Length 50460;
Best Local Similarity 54.7%; Pred. No. 65;
RESULT 579
ID AA31969 standard; DNA; 345 BP.
DE Plant microsatellite marker #930.
PN WO9967421-A1.
PD 29-DEC-1999.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 2.6%; Score 38; DB 3; Length 359;
Best Local Similarity 49.0%; Pred. No. 6.3;
RESULT 580
ID AA31680 standard; DNA; 359 BP.
DE Plant microsatellite marker #641.
PN WO9967421-A1.
PD 29-DEC-1999.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 2.6%; Score 38; DB 3; Length 359;
Best Local Similarity 49.0%; Pred. No. 6.3;
RESULT 581
ID AA674660 standard; cDNA; 381 BP.
DE DNA encoding novel human diagnostic protein #10464.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.6%; Score 38; DB 5; Length 381;
Best Local Similarity 56.3%; Pred. No. 6.5;
RESULT 582
ID AAA31454 standard; DNA; 404 BP.
DE Plant microsatellite marker #415.
PN WO9967421-A1.
PD 29-DEC-1999.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 2.6%; Score 38; DB 3; Length 404;
Best Local Similarity 49.0%; Pred. No. 6.7;
RESULT 583
ID AAA31708 standard; DNA; 414 BP.
DE Plant microsatellite marker #669.
PN WO9967421-A1.
PD 29-DEC-1999.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 2.6%; Score 38; DB 3; Length 414;
Best Local Similarity 49.0%; Pred. No. 6.8;
RESULT 584
ID AB214848 standard; DNA; 450 BP.
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 2653.
PN WO200216655-A2.
PD 28-FEB-2002.
PA (SCRI) SCRIPPS RES INST.
Query Match 2.6%; Score 38; DB 6; Length 450;
Best Local Similarity 48.6%; Pred. No. 7.1;
RESULT 585
ID ADA68519 standard; DNA; 450 BP.
DE Arabidopsis thaliana gene, SEQ ID 577.
PN WO200300898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.6%; Score 38; DB 8; Length 450;
Best Local Similarity 48.6%; Pred. No. 7.1;
RESULT 586
ID AAC49319 standard; DNA; 456 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 60710.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 2.6%; Score 38; DB 3; Length 456;
Best Local Similarity 48.6%; Pred. No. 7.1;
RESULT 587
ID AAC41064 standard; DNA; 501 BP.
DE Zea mays DNA fragment SEQ ID NO: 30519.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 2.6%; Score 38; DB 3; Length 501;
Best Local Similarity 48.6%; Pred. No. 7.5;
RESULT 588
ID ADC76485 standard; DNA; 560 BP.
DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 1754.
PN WO2003020905-A2.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
Query Match 2.6%; Score 38; DB 10; Length 560;
Best Local Similarity 48.6%; Pred. No. 7.9;
RESULT 589
ID ADK55194 standard; DNA; 560 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #2577.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
Query Match 2.6%; Score 38; DB 10; Length 560;
Best Local Similarity 48.6%; Pred. No. 7.9;
RESULT 590
ID ADC77186 standard; DNA; 617 BP.
DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 2115.
PN WO2003020905-A2.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
Query Match 2.6%; Score 38; DB 10; Length 617;
Best Local Similarity 48.6%; Pred. No. 8.3;
RESULT 591
ID ADK56996 standard; DNA; 617 BP.

DE Plant DNA sequence which confers altered metabolic characteristic #4379.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOMC) DOM CHEM CO.
PN (DOMC) DOM AGROSCIENCES LLC.
PA Query Match 2.6%; Score 38; DB 10; Length 617;
Best Local Similarity 48.6%; Pred. No. 8.3;
RESULT 592
ID AB065708 standard; DNA; 695 BP.
DE Arabidopsis thaliana polynucleotide SEQ ID NO 285.
PN US2002059663-A1.
PD 16-MAY-2002.
PA (GORT/) GORTLACH J.
PA (ANYX/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (RAIN/) RAINES T M.
PA (YUY/) YU Y.
PA (PAGE/) PAGE A.
PA (MATH/) MATHW A V.
PA (LEDF/) LEDFORD B L.
PA (WOBS/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
PA (KRICK/) KRICKER M.
PA (SLAT/) SLATER T.
PA (DAVI/) DAVIS K R.
PA (ALBE/) ALLEN K.
PA (HOFF/) HOFFMAN N.
PA (HURB/) HURBAN P.
PA Query Match 2.6%; Score 38; DB 6; Length 695;
Best Local Similarity 48.6%; Pred. No. 8.8;
RESULT 593
ID ABJ32567 standard; DNA; 6907 BP.
DE Human immune system associated gene SEQ ID NO: 540.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIC-) EPIGENOMICS AG.
PA Query Match 2.6%; Score 38; DB 6; Length 6907;
Best Local Similarity 51.8%; Pred. No. 28;
RESULT 594
ID AAA10594 standard; DNA; 10732 BP.
DE Gene encoding a subunit of cellulose synthase.
PN JP2000060568-A.
PD 29-FEB-2000.
PA (MITU/) MITUNO K.
PA (OUIP) OUI PAPER CO.
PA Query Match 2.6%; Score 38; DB 3; Length 10732;
Best Local Similarity 13.8%; Pred. No. 34;
RESULT 595
ID ADJ57067 standard; DNA; 13535 BP.
DE Vector plasmid pBS 15.1 hcmv/GFP+hot spot for CHO cells.
PN WO2004009823-A1.
PD 29-JAN-2004.
PA (LONZ-) LONZA BIOLOGICS PLC.
PA Query Match 2.6%; Score 38; DB 12; Length 13535;
Best Local Similarity 56.3%; Pred. No. 38;
RESULT 596
ID AB168262 standard; DNA; 62944 BP.
DE Kidney cancer related gene sequence SEQ ID NO:6599.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
PA Query Match 2.6%; Score 38; DB 6; Length 62944;
Best Local Similarity 60.8%; Pred. No. 83;
RESULT 597
ID AB166947 standard; DNA; 62944 BP.
DE Lung cancer related gene sequence SEQ ID NO:5284.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
PA Query Match 2.6%; Score 38; DB 6; Length 62944;

Best Local Similarity 60.8%; Pred. No. 83;
RESULT 598
ID ABD32881 standard; DNA; 83943 BP.
DE Mouse cancer-associated genomic DNA MD18-006.
PN WO2004074520-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
PA Query Match 2.6%; Score 38; DB 13; Length 83943;
Best Local Similarity 54.2%; Pred. No. 95;
RESULT 599
ID ABD33157 standard; DNA; 109559 BP.
DE Murine cancer-associated (CA) gene MD07-021.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
PA Query Match 2.6%; Score 38; DB 13; Length 109559;
Best Local Similarity 56.3%; Pred. No. 1.1e+02;
RESULT 600
Query Match 2.6%; Score 38; DB 12; Length 110000;
Best Local Similarity 59.1%; Pred. No. 1.1e+02;
RESULT 601
ID ADA58658 standard; cDNA; 242 BP.
DE Maize sucrose synthase EST #302.
PN US2003135870-A1.
PD 17-JUL-2003.
PA (CHEI/) CHEIKH N.
PA (FISH/) FISHER D K.
PA (LIUJ/) LIU J.
PA Query Match 2.5%; Score 37.8; DB 9; Length 242;
Best Local Similarity 52.9%; Pred. No. 5.9;
RESULT 602
ID ACH18237 standard; cDNA; 391 BP.
DE Human adult heart cDNA #2551.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRWA/) DRWANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
PA Query Match 2.5%; Score 37.8; DB 9; Length 391;
Best Local Similarity 49.3%; Pred. No. 7.5;
RESULT 603
ID ACH24579 standard; cDNA; 449 BP.
DE Human adult ovary cDNA #2359.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRWA/) DRWANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
PA Query Match 2.5%; Score 37.8; DB 9; Length 449;
Best Local Similarity 49.3%; Pred. No. 8;
RESULT 604
ID ACH28432 standard; cDNA; 455 BP.
DE Human adult ovary cDNA #6812.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRWA/) DRWANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
PA Query Match 2.5%; Score 37.8; DB 9; Length 455;
Best Local Similarity 49.3%; Pred. No. 8.1;
RESULT 605
ID ACH17443 standard; cDNA; 459 BP.
DE Human adult heart cDNA #1757.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRWA/) DRWANAC R T.
PA (LABA/) LABAT I.

PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 2.5%; Score 37.8; DB 9; Length 459;
Best Local Similarity 49.3%; Pred. No. 8.1;
RESULT 606
ID ACH16072 standard; cDNA; 465 BP.
DE Human adult heart cDNA #386.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 2.5%; Score 37.8; DB 9; Length 465;
Best Local Similarity 49.3%; Pred. No. 8.2;
RESULT 607
ID ACH26804 standard; cDNA; 478 BP.
DE Human adult ovary cDNA #5184.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 2.5%; Score 37.8; DB 9; Length 478;
Best Local Similarity 49.3%; Pred. No. 8.3;
RESULT 608
ID AAH81659 standard; DNA; 557 BP.
DE Human differential transcription-associated cDNA SEQ ID 168.
PN WO200357058-A2.
PD 09-AUG-2001.
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
Query Match 2.5%; Score 37.8; DB 5; Length 557;
Best Local Similarity 49.3%; Pred. No. 8.9;
RESULT 609
ID ACN40763 standard; cDNA; 1116 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA326826, SEQ ID NO:5754.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 37.8; DB 13; Length 1116;
Best Local Similarity 49.3%; Pred. No. 13;
RESULT 610
ID ADK70382 standard; cDNA; 1160 BP.
DE Respiratory disease differentially expressed cDNA #118.
PN WO2003101283-A2.
PD 11-DEC-2003.
PA (INCY-) INCYTE CORP.
Query Match 2.5%; Score 37.8; DB 13; Length 1160;
Best Local Similarity 49.3%; Pred. No. 13;
RESULT 611
ID AAG45021 standard; cDNA; 1199 BP.
DE cDNA encoding novel human secretory protein. Seq ID No 102.
PN WO200166889-A2.
PD 13-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.5%; Score 37.8; DB 5; Length 1199;
Best Local Similarity 49.3%; Pred. No. 13;
RESULT 612
ID AA193806 standard; cDNA; 1306 BP.
DE Human polynucleotide SEQ ID NO 13866.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.5%; Score 37.8; DB 4; Length 1306;
Best Local Similarity 49.3%; Pred. No. 14;
RESULT 613
ID AD56207 standard; cDNA; 1312 BP.
DE Human cDNA differentially expressed in MYCN activated cells SeqID 13.
PN US2003119009-A1.

PD 26-JUN-2003.
PA (STUA/) STUART S G.
PA (NUCH/) NUCHTERN J G.
PA (PLON/) PLON S E.
PA (SHOH/) SHOHEI J M.
Query Match 2.5%; Score 37.8; DB 10; Length 1312;
Best Local Similarity 49.3%; Pred. No. 14;
RESULT 614
ID ACA26293 standard; DNA; 1404 BP.
DE Prokaryotic essential gene #7950.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 2.5%; Score 37.8; DB 8; Length 1404;
Best Local Similarity 52.2%; Pred. No. 14;
RESULT 615
ID ADA71195 standard; DNA; 1839 BP.
DE Rice gene, SEQ ID 4518.
PN WO200300898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.5%; Score 37.8; DB 8; Length 1839;
Best Local Similarity 50.3%; Pred. No. 16;
RESULT 616
ID ACN90405 standard; DNA; 3397 BP.
DE Breast cancer related marker, seq id 11555.
PN US200309974-A1.
PD 29-MAY-2003.
PA (MILL-) MILENNIUM PHARM INC.
Query Match 2.5%; Score 37.8; DB 11; Length 3397;
Best Local Similarity 49.3%; Pred. No. 22;
RESULT 617
ID AAG65476 standard; DNA; 3682 BP.
DE Human beta-3 adrenergic receptor gene.
PN EP600136-A1.
PD 08-JUN-1994.
PA (CNRS) CNRT NAT RECH SCI.
Query Match 2.5%; Score 37.8; DB 2; Length 3682;
Best Local Similarity 52.9%; Pred. No. 23;
RESULT 618
ID ABO8185 standard; cDNA; 4911 BP.
DE Human kinesin motor protein Hekif21b coding sequence.
PN US6426193-B1.
PD 30-JUL-2002.
PA (CYTO-) CYTOKINETICS INC.
Query Match 2.5%; Score 37.8; DB 6; Length 4911;
Best Local Similarity 44.0%; Pred. No. 26;
RESULT 619
ID ABR52651 standard; DNA; 4911 BP.
DE DNA encoding human kinesin motor protein Hekif21b.
PN US6383796-B1.
PD 07-MAY-2002.
PA (CYTO-) CYTOKINETICS INC.
Query Match 2.5%; Score 37.8; DB 6; Length 4911;
Best Local Similarity 44.0%; Pred. No. 26;
RESULT 620
ID ABS7218 standard; DNA; 4911 BP.
DE Human kinesin-like protein, Hekif21b, gene.
PN US6455293-B1.
PD 24-SEP-2002.
PA (CYTO-) CYTOKINETICS INC.
Query Match 2.5%; Score 37.8; DB 10; Length 4911;
Best Local Similarity 44.0%; Pred. No. 26;
RESULT 621
ID ACC47237 standard; cDNA; 5197 BP.
DE Human SCAP encoding cDNA-Incyte Id. 7290157CBL.
PN WO2003008625-A2.
PD 30-JAN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 2.5%; Score 37.8; DB 8; Length 5197;
Best Local Similarity 44.0%; Pred. No. 27;
RESULT 622
ID ABX1086 standard; DNA; 4299 BP.

DE Human ribosomal RNA (rRNA) gene.
PN US2002160410-A1.
PD 31-OCT-2002.
PA (HADL/) HADLACZY G.
PA (SZAL/) SZALAY A A.
Query Match 2.5%; Score 37.8; DB 8; Length 42999;
Best Local Similarity 45.3%; Pred. No. 78;
RESULT 623
ID ADA02933 standard; DNA; 96599 BP.
DE Mouse Braf carcinoma associated gene, SEQ ID NO.1451.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.5%; Score 37.8; DB 9; Length 96599;
Best Local Similarity 54.7%; Pred. No. 1.2e+02;
RESULT 624
ID ADB72671 standard; DNA; 96599 BP.
DE Mouse Braf gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.5%; Score 37.8; DB 10; Length 96599;
Best Local Similarity 54.7%; Pred. No. 1.2e+02;
RESULT 625
ID ADC85413 standard; DNA; 96599 BP.
DE Mouse Braf genomic sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.5%; Score 37.8; DB 10; Length 96599;
Best Local Similarity 54.7%; Pred. No. 1.2e+02;
RESULT 626
ID ADM74528 standard; DNA; 96599 BP.
DE Murine carcinoma associated (CA) nucleic acid #100.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR/) MORRIS D W.
PA (ENGEL/) ENGELHARD E K.
Query Match 2.5%; Score 37.8; DB 12; Length 96599;
Best Local Similarity 54.7%; Pred. No. 1.2e+02;
RESULT 627
ID ADC77195 standard; DNA; 526 BP.
DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 2124.
PN WO2003020905-A2.
PD 13-MAR-2003.
PA (DOMC-) DOM CHEM CO.
Query Match 2.5%; Score 37.6; DB 10; Length 526;
Best Local Similarity 47.5%; Pred. No. 9.9;
RESULT 628
ID ADC75911 standard; DNA; 526 BP.
DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 835.
PN WO2003020905-A2.
PD 13-MAR-2003.
PA (DOMC-) DOM CHEM CO.
Query Match 2.5%; Score 37.6; DB 10; Length 526;
Best Local Similarity 47.5%; Pred. No. 9.9;
RESULT 629
ID ADS7005 standard; DNA; 526 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #4388.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOMC-) DOM CHEM CO.
Query Match 2.5%; Score 37.6; DB 10; Length 526;
Best Local Similarity 47.5%; Pred. No. 9.9;
RESULT 630
ID ADS5189 standard; DNA; 526 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #2572.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOMC-) DOM CHEM CO.
Query Match 2.5%; Score 37.6; DB 10; Length 526;
Best Local Similarity 47.5%; Pred. No. 9.9;
RESULT 631
ID ADS5189 standard; DNA; 526 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #2572.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOMC-) DOM CHEM CO.
Query Match 2.5%; Score 37.6; DB 10; Length 526;
Best Local Similarity 47.5%; Pred. No. 9.9;

Best Local Similarity 47.5%; Pred. No. 9.9;
RESULT 631
ID ACU19198 standard; DNA; 604 BP.
DE DNA clone originating in barley containing SNP encoding sequence #9189.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UYNI-) UNIV JAPAN OKAYAMA.
Query Match 2.5%; Score 37.6; DB 9; Length 604;
Best Local Similarity 49.0%; Pred. No. 11;
RESULT 632
ID ACU19212 standard; DNA; 708 BP.
DE DNA clone originating in barley containing SNP encoding sequence #9203.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UYNI-) UNIV JAPAN OKAYAMA.
Query Match 2.5%; Score 37.6; DB 9; Length 708;
Best Local Similarity 49.0%; Pred. No. 11;
RESULT 633
ID ACU19226 standard; DNA; 711 BP.
DE DNA clone originating in barley containing SNP encoding sequence #9217.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UYNI-) UNIV JAPAN OKAYAMA.
Query Match 2.5%; Score 37.6; DB 9; Length 711;
Best Local Similarity 49.0%; Pred. No. 11;
RESULT 634
ID ADS51517 standard; cDNA; 799 BP.
DE Bacterial polynucleotide #6260.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 2.5%; Score 37.6; DB 13; Length 799;
Best Local Similarity 47.1%; Pred. No. 12;
RESULT 635
ID ABD06635 standard; DNA; 1344 BP.
DE Pseudomonas aeruginosa polynucleotide #5239.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.5%; Score 37.6; DB 11; Length 1344;
Best Local Similarity 51.2%; Pred. No. 16;
RESULT 636
ID ABD06577 standard; DNA; 1794 BP.
DE Pseudomonas aeruginosa polynucleotide #5181.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.5%; Score 37.6; DB 11; Length 1794;
Best Local Similarity 51.2%; Pred. No. 18;
RESULT 637
ID ABD06690 standard; DNA; 2547 BP.
DE Pseudomonas aeruginosa polynucleotide #5294.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.5%; Score 37.6; DB 11; Length 2547;
Best Local Similarity 51.2%; Pred. No. 22;
RESULT 638
ID ADD00948 standard; cDNA; 4749 BP.
DE Human jagged 2 encoding cDNA SEQ ID NO.3.
PN WO2003077848-A2.
PD 25-SEP-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 2.5%; Score 37.6; DB 10; Length 4749;
Best Local Similarity 52.6%; Pred. No. 30;
RESULT 639
ID ADH62908 standard; DNA; 4749 BP.
DE Human jagged 2 DNA #1.
PN US2003170636-A1.

PD 11-SEP-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 2.5%; Score 37.6; DB 10; Length 4749;
Best Local Similarity 52.6%; Pred. No. 30;
RESULT 640
ID ADH57063 standard; DNA; 4749 BP.
DE DNA of a human Jagged 2 RNA sequence Segid 3.
PN US2003207839-A1.
PD 06-NOV-2003.
PA (FREI/) FREIER S. M.
Query Match 2.5%; Score 37.6; DB 10; Length 4749;
Best Local Similarity 52.6%; Pred. No. 30;
RESULT 641
ID ADD00955 standard; cDNA; 4974 BP.
DE Human Jagged 2 encoding cDNA SEQ ID NO:10.
PN WO2003077848-A2.
PD 25-SEP-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 2.5%; Score 37.6; DB 10; Length 4974;
Best Local Similarity 52.6%; Pred. No. 30;
RESULT 642
ID ADH62915 standard; DNA; 4974 BP.
DE Human Jagged 2 DNA #2.
PN US2003170636-A1.
PD 11-SEP-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 2.5%; Score 37.6; DB 10; Length 4974;
Best Local Similarity 52.6%; Pred. No. 30;
RESULT 643
ID ADH57070 standard; DNA; 4974 BP.
DE DNA of a human Jagged 2 RNA sequence Segid 10.
PN US2003207839-A1.
PD 06-NOV-2003.
PA (FREI/) FREIER S. M.
Query Match 2.5%; Score 37.6; DB 10; Length 4974;
Best Local Similarity 52.6%; Pred. No. 30;
RESULT 644
ID ADN03615 standard; cDNA; 5077 BP.
DE Antipeptidic cDNA sequence #5.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GEHT) GENENTECH INC.
Query Match 2.5%; Score 37.6; DB 12; Length 5077;
Best Local Similarity 52.6%; Pred. No. 31;
RESULT 645
ID ADR83400 standard; DNA; 5077 BP.
DE Human Jagged 2 DNA, target gene of miRNA.
PN WO2004076622-A2.
PD 10-SEP-2004.
PA (NMAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
Query Match 2.5%; Score 37.6; DB 13; Length 5077;
Best Local Similarity 52.6%; Pred. No. 31;
RESULT 646
ID ADR73469 standard; DNA; 5077 BP.
DE Human Jagged 2, JAG2, gene.
PN WO2004076682-A2.
PD 10-SEP-2004.
PA (SURR-) SURROMED INC.
Query Match 2.5%; Score 37.6; DB 13; Length 5077;
Best Local Similarity 52.6%; Pred. No. 31;
RESULT 647
ID ABD32670 standard; DNA; 111331 BP.
DE Mouse cancer-associated genomic DNA MD17-083.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.5%; Score 37.6; DB 13; Length 111331;
Best Local Similarity 51.8%; Pred. No. 1.4e+02;
RESULT 648
ID ABD32610 standard; DNA; 115780 BP.
DE Mouse cancer-associated genomic DNA MD12-017.
PN WO2004074320-A2.
PD 02-SEP-2004.

PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.5%; Score 37.6; DB 13; Length 115780;
Best Local Similarity 46.2%; Pred. No. 1.4e+02;
RESULT 649
ID ADD50650 standard; DNA; 175590 BP.
DE BAC sequence #1 containing hCHT DNA.
PN US2003114399-A1.
PD 19-JUN-2003.
PA (BLAK/) BLAKELY R. D.
PA (APPA/) APPASUNDARAM S.
PA (FERG/) FERGUSON S.
Query Match 2.5%; Score 37.6; DB 10; Length 175590;
Best Local Similarity 51.8%; Pred. No. 1.8e+02;
RESULT 650
ID ACN44514 standard; DNA; 256493 BP.
DE Human genomic sequence hCG17361.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.5%; Score 37.6; DB 11; Length 256493;
Best Local Similarity 46.0%; Pred. No. 2.1e+02;
RESULT 651
ID ADH00876 standard; DNA; 327 BP.
DE Kidney disease-associated gene-related mouse DNA sequence Segid2005.
PN WO2003091427-A1.
PD 06-NOV-2003.
PA (KANSAI) KANSAI TECHNOLOGY LICENSING ORG CO LTD.
Query Match 2.5%; Score 37.4; DB 12; Length 327;
Best Local Similarity 58.6%; Pred. No. 8.9;
RESULT 652
ID ADB59059 standard; DNA; 511 BP.
DE Toxicity-related gene, SEQ ID 4085.
PN WO2003064624-A2.
PD 07-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 2.5%; Score 37.4; DB 10; Length 511;
Best Local Similarity 47.0%; Pred. No. 11;
RESULT 653
ID ADB53812 standard; DNA; 511 BP.
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:4354.
PN WO2003065593-A2.
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 2.5%; Score 37.4; DB 10; Length 511;
Best Local Similarity 47.0%; Pred. No. 11;
RESULT 654
ID ADB68842 standard; DNA; 536 BP.
DE Minority luxI consensus sequence DNA 14.
PN WO2003057802-A2.
PD 17-JUL-2003.
PA (FRANU) FRADUNHOFER USA INC.
Query Match 2.5%; Score 37.4; DB 10; Length 536;
Best Local Similarity 13.4%; Pred. No. 11;
RESULT 655
ID AC119217 standard; DNA; 559 BP.
DE DNA clone originating in barley containing SNP encoding sequence #9208.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UNIV-) UNIV JAPAN OKAYAMA.
Query Match 2.5%; Score 37.4; DB 9; Length 559;
Best Local Similarity 49.2%; Pred. No. 12;
RESULT 656
ID AC119219 standard; DNA; 593 BP.
DE DNA clone originating in barley containing SNP encoding sequence #9210.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UNIV-) UNIV JAPAN OKAYAMA.
Query Match 2.5%; Score 37.4; DB 9; Length 593;
Best Local Similarity 49.2%; Pred. No. 12;
RESULT 657
ID AC119199 standard; DNA; 593 BP.
DE DNA clone originating in barley containing SNP encoding sequence #9190.
PN WO2003057877-A1.

PD 17-JUL-2003.
PA (UYN1-) UNIV JAPAN OKAYAMA.
Query Match 2.5%; Score 37.4; DB 9; Length 593;
Best Local Similarity 49.2%; Pred. No. 12;
RESULT 658
ID ACL19225 standard; DNA; 607 BP.
DE DNA clone originating in barley containing SNP encoding sequence #9216.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UYN1-) UNIV JAPAN OKAYAMA.
Query Match 2.5%; Score 37.4; DB 9; Length 607;
Best Local Similarity 49.2%; Pred. No. 12;
RESULT 659
ID ACL19201 standard; DNA; 608 BP.
DE DNA clone originating in barley containing SNP encoding sequence #9192.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UYN1-) UNIV JAPAN OKAYAMA.
Query Match 2.5%; Score 37.4; DB 9; Length 608;
Best Local Similarity 49.2%; Pred. No. 12;
RESULT 660
ID ACL19204 standard; DNA; 621 BP.
DE DNA clone originating in barley containing SNP encoding sequence #9195.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UYN1-) UNIV JAPAN OKAYAMA.
Query Match 2.5%; Score 37.4; DB 9; Length 621;
Best Local Similarity 49.2%; Pred. No. 12;
RESULT 661
ID ACL19206 standard; DNA; 623 BP.
DE DNA clone originating in barley containing SNP encoding sequence #9197.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UYN1-) UNIV JAPAN OKAYAMA.
Query Match 2.5%; Score 37.4; DB 9; Length 623;
Best Local Similarity 49.2%; Pred. No. 12;
RESULT 662
ID ACL19208 standard; DNA; 629 BP.
DE DNA clone originating in barley containing SNP encoding sequence #9199.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UYN1-) UNIV JAPAN OKAYAMA.
Query Match 2.5%; Score 37.4; DB 9; Length 629;
Best Local Similarity 49.2%; Pred. No. 12;
RESULT 663
ID ACL19205 standard; DNA; 633 BP.
DE DNA clone originating in barley containing SNP encoding sequence #9196.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UYN1-) UNIV JAPAN OKAYAMA.
Query Match 2.5%; Score 37.4; DB 9; Length 633;
Best Local Similarity 49.2%; Pred. No. 12;
RESULT 664
ID ACL19221 standard; DNA; 664 BP.
DE DNA clone originating in barley containing SNP encoding sequence #9212.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UYN1-) UNIV JAPAN OKAYAMA.
Query Match 2.5%; Score 37.4; DB 9; Length 664;
Best Local Similarity 49.2%; Pred. No. 13;
RESULT 665
ID ACL19213 standard; DNA; 669 BP.
DE DNA clone originating in barley containing SNP encoding sequence #9204.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UYN1-) UNIV JAPAN OKAYAMA.
Query Match 2.5%; Score 37.4; DB 9; Length 669;
Best Local Similarity 49.2%; Pred. No. 13;
RESULT 666
ID ACL19216 standard; DNA; 670 BP.
DE DNA clone originating in barley containing SNP encoding sequence #9207.
PN WO2003057877-A1.
PD 17-JUL-2003.

PA (UYN1-) UNIV JAPAN OKAYAMA.
Query Match 2.5%; Score 37.4; DB 9; Length 670;
Best Local Similarity 49.2%; Pred. No. 13;
RESULT 667
ID ACL19220 standard; DNA; 696 BP.
DE DNA clone originating in barley containing SNP encoding sequence #9211.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UYN1-) UNIV JAPAN OKAYAMA.
Query Match 2.5%; Score 37.4; DB 9; Length 696;
Best Local Similarity 49.2%; Pred. No. 13;
RESULT 668
ID ACL19223 standard; DNA; 710 BP.
DE DNA clone originating in barley containing SNP encoding sequence #9214.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UYN1-) UNIV JAPAN OKAYAMA.
Query Match 2.5%; Score 37.4; DB 9; Length 710;
Best Local Similarity 49.2%; Pred. No. 13;
RESULT 669
ID ADP29084 standard; DNA; 1044 BP.
DE Human secreted protein encoding sequence SEQ ID #1082.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 2.5%; Score 37.4; DB 12; Length 1044;
Best Local Similarity 47.6%; Pred. No. 16;
RESULT 670
ID ADJ39564 standard; cDNA; 1930 BP.
DE Plant cDNA #564.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOF/) GOF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICKS D.
PA (ZHUT/) ZHU T.
Query Match 2.5%; Score 37.4; DB 12; Length 1930;
Best Local Similarity 53.8%; Pred. No. 21;
RESULT 671
ID ABX72264 standard; cDNA; 2209 BP.
DE Human NOVX polynucleotide #95.
PN WO200281498-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 2.5%; Score 37.4; DB 8; Length 2209;
Best Local Similarity 47.6%; Pred. No. 23;
RESULT 672
ID AAD34007 standard; cDNA; 2258 BP.
DE Human HIPHM 0000029 protein encoding cDNA.
PN GB2365432-A.
PD 20-FEB-2002.
PA (GLAX) GLAXO GROUP LTD.
Query Match 2.5%; Score 37.4; DB 6; Length 2258;
Best Local Similarity 47.6%; Pred. No. 23;
RESULT 673
ID ADP63696 standard; cDNA; 2336 BP.
DE Novel human cDNA sequence #857.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) REAS ASSOC BIOTECHNOLOGY.
Query Match 2.5%; Score 37.4; DB 12; Length 2336;
Best Local Similarity 53.8%; Pred. No. 24;
RESULT 674
ID ACF79238 standard; cDNA; 2388 BP.
DE Human neurotransmitter transporter variant polynucleotide.
PN WO2003059947-A1.

PD 24-JUL-2003.
PA (FARB) BAYER AG.
Query Match 2.5%; Score 37.4; DB 10; Length 2388;
Best Local Similarity 47.6%; Pred. No. 24;
RESULT 675
ID AC79237 standard; cDNA; 2432 BP.
DE Human neurotransmitter transporter polynucleotide.
PN WO2003059947-A1.
PD 24-JUL-2003.
PA (FARB) BAYER AG.
Query Match 2.5%; Score 37.4; DB 10; Length 2432;
Best Local Similarity 47.6%; Pred. No. 24;
RESULT 676
ID AAT09866 standard; cDNA; 2486 BP.
DE Human neurotransmitter transporter protein cDNA.
PN WO9531539-A1.
PD 23-NOV-1995.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.5%; Score 37.4; DB 2; Length 2486;
Best Local Similarity 47.6%; Pred. No. 24;
RESULT 677
ID ACC43635 standard; DNA; 2490 BP.
DE Nucleotide sequence of the human F-box polypeptide FBW3B.
PN FR2828208-A1.
PD 07-FEB-2003.
PA (CYTO-) CYTOMICS SYSTEMS SA.
Query Match 2.5%; Score 37.4; DB 8; Length 2490;
Best Local Similarity 58.6%; Pred. No. 24;
RESULT 678
ID AD097161 standard; DNA; 107432 BP.
DE Mouse cancer associated sequence MD08-009, SEQ ID 137.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.5%; Score 37.4; DB 12; Length 107432;
Best Local Similarity 55.9%; Pred. No. 1.6e+02;
RESULT 679
ID AA184688 standard; cDNA; 439 BP.
DE Human polynucleotide SEQ ID NO 4748.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.5%; Score 37.2; DB 4; Length 439;
Best Local Similarity 50.3%; Pred. No. 12;
RESULT 680
ID AAC56719 standard; DNA; 476 BP.
DE Eucalyptus grandis transcription factor DNA sequence #590.
PN WO2000053724-A2.
PD 14-SEP-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 2.5%; Score 37.2; DB 3; Length 476;
Best Local Similarity 49.0%; Pred. No. 12;
RESULT 681
ID ABD17057 standard; DNA; 864 BP.
DE Pseudomonas aeruginosa polynucleotide #15661.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.5%; Score 37.2; DB 11; Length 864;
Best Local Similarity 44.7%; Pred. No. 16;
RESULT 682
ID ABD17123 standard; DNA; 1428 BP.
DE Pseudomonas aeruginosa polynucleotide #15727.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.5%; Score 37.2; DB 11; Length 1428;
Best Local Similarity 44.7%; Pred. No. 21;
RESULT 683
ID ABK92063 standard; DNA; 1782 BP.
DE DNA encoding novel transmembrane segment 2-like protein #4.
PN WO200229058-A2.

PD 11-APR-2002.
PA (CURA-) CURAGEN CORP.
Query Match 2.5%; Score 37.2; DB 6; Length 1782;
Best Local Similarity 54.3%; Pred. No. 23;
RESULT 684
ID AD847785 standard; DNA; 1881 BP.
DE Human NOV45d gene SEQ ID NO:147.
PN WO2003076642-A2.
PD 18-SEP-2003.
PA (CURA-) CURAGEN CORP.
Query Match 2.5%; Score 37.2; DB 10; Length 1881;
Best Local Similarity 54.3%; Pred. No. 24;
RESULT 685
ID ADH41902 standard; DNA; 1881 BP.
DE Novel human nucleic acid NOV36f.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 2.5%; Score 37.2; DB 12; Length 1881;
Best Local Similarity 54.3%; Pred. No. 24;
RESULT 686
ID ADU79055 standard; DNA; 1881 BP.
DE Human NOVX protein NOV45D gene sequence.
PN US2004014053-A1.
PD 22-JAN-2004.
PA (ZERR/) ZERRHUSEN B D.
PA (PAT/) PATTRAJAN M.
PA (KEKU/) KEKUDA R.
PA (MILL/) MILLER C E.
PA (RIEG/) RIEGER D K.
PA (PENNA/) PENNA C E A.
PA (SHIM/) SHIMKETS R A.
PA (LILL/) LI L.
PA (BERG/) BERGHS C.
PA (ZHON/) ZHONG M.
PA (CASM/) CASMAN S J.
PA (VOSS/) VOSS E Z.
PA (BOLD/) BOLDIG F L.
PA (PADI/) PADIGARU M.
PA (SMIT/) SMITHSON G.
PA (JIMW/) JI W.
PA (GORM/) GORMAN L.
PA (VERN/) VERNET C A M.
PA (LEIT/) LEITE M W.
PA (GUOX/) GUO X S.
PA (ANDE/) ANDERSON D W.
PA (SPYT/) SPYTEK K A.
PA (GERL/) GERLACH V.
PA (BURG/) BURGESS C E.
PA (KHRA/) KHRAMTSOV N V.
PA (ORTT/) ORT T.
PA (ELLE/) ELLERMAN K.
PA (RAST/) RASTELLI L.
PA (AGEB/) AGE M L.
PA (CHAU/) CHAUDHURI A.
PA (CHAN/) CHANT J S.
PA (DIP/) DIPPEO V A.
PA (EDIN/) EDINGER S R.
PA (EISE/) EISEN A J.
PA (GANG/) GANGOLLI E A.
PA (GIOT/) GIOT L.
PA (OOIC/) OOI C E.
PA (ROTH/) ROTHENBERG M E.
PA (SPAD/) SPADERNA S K.
PA (HJAL/) HJALT T.
PA (LIUX/) LIU X.
PA (TAUP/) TAUPIER R J.
PA (CATY/) CATTERTON E.
PA (SHEN/) SHENDY S G.
Query Match 2.5%; Score 37.2; DB 12; Length 1881;
Best Local Similarity 54.3%; Pred. No. 24;
RESULT 687
ID ABD17019 standard; DNA; 2679 BP.

DE Pseudomonas aeruginosa polynucleotide #15623.
PN US651795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.5%; Score 37.2; DB 11; Length 2679;
Best Local Similarity 44.7%; Pred. No. 29;
RESULT 688
ID AAF32508 standard; cDNA; 5068 BP.
DE Human male enhanced antigen-2 (MEA-2) nucleotide sequence SEQ ID NO.1.
PN JP2000316580-A.
PD 21-NOV-2000.
PA (ITOH-) ITO HAM KK.
Query Match 2.5%; Score 37.2; DB 5; Length 5068;
Best Local Similarity 48.2%; Pred. No. 39;
RESULT 689
ID AAL37335 standard; DNA; 7791 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 3700.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.5%; Score 37.2; DB 4; Length 7791;
Best Local Similarity 51.2%; Pred. No. 49;
RESULT 690
ID ABX60323 standard; cDNA; 7791 BP.
DE cDNA encoding novel human musculoskeletal system antigen #2667.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.5%; Score 37.2; DB 8; Length 7791;
Best Local Similarity 51.2%; Pred. No. 49;
RESULT 691
ID ADJ31073 standard; DNA; 7791 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3700.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.5%; Score 37.2; DB 12; Length 7791;
Best Local Similarity 51.2%; Pred. No. 49;
RESULT 692
ID ABD33078 standard; DNA; 21457 BP.
DE Murine cancer associated (CA) gene MD07-003.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.5%; Score 37.2; DB 13; Length 21457;
Best Local Similarity 56.6%; Pred. No. 81;
RESULT 693
ID ACC60906 standard; DNA; 43064 BP.
DE Human CYP1A2 gene SEQ ID NO:76.
PN WO2003014387-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 37.2; DB 8; Length 43064;
Best Local Similarity 50.6%; Pred. No. 1.1e+02;
RESULT 694
ID AAL51405 standard; DNA; 80959 BP.
DE Human secreted protein gene sequence, SEQ ID NO 3.
Query Match 2.5%; Score 37.2; DB 8; Length 80959;
Best Local Similarity 48.6%; Pred. No. 1.6e+02;
RESULT 695
ID ACN45182 standard; DNA; 261817 BP.
DE Human genomic sequence hCG14925.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.5%; Score 37.2; DB 11; Length 261817;
Best Local Similarity 53.4%; Pred. No. 2.8e+02;
RESULT 696
ID ADA58478 standard; cDNA; 289 BP.
DE Maize sucrose synthase EST #122.
PN US2003135870-A1.

PD 17-JUL-2003.
PA (CHRI/) CHIERH N.
PA (FISH/) FISHER D K.
PA (LIUV/) LIU J.
Query Match 2.5%; Score 37; DB 9; Length 289;
Best Local Similarity 53.0%; Pred. No. 11;
RESULT 697
ID ABD09208 standard; DNA; 429 BP.
DE Pseudomonas aeruginosa polynucleotide #7812.
PN US651795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.5%; Score 37; DB 11; Length 429;
Best Local Similarity 45.6%; Pred. No. 13;
RESULT 698
ID ACL19215 standard; DNA; 439 BP.
DE DNA clone originating in barley containing SNP encoding sequence #9206.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UYNI-) UNIV JAPAN OKAYAMA.
Query Match 2.5%; Score 37; DB 9; Length 439;
Best Local Similarity 48.7%; Pred. No. 13;
RESULT 699
ID AAC43517 standard; DNA; 549 BP.
DE Zea mays DNA fragment SEQ ID NO: 39522.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 2.5%; Score 37; DB 3; Length 549;
Best Local Similarity 54.9%; Pred. No. 15;
RESULT 700
ID ADR38458 standard; DNA; 1002 BP.
DE Streptomyces sp KNR269 aldehyde oxidase beta subunit DNA Seq 5.
PN WO2004072281-A1.
PD 26-AUG-2004.
PA (KXNF) KANEXA CORP.
Query Match 2.5%; Score 37; DB 13; Length 1002;
Best Local Similarity 48.0%; Pred. No. 20;
RESULT 701
ID ABX65499 standard; DNA; 1024 BP.
DE Helicobacter pylori selected interacting domain (SID) DNA #98.
PN WO200266501-A2.
PD 29-AUG-2002.
PA (HYBR-) HYBRIGENICS.
PA (INSP) INST PASTEUR.
Query Match 2.5%; Score 37; DB 6; Length 1024;
Best Local Similarity 56.0%; Pred. No. 20;
RESULT 702
ID ACA23920 standard; DNA; 1092 BP.
DE Prokaryotic essential gene #5577.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 2.5%; Score 37; DB 8; Length 1092;
Best Local Similarity 53.9%; Pred. No. 21;
RESULT 703
ID ABD08997 standard; DNA; 1434 BP.
DE Pseudomonas aeruginosa polynucleotide #7601.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.5%; Score 37; DB 11; Length 1434;
Best Local Similarity 45.6%; Pred. No. 24;
RESULT 704
ID ABD09346 standard; DNA; 1626 BP.
DE Pseudomonas aeruginosa polynucleotide #7950.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.5%; Score 37; DB 11; Length 1626;
Best Local Similarity 45.6%; Pred. No. 25;
RESULT 705
ID AAF85145 standard; DNA; 1800 BP.
DE Nucleotide sequence of the relaxase virD2.

PN WO200130810-A2.
PD 03-MAY-2001.
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
Query Match 2.5%; Score 37; DB 4; Length 1800;
Best Local Similarity 56.0%; Pred. No. 27;
RESULT 706
ID AAF85146 standard; DNA; 1800 BP.
DE Nucleotide sequence of the relaxase yirD2.
PN WO200130810-A2.
PD 03-MAY-2001.
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
Query Match 2.5%; Score 37; DB 4; Length 1800;
Best Local Similarity 56.0%; Pred. No. 27;
RESULT 707
ID AAX14387 standard; DNA; 1934 BP.
DE H. pylori GHP0 504 gene.
PN WO9843478-A1.
PD 08-OCT-1998.
PA (INMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
PA (HMA-) HUMAN GENOME SCI INC.
Query Match 2.5%; Score 37; DB 2; Length 1934;
Best Local Similarity 56.0%; Pred. No. 28;
RESULT 708
ID ABD08927 standard; DNA; 2169 BP.
DE Pseudomonas aeruginosa polynucleotide #7531.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.5%; Score 37; DB 11; Length 2169;
Best Local Similarity 45.6%; Pred. No. 29;
RESULT 709
ID ABV74815 standard; DNA; 3644 BP.
DE Human scavenger receptor class A protein ADSE coding sequence #2.
PN WO200264770-A1.
PD 22-AUG-2002.
PA (MOCH) MOCHIDA PHARM CO LTD.
Query Match 2.5%; Score 37; DB 8; Length 3644;
Best Local Similarity 57.3%; Pred. No. 38;
RESULT 710
ID ADD08990 standard; DNA; 44442 BP.
DE Human pancorin genomic DNA SEQ ID NO:15.
PN WO2003085377-A2.
PD 16-OCT-2003.
PA (AMHP) WYETH.
Query Match 2.5%; Score 37; DB 10; Length 44442;
Best Local Similarity 62.4%; Pred. No. 1.3e+02;
RESULT 711
ID ADM80676 standard; DNA; 46374 BP.
DE Human USH3A gene genomic sequence SegID5.
PN WO2003097685-A1.
PD 27-NOV-2003.
PA (YEDA) YEDA RES & DEV CO LTD.
Query Match 2.5%; Score 37; DB 12; Length 46374;
Best Local Similarity 49.7%; Pred. No. 1.4e+02;
RESULT 712
ID ABS52847 standard; DNA; 90541 BP.
DE Human SR protein-specific kinase 2, SRPK2, genomic DNA.
PN US2002094560-A1.
PD 18-JUL-2002.
PA (ABUT/) ABU-THREIDER J.
PA (GONG/) GONG F.
PA (KERC/) KETCHUM K A.
PA (DFRA/) DI FRANCESCO V.
PA (BEAS/) BEASLEY E M.
Query Match 2.5%; Score 37; DB 6; Length 90541;
Best Local Similarity 52.2%; Pred. No. 1.9e+02;
RESULT 713
ID ADJ37690 standard; DNA; 90541 BP.
DE Human kinase genomic DNA.
PN US2003175927-A1.
PD 18-SEP-2003.
PA (APPL-) APPLERA CORP.
Query Match 2.5%; Score 37; DB 10; Length 90541;

Best Local Similarity 52.2%; Pred. No. 1.9e+02;
RESULT 714
ID ADJ31219 standard; DNA; 90541 BP.
DE Human SRPK2 kinase protein alternative splice form genomic DNA.
PN US2004157297-A1.
PD 12-AUG-2004.
PA (APPL-) APPLERA CORP.
Query Match 2.5%; Score 37; DB 13; Length 90541;
Best Local Similarity 52.2%; Pred. No. 1.9e+02;
RESULT 715
ID AAH88704 standard; DNA; 160755 BP.
DE Human DNA sequence SEQ ID 544.
PN WO200151659-A2.
PD 19-JUL-2001.
PA (GBST) GENSET.
Query Match 2.5%; Score 37; DB 4; Length 160755;
Best Local Similarity 39.7%; Pred. No. 2.5e+02;
RESULT 716
ID ADA58682 standard; cDNA; 262 BP.
DE Maize sucrose synthase EST #326.
PN US2003135870-A1.
PD 17-JUL-2003.
PA (CHRI/) CHIRIKH N.
PA (FISH/) FISHER D K.
PA (LIUJ/) LIU J.
Query Match 2.5%; Score 36.8; DB 9; Length 262;
Best Local Similarity 51.9%; Pred. No. 12;
RESULT 717
ID AAC36202 standard; DNA; 508 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 12916.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 2.5%; Score 36.8; DB 3; Length 508;
Best Local Similarity 54.4%; Pred. No. 16;
RESULT 718
ID ACH78156 standard; DNA; 518 BP.
DE Human genome derived single exon probe #11351.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 2.5%; Score 36.8; DB 12; Length 518;
Best Local Similarity 50.6%; Pred. No. 16;
RESULT 719
ID ACH78575 standard; DNA; 518 BP.
DE Human genome derived single exon probe #11770.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 2.5%; Score 36.8; DB 12; Length 518;
Best Local Similarity 50.6%; Pred. No. 16;
RESULT 720
ID AB066069 standard; DNA; 636 BP.
DE Arabidopsis thaliana polynucleotide SEQ ID NO 646.
PN US2002059663-A1.
PD 16-MAY-2002.
PA (GORT/) GORTLACH J.
PA (ANYV/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (RAIN/) RAINES T M.
PA (YUYV/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHEW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
PA (KRIC/) KRICKER M.

PA (SLAT/) SLATER T.
PA (DAVI/) DAVIS K R.
PA (ALLE/) ALLEN K.
PA (HOFF/) HOFFMAN N.
PA (HURB/) HURBAN P.
Query Match 2.5%; Score 36.8; DB 6; Length 636;
Best Local Similarity 49.0%; Pred. No. 18;
RESULT 721
ID ABD03162 standard; DNA; 873 BP.
DE Pseudomonas aeruginosa polynucleotide #1766.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.5%; Score 36.8; DB 11; Length 873;
Best Local Similarity 54.4%; Pred. No. 21;
RESULT 722
ID ABD03306 standard; DNA; 2169 BP.
DE Pseudomonas aeruginosa polynucleotide #1910.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.5%; Score 36.8; DB 11; Length 2169;
Best Local Similarity 54.4%; Pred. No. 33;
RESULT 723
ID AAF82218 standard; DNA; 2796 BP.
DE Melon ethylene receptor gene promoter-related sequence.
PN JP2001037484-A.
PD 13-FEB-2001.
PA (IBAR-) IBARAKI PREFECTURE.
Query Match 2.5%; Score 36.8; DB 5; Length 2796;
Best Local Similarity 49.5%; Pred. No. 38;
RESULT 724
ID ABD03441 standard; DNA; 2946 BP.
DE Pseudomonas aeruginosa polynucleotide #2045.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.5%; Score 36.8; DB 11; Length 2946;
Best Local Similarity 54.4%; Pred. No. 39;
RESULT 725
ID AB106732 standard; cDNA; 4298 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 14678.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 2.5%; Score 36.8; DB 4; Length 4298;
Best Local Similarity 49.6%; Pred. No. 47;
RESULT 726
ID AAX84332 standard; DNA; 5059 BP.
DE Stealth virus nucleic acid clone, SEQ ID NO: 24.
Query Match 2.5%; Score 36.8; DB 2; Length 5059;
Best Local Similarity 19.2%; Pred. No. 51;
RESULT 727
ID AAQ79728 standard; DNA; 6100 BP.
DE Human U5/3 tumour suppressor gene (genomic sequence).
PN US6315000-A.
PD 24-MAY-1994.
PA (CHIL-) CHILDRENS HOSPITAL MEDICAL CENT.
Query Match 2.5%; Score 36.8; DB 2; Length 6100;
Best Local Similarity 55.5%; Pred. No. 56;
RESULT 728
ID AAT62440 standard; DNA; 6100 BP.
DE Human U5/3 growth factor genomic sequence.
PN US606029-A.
PD 25-FEB-1997.
PA (CHIL-) CHILDRENS HOSPITAL MEDICAL CENT.
Query Match 2.5%; Score 36.8; DB 2; Length 6100;
Best Local Similarity 55.5%; Pred. No. 56;
RESULT 729
ID ABL68609 standard; DNA; 9980 BP.
DE Kidney cancer related gene sequence SEQ ID NO:6946.
PN WO200194629-A2.
PD 13-DEC-2001.

PA (AVALL-) AVALON PHARM.
Query Match 2.5%; Score 36.8; DB 6; Length 9980;
Best Local Similarity 55.5%; Pred. No. 71;
RESULT 730
ID ABN96855 standard; DNA; 9980 BP.
DE Gene #3353 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 2.5%; Score 36.8; DB 6; Length 9980;
Best Local Similarity 55.5%; Pred. No. 71;
RESULT 731
ID AAA29063 standard; DNA; 35828 BP.
DE Murine TGF-beta binding protein (BBER) genomic MLUI-AvIII DNA fragment.
PN WO200032773-A1.
PD 08-JUN-2000.
PA (DARW-) DARWIN DISCOVERY LTD.
Query Match 2.5%; Score 36.8; DB 3; Length 35828;
Best Local Similarity 69.4%; Pred. No. 1.4e+02;
RESULT 732
ID AAD50739 standard; DNA; 64467 BP.
DE Human kinase gene.
Query Match 2.5%; Score 36.8; DB 8; Length 64467;
Best Local Similarity 56.7%; Pred. No. 1.8e+02;
RESULT 733
ID ACH00100 standard; DNA; 64467 BP.
DE Human kinase protein genomic DNA.
Query Match 2.5%; Score 36.8; DB 9; Length 64467;
Best Local Similarity 56.7%; Pred. No. 1.8e+02;
RESULT 734
ID ADD15783 standard; DNA; 64467 BP.
DE Human MEK kinase subfamily kinase genomic DNA.
PN US6582946-B1.
PD 24-JUN-2003.
PA (APPL-) APPLERA CORP.
Query Match 2.5%; Score 36.8; DB 10; Length 64467;
Best Local Similarity 56.7%; Pred. No. 1.8e+02;
RESULT 735
ID ADP45591 standard; DNA; 92500 BP.
DE Human intercellular adhesion molecule ICAM-1/ICAM-4/ICAM-5 cDNA.
Query Match 2.5%; Score 36.8; DB 12; Length 92500;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
RESULT 736
ID ADF13110 standard; DNA; 118067 BP.
DE Hypomethylation site in human breast cancer Cpg island locus HBC-37.
PN US2003129602-A1.
PD 10-JUL-2003.
PA (HUAN/) HUANG T H.
Query Match 2.5%; Score 36.8; DB 12; Length 118067;
Best Local Similarity 55.5%; Pred. No. 2.4e+02;
RESULT 737
ID ADI37256 standard; DNA; 118067 BP.
DE Hypomethylation in cancer (HBC) locus-37.
PN US6605432-B1.
PD 12-AUG-2003.
PA (UMOR-) UNIV MISSOURI.
Query Match 2.5%; Score 36.8; DB 12; Length 118067;
Best Local Similarity 55.5%; Pred. No. 2.4e+02;
RESULT 738
ID ABR83562 standard; cDNA; 139904 BP.
DE Human cDNA differentially expressed in granulocytic cells #133.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 2.5%; Score 36.8; DB 6; Length 139904;
Best Local Similarity 58.0%; Pred. No. 2.7e+02;
RESULT 739
ID ACA64924 standard; DNA; 201239 BP.
DE Human PLZF DNA corresponding to AF060568.
PN DE10127572-A1.
PD 05-DEC-2002.
PA (PATR-) PATHOARRAY GMBH.
Query Match 2.5%; Score 36.8; DB 8; Length 201239;

Best Local Similarity 48.1%; Pred. No. 3.2e+02;
RESULT 740
ID ADA58461 standard; cDNA; 295 BP.
DE Maize sucrose synthase EST #105.
PN US2003135870-A1.
PD 17-JUL-2003.
PA (CHEI/) CHEIKH N.
PA (FISH/) FISHER D K.
PA (LIU/) LIU J.
Query Match 2.5%; Score 36.6; DB 9; Length 295;
Best Local Similarity 56.1%; Pred. No. 14;
RESULT 741
ID ADA58383 standard; cDNA; 340 BP.
DE Maize sucrose synthase EST #27.
PN US2003135870-A1.
PD 17-JUL-2003.
PA (CHEI/) CHEIKH N.
PA (FISH/) FISHER D K.
PA (LIU/) LIU J.
Query Match 2.5%; Score 36.6; DB 9; Length 340;
Best Local Similarity 58.9%; Pred. No. 15;
RESULT 742
ID ABX52791 standard; cDNA; 438 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #2720.
PN US2002137160-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WAR/) WARREN W C.
Query Match 2.5%; Score 36.6; DB 8; Length 438;
Best Local Similarity 46.9%; Pred. No. 17;
RESULT 743
ID ADA48906 standard; DNA; 689 BP.
DE Wheat gene conferring disease resistance in plants.
PN WO200300905-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.5%; Score 36.6; DB 9; Length 689;
Best Local Similarity 49.7%; Pred. No. 22;
RESULT 744
ID ADC08648 standard; DNA; 689 BP.
DE Wheat DNA sequence Seq ID953 related to grain filling.
PN WO200300905-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.5%; Score 36.6; DB 10; Length 689;
Best Local Similarity 49.7%; Pred. No. 22;
RESULT 745
ID ADJ41713 standard; cDNA; 689 BP.
DE Plant cDNA #2713.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOLF/) GOLF S A.
PA (KATA/) KATAGIRI F.
PA (KEEP/) KEEPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
PA (ZHU/) ZHU T.
Query Match 2.5%; Score 36.6; DB 12; Length 689;
Best Local Similarity 49.7%; Pred. No. 22;
RESULT 746
ID AAH74539 standard; cDNA; 905 BP.
DE Nucleotide sequence of a chitobiosidase polypeptide.
PN WO200146387-A1.
PD 28-JUN-2001.
PA (CORR) CORNELL RES FOUND INC.
Query Match 2.5%; Score 36.6; DB 4; Length 905;
Best Local Similarity 49.7%; Pred. No. 22;
RESULT 747
ID ADA69391 standard; DNA; 1182 BP.
DE Rice gene, SEQ ID 2714.
PN WO200300898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.5%; Score 36.6; DB 8; Length 1182;
Best Local Similarity 49.7%; Pred. No. 28;
RESULT 748
ID ADA47947 standard; DNA; 1182 BP.
DE Rice gene conferring disease resistance in plants.
PN WO200300906-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.5%; Score 36.6; DB 9; Length 1182;
Best Local Similarity 49.7%; Pred. No. 28;
RESULT 749
ID ADC07965 standard; DNA; 1182 BP.
DE Rice DNA sequence Seq ID231 related to grain filling.
PN WO200300905-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.5%; Score 36.6; DB 10; Length 1182;
Best Local Similarity 49.7%; Pred. No. 28;
RESULT 750
ID ADJ39882 standard; cDNA; 1182 BP.
DE Plant cDNA #882.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOLF/) GOLF S A.
PA (KATA/) KATAGIRI F.
PA (KEEP/) KEEPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
PA (ZHU/) ZHU T.
Query Match 2.5%; Score 36.6; DB 12; Length 1182;
Best Local Similarity 49.7%; Pred. No. 28;
RESULT 751
ID AAZ06824 standard; DNA; 1294 BP.
DE Streptomyces albidoflavus chitobiosidase DNA.
PN WO9942594-A1.
PD 26-AUG-1999.
PA (CORR) CORNELL RES FOUND INC.
Query Match 2.5%; Score 36.6; DB 2; Length 1294;
Best Local Similarity 50.9%; Pred. No. 29;
RESULT 752
ID AAH74537 standard; DNA; 1294 BP.
DE Nucleotide sequence of a chitobiosidase polypeptide.
PN WO200146387-A1.
PD 28-JUN-2001.
PA (CORR) CORNELL RES FOUND INC.
Query Match 2.5%; Score 36.6; DB 4; Length 1294;
Best Local Similarity 50.9%; Pred. No. 29;
RESULT 753
ID ADQ25850 standard; DNA; 4145 BP.
DE Rat G-protein coupled receptor 88 coding sequence.
PN WO2004054617-A1.
PD 01-JUL-2004.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 2.5%; Score 36.6; DB 12; Length 4145;
Best Local Similarity 51.5%; Pred. No. 53;
RESULT 754
ID AAH41184 standard; DNA; 4164 BP.
DE Rat G-protein-coupled receptor, stry, coding sequence.
PN WO200136634-A1.
PD 25-MAY-2001.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.

Query Match 2.5%; Score 36.6; DB 5; Length 4164;
Best Local Similarity 51.5%; Pred. No. 53;
RESULT 755
ID ADE59567 standard; DNA; 5761 BP.
DE Human gene XM_038377, SEQ ID NO 5463.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GHEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 2.5%; Score 36.6; DB 10; Length 5761;
Best Local Similarity 57.0%; Pred. No. 62;
RESULT 756
ID ADE59563 standard; DNA; 5761 BP.
DE Human gene XM_038377, SEQ ID NO 5459.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GHEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 2.5%; Score 36.6; DB 10; Length 5761;
Best Local Similarity 57.0%; Pred. No. 62;
RESULT 757
ID ACN44528 standard; DNA; 49806 BP.
DE Mouse genomic sequence mCG20647.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.5%; Score 36.6; DB 11; Length 49806;
Best Local Similarity 57.4%; Pred. No. 1.8e+02;
RESULT 758
ID AD570697 standard; cDNA; 272 BP.
DE Corn seedling-derived polynucleotide (cpds), SEQ ID 5713.
PN US200337110-A9.
PD 25-DEC-2003.
PA (INCY-) INCYTE PHARM INC.
Query Match 2.5%; Score 36.4; DB 7; Length 272;
Best Local Similarity 58.1%; Pred. No. 15;
RESULT 759
ID ADP29106 standard; DNA; 279 BP.
DE Human secreted protein encoding sequence SEQ ID #1104.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 2.5%; Score 36.4; DB 12; Length 279;
Best Local Similarity 48.9%; Pred. No. 16;
RESULT 760
ID ADA49220 standard; DNA; 399 BP.
DE Maize gene conferring disease resistance in plants.
PN WO200300906-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.5%; Score 36.4; DB 9; Length 399;
Best Local Similarity 52.7%; Pred. No. 19;
RESULT 761
ID AC119211 standard; DNA; 409 BP.
DE DNA clone originating in barley containing SNP encoding sequence #9202.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UNIV-) UNIV JAPAN OKAYAMA.
Query Match 2.5%; Score 36.4; DB 9; Length 409;
Best Local Similarity 46.7%; Pred. No. 19;
RESULT 762
ID AC119207 standard; DNA; 418 BP.
DE DNA clone originating in barley containing SNP encoding sequence #9198.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UNIV-) UNIV JAPAN OKAYAMA.
Query Match 2.5%; Score 36.4; DB 9; Length 418;
Best Local Similarity 48.1%; Pred. No. 19;
RESULT 763
ID ADA69502 standard; DNA; 450 BP.
DE Rice gene, SEQ ID 2825.
PN WO200300898-A1.
PD 03-JAN-2003.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.5%; Score 36.4; DB 8; Length 450;
Best Local Similarity 48.1%; Pred. No. 20;
RESULT 764
ID ADA48603 standard; DNA; 450 BP.
DE Rice gene conferring disease resistance in plants.
PN WO200300906-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.5%; Score 36.4; DB 9; Length 450;
Best Local Similarity 48.1%; Pred. No. 20;
RESULT 765
ID ADJ44943 standard; cDNA; 450 BP.
DE Plant cDNA #5943.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
PA (ZHUT/) ZHU T.
Query Match 2.5%; Score 36.4; DB 12; Length 450;
Best Local Similarity 48.1%; Pred. No. 20;
RESULT 766
ID ABV59448 standard; cDNA; 456 BP.
DE Human prostate expression marker cDNA 59439.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.5%; Score 36.4; DB 5; Length 456;
Best Local Similarity 55.6%; Pred. No. 20;
RESULT 767
ID ACH22587 standard; cDNA; 486 BP.
DE Human adult ovary cDNA #967.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STRAC/) STRACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 2.5%; Score 36.4; DB 9; Length 486;
Best Local Similarity 49.5%; Pred. No. 21;
RESULT 768
ID ADA69813 standard; DNA; 516 BP.
DE Rice gene, SEQ ID 3136.
PN WO200300898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.5%; Score 36.4; DB 8; Length 516;
Best Local Similarity 48.5%; Pred. No. 21;
RESULT 769
ID AC119210 standard; DNA; 517 BP.
DE DNA clone originating in barley containing SNP encoding sequence #9201.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UNIV-) UNIV JAPAN OKAYAMA.
Query Match 2.5%; Score 36.4; DB 9; Length 517;
Best Local Similarity 46.7%; Pred. No. 21;
RESULT 770
ID ADA4885 standard; DNA; 600 BP.
DE Banana gene conferring disease resistance in plants.
PN WO200300906-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.5%; Score 36.4; DB 9; Length 600;
Best Local Similarity 48.1%; Pred. No. 23;

RESULT 771
ID ADJ42628 standard; cDNA; 606 BP.
DE Plant cDNA #3628.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOF/) GOF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RIQUE D.
PA (ZHUT/) ZHU T.
Query Match
Best Local Similarity 2.5%; Score 36.4; DB 12; Length 606;
56.8%; Pred. No. 23;
RESULT 772
ID ADJ6477 standard; DNA; 647 BP.
DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 1746.
PN WO2003020905-A2.
PD 13-MAR-2003.
PA (DOMC) DOM CHEM CO.
Query Match
Best Local Similarity 2.5%; Score 36.4; DB 10; Length 647;
48.1%; Pred. No. 24;
RESULT 773
ID ADK59088 standard; DNA; 647 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #6471.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOMC) DOM CHEM CO.
Query Match
Best Local Similarity 2.5%; Score 36.4; DB 10; Length 647;
48.1%; Pred. No. 24;
RESULT 774
ID ADJ42638 standard; cDNA; 662 BP.
DE Plant cDNA #3638.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOF/) GOF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RIQUE D.
PA (ZHUT/) ZHU T.
Query Match
Best Local Similarity 2.5%; Score 36.4; DB 12; Length 662;
48.1%; Pred. No. 24;
RESULT 775
ID ADJ75915 standard; DNA; 716 BP.
DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 839.
PN WO2003020905-A2.
PD 13-MAR-2003.
PA (DOMC) DOM CHEM CO.
Query Match
Best Local Similarity 2.5%; Score 36.4; DB 10; Length 716;
48.1%; Pred. No. 25;
RESULT 776
ID ADJ76482 standard; DNA; 784 BP.
DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 1751.
PN WO2003020905-A2.
PD 13-MAR-2003.
PA (DOMC) DOM CHEM CO.
Query Match
Best Local Similarity 2.5%; Score 36.4; DB 10; Length 784;
48.1%; Pred. No. 26;
RESULT 777
ID ADJ7183 standard; DNA; 784 BP.
DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 2112.
PN WO2003020905-A2.

PD 13-MAR-2003.
PA (DOMC) DOM CHEM CO.
Query Match
Best Local Similarity 2.5%; Score 36.4; DB 10; Length 784;
48.1%; Pred. No. 26;
RESULT 778
ID ADK56993 standard; DNA; 784 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #4376.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOMC) DOM CHEM CO.
Query Match
Best Local Similarity 2.5%; Score 36.4; DB 10; Length 784;
48.1%; Pred. No. 26;
RESULT 779
ID ADK59091 standard; DNA; 784 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #6474.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOMC) DOM CHEM CO.
Query Match
Best Local Similarity 2.5%; Score 36.4; DB 10; Length 784;
48.1%; Pred. No. 26;
RESULT 780
ID ADJ42632 standard; cDNA; 868 BP.
DE Plant cDNA #3632.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOF/) GOF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RIQUE D.
PA (ZHUT/) ZHU T.
Query Match
Best Local Similarity 2.5%; Score 36.4; DB 12; Length 868;
48.1%; Pred. No. 27;
RESULT 781
ID AAS80397 standard; cDNA; 1203 BP.
DE DNA encoding novel human diagnostic protein #16201.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 2.5%; Score 36.4; DB 5; Length 1203;
51.9%; Pred. No. 32;
RESULT 782
ID ABL67798 standard; DNA; 1306 BP.
DE Oesophagus cancer related gene sequence SEQ ID NO:6135.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match
Best Local Similarity 2.5%; Score 36.4; DB 6; Length 1306;
48.1%; Pred. No. 34;
RESULT 783
ID ABL65422 standard; DNA; 1306 BP.
DE Lung cancer related gene sequence SEQ ID NO:3759.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match
Best Local Similarity 2.5%; Score 36.4; DB 6; Length 1306;
48.1%; Pred. No. 34;
RESULT 784
ID ABL66524 standard; DNA; 1306 BP.
DE Lung cancer related gene sequence SEQ ID NO:4861.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match
Best Local Similarity 2.5%; Score 36.4; DB 6; Length 1306;
48.1%; Pred. No. 34;
RESULT 785

ID ADN04465 standard; cDNA; 1367 BP.
DE Antisporadic cDNA sequence #434.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 2.5%; Score 36.4; DB 12; Length 1367;
Best Local Similarity 48.1%; Pred. No. 34;
RESULT 786
ID ADE47781 standard; DNA; 1710 BP.
DE Human NOV45b gene SEQ ID NO:143.
PN WO2003076642-A2.
PD 18-SEP-2003.
PA (CURA-) CURAGEN CORP.
Query Match 2.5%; Score 36.4; DB 10; Length 1710;
Best Local Similarity 58.2%; Pred. No. 38;
RESULT 787
ID ADH41898 standard; DNA; 1710 BP.
DE Novel human nucleic acid NOV36d.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 2.5%; Score 36.4; DB 12; Length 1710;
Best Local Similarity 58.2%; Pred. No. 38;
RESULT 788
ID ADJ79051 standard; DNA; 1710 BP.
DE Human NOVX protein NOV45b gene sequence.
PN US2004014053-A1.
PD 22-JAN-2004.
PA (ZERRH) ZERRHUSEN B. D.
PA (PATT) PATTURAJAN M.
PA (KEKU) KEKUDA R.
PA (MILL) MILLER C. E.
PA (RIBG) RIEGER D. K.
PA (PENNA) PENNA C. E. A.
PA (SHIM) SHIMKETS R. A.
PA (LILL) LI L.
PA (BERG) BERGHS C.
PA (ZHON) ZHONG M.
PA (CASM) CASMAN S. J.
PA (VOSS) VOSS E. Z.
PA (BOLD) BOLDOG F. L.
PA (PADI) PADIGARU M.
PA (SMIT) SMITHSON G.
PA (UTW) UT W.
PA (GORM) GORMAN L.
PA (VERN) VERNET C. A. M.
PA (LEIT) LEITE M. W.
PA (GROX) GRO X. S.
PA (ANDE) ANDERSON D. W.
PA (SPYR) SPYTER K. A.
PA (GERL) GERLACH V.
PA (BURG) BURGESS C. E.
PA (KHRA) KHRAMTSOV N. V.
PA (ORTT) ORT T.
PA (ELLE) ELLERMAN K.
PA (RAST) RASTELLI L.
PA (AGEE) AGE E. M. L.
PA (CHAU) CHAUDHURI A.
PA (CHAN) CHANT J. S.
PA (DIP) DIPIPPO V. A.
PA (EDIN) EDINGER S. R.
PA (EISE) EISEN A. J.
PA (GANG) GANGOLLI E. A.
PA (GIOT) GIOT L.
PA (OOIC) OOI C. E.
PA (ROTH) ROTHENBERG M. E.
PA (SPAD) SPADERNA S. K.
PA (HTAL) HTALT T.
PA (LUX) LUX X.
PA (TAUP) TAUPLER R. J.
PA (CAT) CATERTON E.
PA (SHEN) SHENY S. G.
Query Match 2.5%; Score 36.4; DB 12; Length 1710;

Best Local Similarity 58.2%; Pred. No. 38;
RESULT 789
ID ABLE7803 standard; DNA; 2746 BP.
DE Oesophagus cancer related gene sequence SEQ ID NO:6140.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL) AVALLON PHARM.
Query Match 2.5%; Score 36.4; DB 6; Length 2746;
Best Local Similarity 48.1%; Pred. No. 49;
RESULT 790
ID ADM67108 standard; DNA; 2947 BP.
DE Murine adipocyte specific DNA SeqID 243.
PN WO2004011618-A2.
PD 05-FEB-2004.
PA (HNGE) HNGENE INC.
Query Match 2.5%; Score 36.4; DB 12; Length 2947;
Best Local Similarity 49.5%; Pred. No. 50;
RESULT 791
ID ABS78681 standard; DNA; 5877 BP.
DE Kitasatospora sp. DNA encoding PKSE.
PN CA2387401-A1.
PD 04-SEP-2002.
PA (ECOP) ECOPHA BIOSCIENCES INC.
Query Match 2.5%; Score 36.4; DB 6; Length 5877;
Best Local Similarity 50.0%; Pred. No. 71;
RESULT 792
ID AAS42021 standard; DNA; 32121 BP.
DE Genomic sequence #337 encoding novel human enzyme polypeptide.
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.5%; Score 36.4; DB 4; Length 32121;
Best Local Similarity 50.6%; Pred. No. 1.7e+02;
RESULT 793
ID AAS35076 standard; DNA; 32121 BP.
DE DNA #26 encoding human neoplastic disease associated polypeptide.
PN WO200155163-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.5%; Score 36.4; DB 4; Length 32121;
Best Local Similarity 50.6%; Pred. No. 1.7e+02;
RESULT 794
ID ADC46518 standard; DNA; 32121 BP.
DE Human neoplastic disease-associated gene 55 DNA #1.
PN US2003082758-A1.
PD 01-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.5%; Score 36.4; DB 10; Length 32121;
Best Local Similarity 50.6%; Pred. No. 1.7e+02;
RESULT 795
ID ACN44094 standard; DNA; 35236 BP.
DE Human genomic sequence hCG23314.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.5%; Score 36.4; DB 11; Length 35236;
Best Local Similarity 54.7%; Pred. No. 1.7e+02;
RESULT 796
ID AAK79963 standard; DNA; 57144 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34775.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.5%; Score 36.4; DB 4; Length 57144;
Best Local Similarity 50.6%; Pred. No. 2.2e+02;
RESULT 797
ID ACN44608 standard; DNA; 90043 BP.
DE Mouse genomic sequence mCG22175.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.5%; Score 36.4; DB 11; Length 90043;
Best Local Similarity 55.6%; Pred. No. 2.8e+02;

RESULT 798
ID ABD33254 standard; DNA; 97415 BP.
DE Murine cancer-associated (CA) gene MD07-043.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.5%; Score 36.4; DB 13; Length 97415;
Best Local Similarity 48.5%; Pred. No. 2.9e+02;
RESULT 799
ID AAD16230 standard; DNA; 107820 BP.
DE Human ATP-binding cassette transporter ABC6 (MRP6) complementary gene.
Query Match 2.5%; Score 36.4; DB 4; Length 107820;
Best Local Similarity 53.5%; Pred. No. 3e+02;
RESULT 800
ID ABD33489 standard; DNA; 151858 BP.
DE Murine cancer-associated (CA) gene MD07-095.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.5%; Score 36.4; DB 13; Length 151858;
Best Local Similarity 55.6%; Pred. No. 3.6e+02;
RESULT 801
ID ACF62733 standard; DNA; 172984 BP.
DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:661.
PN WO2003013534-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 36.4; DB 8; Length 172984;
Best Local Similarity 53.5%; Pred. No. 3.8e+02;
RESULT 802
ID ADB20848 standard; DNA; 172984 BP.
DE MRP1 based cancer related nucleic acid SEQ ID NO:661.
PN WO2003013533-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 36.4; DB 8; Length 172984;
Best Local Similarity 53.5%; Pred. No. 3.8e+02;
RESULT 803
ID ADB87937 standard; DNA; 172984 BP.
DE Human UGT1A1 gene sequence SEQ ID NO:661.
PN WO2003013536-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 36.4; DB 10; Length 172984;
Best Local Similarity 53.5%; Pred. No. 3.8e+02;
RESULT 804
ID ADB96920 standard; DNA; 172984 BP.
DE Human MDR1 related DNA sequence SEQ ID NO:661.
PN WO2003013537-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 36.4; DB 10; Length 172984;
Best Local Similarity 53.5%; Pred. No. 3.8e+02;
RESULT 805
ID ADB92111 standard; DNA; 172984 BP.
DE Human MDR1 related DNA sequence SEQ ID NO:661.
PN WO2003013535-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 36.4; DB 10; Length 172984;
Best Local Similarity 53.5%; Pred. No. 3.8e+02;
RESULT 806
ID ACF62750 standard; DNA; 186591 BP.
DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:682.
PN WO2003013534-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 36.4; DB 8; Length 186591;
Best Local Similarity 53.5%; Pred. No. 3.9e+02;
RESULT 807
ID ADB20869 standard; DNA; 186591 BP.
DE MRP1 based cancer related nucleic acid SEQ ID NO:682.
PN WO2003013533-A2.

PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 36.4; DB 8; Length 186591;
Best Local Similarity 53.5%; Pred. No. 3.9e+02;
RESULT 808
ID ADB87958 standard; DNA; 186591 BP.
DE Human UGT1A1 gene sequence SEQ ID NO:682.
PN WO2003013536-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 36.4; DB 10; Length 186591;
Best Local Similarity 53.5%; Pred. No. 3.9e+02;
RESULT 809
ID ADB96941 standard; DNA; 186591 BP.
DE Human MDR1 related DNA sequence SEQ ID NO:682.
PN WO2003013537-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 36.4; DB 10; Length 186591;
Best Local Similarity 53.5%; Pred. No. 3.9e+02;
RESULT 810
ID ADB92132 standard; DNA; 186591 BP.
DE Human MDR1 related DNA sequence SEQ ID NO:682.
PN WO2003013533-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 36.4; DB 10; Length 186591;
Best Local Similarity 53.5%; Pred. No. 3.9e+02;
RESULT 811
ID ACF62735 standard; DNA; 208648 BP.
DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:663.
PN WO2003013534-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 36.4; DB 8; Length 208648;
Best Local Similarity 53.5%; Pred. No. 4.2e+02;
RESULT 812
ID ACF62740 standard; DNA; 208648 BP.
DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:668.
PN WO2003013534-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 36.4; DB 8; Length 208648;
Best Local Similarity 53.5%; Pred. No. 4.2e+02;
RESULT 813
ID ADB20850 standard; DNA; 208648 BP.
DE MRP1 based cancer related nucleic acid SEQ ID NO:663.
PN WO2003013533-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 36.4; DB 8; Length 208648;
Best Local Similarity 53.5%; Pred. No. 4.2e+02;
RESULT 814
ID ADB20855 standard; DNA; 208648 BP.
DE MRP1 based cancer related nucleic acid SEQ ID NO:668.
PN WO2003013533-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 36.4; DB 8; Length 208648;
Best Local Similarity 53.5%; Pred. No. 4.2e+02;
RESULT 815
ID ADB87944 standard; DNA; 208648 BP.
DE Human UGT1A1 gene sequence SEQ ID NO:668.
PN WO2003013536-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 36.4; DB 10; Length 208648;
Best Local Similarity 53.5%; Pred. No. 4.2e+02;
RESULT 816
ID ADB87939 standard; DNA; 208648 BP.
DE Human UGT1A1 gene sequence SEQ ID NO:663.
PN WO2003013536-A2.
PD 20-FEB-2003.

PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 36.4; DB 10; Length 208648;
Best Local Similarity 53.5%; Pred. No. 4.2e+02;
RESULT 817
ID ADB96922 standard; DNA; 208648 BP.
DE Human MDRI related DNA sequence SEQ ID NO:663.
PN WO2003013537-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 36.4; DB 10; Length 208648;
Best Local Similarity 53.5%; Pred. No. 4.2e+02;
RESULT 818
ID ADB96927 standard; DNA; 208648 BP.
DE Human MDRI related DNA sequence SEQ ID NO:668.
PN WO2003013537-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 36.4; DB 10; Length 208648;
Best Local Similarity 53.5%; Pred. No. 4.2e+02;
RESULT 819
ID ADB92113 standard; DNA; 208648 BP.
DE Human MDRI related DNA sequence SEQ ID NO:663.
PN WO2003013535-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 36.4; DB 10; Length 208648;
Best Local Similarity 53.5%; Pred. No. 4.2e+02;
RESULT 820
ID ADB92118 standard; DNA; 208648 BP.
DE Human MDRI related DNA sequence SEQ ID NO:668.
PN WO2003013535-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 2.5%; Score 36.4; DB 10; Length 208648;
Best Local Similarity 53.5%; Pred. No. 4.2e+02;
RESULT 821
ID ADA58486 standard; cDNA; 294 BP.
DE Maize sucrose synthase EST #130.
PN US2003135870-A1.
PD 17-JUL-2003.
PA (CHEI/) CHEIKH N.
PA (FISH/) FISHER D K.
PA (LILU/) LILU J.
Query Match 2.4%; Score 36.2; DB 9; Length 294;
Best Local Similarity 59.0%; Pred. No. 18;
RESULT 822
ID AA182080 standard; cDNA; 433 BP.
DE Human polynucleotide SEQ ID NO 2140.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.4%; Score 36.2; DB 4; Length 433;
Best Local Similarity 54.0%; Pred. No. 22;
RESULT 823
ID ABS73398 standard; DNA; 1086 BP.
DE DNA encoding human GPCR HP1948 mutant 1128F.
PN WO200268600-A2.
PD 06-SEP-2002.
PA (AREN-) ARENA PHARM INC.
Query Match 2.4%; Score 36.2; DB 6; Length 1086;
Best Local Similarity 54.0%; Pred. No. 35;
RESULT 824
ID AAX87371 standard; cDNA; 1120 BP.
DE Human myosin light chain cDNA.
PN WO9936531-A1.
PD 22-JUL-1999.
PA (ZENB-) ZENECA LTD.
Query Match 2.4%; Score 36.2; DB 2; Length 1120;
Best Local Similarity 48.8%; Pred. No. 35;
RESULT 825
ID AAD07361 standard; DNA; 1120 BP.
DE Human DNA encoding myosin light chain protein (marker 12).
PN WO200136674-A2.

PD 25-MAY-2001.
PA (ASTR-) ASTRAZENECA AB.
PA (ASTR-) ASTRAZENECA UK LTD.
Query Match 2.4%; Score 36.2; DB 4; Length 1120;
Best Local Similarity 48.8%; Pred. No. 35;
RESULT 826
ID AB162349 standard; DNA; 1120 BP.
DE Colon adenocarcinoma related gene sequence SEQ ID NO:686.
PN WO200194639-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 2.4%; Score 36.2; DB 6; Length 1120;
Best Local Similarity 48.8%; Pred. No. 35;
RESULT 827
ID AB169454 standard; DNA; 1120 BP.
DE Prostate cancer related gene sequence SEQ ID NO:7791.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 2.4%; Score 36.2; DB 6; Length 1120;
Best Local Similarity 48.8%; Pred. No. 35;
RESULT 828
ID ADN03695 standard; cDNA; 1120 BP.
DE Antiproliferative cDNA sequence #45.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH-) GENENTECH INC.
Query Match 2.4%; Score 36.2; DB 12; Length 1120;
Best Local Similarity 48.8%; Pred. No. 35;
RESULT 829
ID ADM33386 standard; cDNA; 1120 BP.
DE Human PRO1267 encoding cDNA SEQ ID NO:3.
PN WO2004028447-A2.
PD 08-APR-2004.
PA (GETH-) GENENTECH INC.
Query Match 2.4%; Score 36.2; DB 12; Length 1120;
Best Local Similarity 48.8%; Pred. No. 35;
RESULT 830
ID ADP13398 standard; DNA; 1120 BP.
DE Renal cell carcinoma differentially expressed gene #134.
PN WO2004048933-A2.
PD 10-JUN-2004.
PA (AMHP-) WYETH.
PA (TWIN/) TWINE N C.
PA (BURC/) BURCZYNSKI M E.
PA (TREP/) TREPICCHIO W L.
PA (DORN/) DORNER A.
PA (STOV/) STOVER J A.
PA (SLON/) SLONI D K.
Query Match 2.4%; Score 36.2; DB 12; Length 1120;
Best Local Similarity 48.8%; Pred. No. 35;
RESULT 831
ID ADQ22648 standard; DNA; 1303 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5468.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.4%; Score 36.2; DB 12; Length 1303;
Best Local Similarity 45.9%; Pred. No. 38;
RESULT 832
ID ADL62786 standard; DNA; 1941 BP.
DE Human ovarian cancer DNA marker #20998.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNium PREDICTIVE MEDICINE INC.
Query Match 2.4%; Score 36.2; DB 5; Length 1941;
Best Local Similarity 46.9%; Pred. No. 47;
RESULT 833
ID ABD16767 standard; DNA; 1989 BP.
DE Pseudomonas aeruginosa polynucleotide #15371.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.

Query Match 2.4%; Score 36.2; DB 11; Length 1989;
Best Local Similarity 48.3%; Pred. No. 47;
RESULT 834
ID ADA52522 standard; cDNA; 2044 BP.
DE Human coding sequence, SEQ ID 90.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 2.4%; Score 36.2; DB 10; Length 2044;
Best Local Similarity 55.0%; Pred. No. 48;
RESULT 835
ID ABD16858 standard; DNA; 2058 BP.
DE Pseudomonas aeruginosa polynucleotide #15462.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.4%; Score 36.2; DB 11; Length 2058;
Best Local Similarity 48.3%; Pred. No. 48;
RESULT 836
ID ACA51409 standard; DNA; 2355 BP.
DE Prokaryotic essential gene #33066.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 2.4%; Score 36.2; DB 8; Length 2355;
Best Local Similarity 46.9%; Pred. No. 51;
RESULT 837
ID ABD16799 standard; DNA; 2637 BP.
DE Pseudomonas aeruginosa polynucleotide #15403.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.4%; Score 36.2; DB 11; Length 2637;
Best Local Similarity 48.3%; Pred. No. 54;
RESULT 838
ID AAA8444 standard; DNA; 2893 BP.
DE Human deamin gene 5' flanking region, including the promoter region.
PN EP99278-A1.
PD 10-MAY-2000.
PA (UTPA-) UNIV PARIS VII.
Query Match 2.4%; Score 36.2; DB 3; Length 2893;
Best Local Similarity 52.3%; Pred. No. 57;
RESULT 839
ID ABT16471 standard; DNA; 3270 BP.
DE Human intracellular signalling protein coding sequence - SEQ ID No 24.
PN WO200210108-A2.
PD 19-DEC-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 2.4%; Score 36.2; DB 10; Length 3270;
Best Local Similarity 59.0%; Pred. No. 60;
RESULT 840
ID AAD49464 standard; cDNA; 5230 BP.
DE Human vesicle-associated protein-8 (VAP)-8 cDNA.
PN WO200286061-A2.
PD 31-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 2.4%; Score 36.2; DB 10; Length 5230;
Best Local Similarity 50.3%; Pred. No. 76;
RESULT 841
ID ADL13006 standard; cDNA; 5467 BP.
DE Human steroid-induced C3A liver cell cDNA #735.
PN US6673549-B1.
PD 06-JAN-2004.
PA (INCY-) INCYTE CORP.
Query Match 2.4%; Score 36.2; DB 12; Length 5467;
Best Local Similarity 50.3%; Pred. No. 78;
RESULT 842
ID AA055145 standard; DNA; 9515 BP.
DE Pseudomonas aeruginosa probe P2-2.
PN WO9401583-A1.
PD 20-JAN-1994.
PA (FUSO) FUSO PHARM IND LTD.

Query Match 2.4%; Score 36.2; DB 2; Length 9515;
Best Local Similarity 44.5%; Pred. No. 1e+02;
RESULT 843
ID AB277356 standard; DNA; 9515 BP.
DE Nucleotide sequence designated PS-2.
PN WO2002101037-A1.
PD 19-DEC-2002.
PA (FUSO) FUSO PHARM IND LTD.
Query Match 2.4%; Score 36.2; DB 8; Length 9515;
Best Local Similarity 44.5%; Pred. No. 1e+02;
RESULT 844
ID AAL51844 standard; DNA; 9515 BP.
DE Pseudomonas aeruginosa microbe identification-related DNA sequence.
PN WO200299133-A1.
PD 12-DEC-2002.
PA (FUSO) FUSO PHARM IND LTD.
PA (OHNO/) OHNO T.
Query Match 2.4%; Score 36.2; DB 10; Length 9515;
Best Local Similarity 44.5%; Pred. No. 1e+02;
RESULT 845
ID AAD40350 standard; DNA; 11771 BP.
DE Bovine DGAT1 gene.
Query Match 2.4%; Score 36.2; DB 6; Length 11771;
Best Local Similarity 50.9%; Pred. No. 1.1e+02;
RESULT 846
ID AB277045 standard; DNA; 14117 BP.
DE Bovine DGAT gene SEQ ID NO:3.
PN WO2003004630-A2.
PD 16-JAN-2003.
PA (ARBE-) ARBEITSGEMEINSCHAFT DEUT RINDERZUCHTER.
Query Match 2.4%; Score 36.2; DB 10; Length 14117;
Best Local Similarity 50.9%; Pred. No. 1.2e+02;
RESULT 847
ID AB277044 standard; DNA; 14117 BP.
DE Bovine DGAT gene SEQ ID NO:1.
PN WO2003004630-A2.
PD 16-JAN-2003.
PA (ARBE-) ARBEITSGEMEINSCHAFT DEUT RINDERZUCHTER.
Query Match 2.4%; Score 36.2; DB 10; Length 14117;
Best Local Similarity 50.9%; Pred. No. 1.2e+02;
RESULT 848
ID AAT68715 standard; DNA; 15872 BP.
DE Streptomyces venezuelae polyketide synthase vep ORF1.
PN WO9722711-A1.
PD 26-JUN-1997.
PA (MINU) UNIV MINNESOTA.
Query Match 2.4%; Score 36.2; DB 2; Length 15872;
Best Local Similarity 52.3%; Pred. No. 1.3e+02;
RESULT 849
ID AAZ87283 standard; DNA; 15872 BP.
DE S. venezuelae vep ORF 1, SEQ ID NO:1.
PN WO200000620-A2.
PD 06-JAN-2000.
PA (MINU) UNIV MINNESOTA.
Query Match 2.4%; Score 36.2; DB 3; Length 15872;
Best Local Similarity 52.3%; Pred. No. 1.3e+02;
RESULT 850
ID AD191929 standard; DNA; 15872 BP.
DE Streptomyces venezuelae vep ORF1 coding sequence.
PN US2003194784-A1.
PD 16-OCT-2003.
PA (SHER/) SHERMAN D H.
PA (LITU/) LITU H.
PA (XUEY/) XUE Y.
PA (ZHAO/) ZHAO L.
Query Match 2.4%; Score 36.2; DB 12; Length 15872;
Best Local Similarity 52.3%; Pred. No. 1.3e+02;
RESULT 851
ID ACN44556 standard; DNA; 22262 BP.
DE Mouse genomic sequence mCG21411.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.

Query Match 2.4%; Score 36.2; DB 11; Length 2262;
Best Local Similarity 54.0%; Pred. No. 1.6e+02;
RESULT 852
ID AAT93095 standard; cDNA; 24379 BP.
DE Streptomyces firenolicin gene cluster.
PN EP806480-A2.
PD 12-NOV-1997.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Query Match 2.4%; Score 36.2; DB 2; Length 24379;
Best Local Similarity 55.0%; Pred. No. 1.6e+02;
RESULT 853
ID AAV25925 standard; cDNA; 24379 BP.
DE Streptomyces roseofulvus firenolicin gene cluster.
PN JP10094395-A.
PD 14-APR-1998.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Query Match 2.4%; Score 36.2; DB 2; Length 24379;
Best Local Similarity 55.0%; Pred. No. 1.6e+02;
RESULT 854
ID ABD33195 standard; DNA; 27485 BP.
DE Human cancer-associated (CA) gene HD07-029.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 36.2; DB 13; Length 27485;
Best Local Similarity 51.7%; Pred. No. 1.7e+02;
RESULT 855
ID AAT80413 standard; DNA; 43280 BP.
DE Tylectone synthase gene cluster.
PN EP791655-A2.
PD 27-AUG-1997.
PA (ELIT) LITLY & CO BLI.
Query Match 2.4%; Score 36.2; DB 2; Length 43280;
Best Local Similarity 52.3%; Pred. No. 2.2e+02;
RESULT 856
ID ADR28249 standard; DNA; 59999 BP.
DE Human low density lipoprotein (LDL) receptor gene sequence SegID1.
PN WO2004067740-A1.
PD 12-AUG-2004.
PA (EFAR-) EFARMES SA.
Query Match 2.4%; Score 36.2; DB 13; Length 59999;
Best Local Similarity 55.0%; Pred. No. 2.6e+02;
RESULT 857
ID ABD33301 standard; DNA; 89829 BP.
DE Murine cancer-associated (CA) gene MD07-054.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 36.2; DB 13; Length 89829;
Best Local Similarity 60.8%; Pred. No. 3.1e+02;
RESULT 858
Query Match 2.4%; Score 36.2; DB 13; Length 110000;
Best Local Similarity 56.2%; Pred. No. 3.5e+02;
RESULT 859
ID ADG97107 standard; DNA; 121124 BP.
DE Mouse cancer associated sequence MD08-002, SEQ ID 83.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 36.2; DB 13; Length 121124;
Best Local Similarity 56.2%; Pred. No. 3.6e+02;
RESULT 860
ID ABD3268 standard; DNA; 238417 BP.
DE Human cancer-associated genomic DNA HD17-053.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 36.2; DB 13; Length 238417;
Best Local Similarity 48.3%; Pred. No. 5e+02;
RESULT 861
ID ADQ19085 standard; DNA; 452 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1904.
PN WO2004048938-A2.

PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.4%; Score 36; DB 12; Length 452;
Best Local Similarity 55.5%; Pred. No. 26;
RESULT 862
ID AAC41067 standard; DNA; 489 BP.
DE Zea mays DNA fragment SEQ ID NO: 30530.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 2.4%; Score 36; DB 3; Length 489;
Best Local Similarity 46.7%; Pred. No. 27;
RESULT 863
ID AAC40977 standard; DNA; 507 BP.
DE Zea mays DNA fragment SEQ ID NO: 30205.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 2.4%; Score 36; DB 3; Length 507;
Best Local Similarity 46.7%; Pred. No. 27;
RESULT 864
ID ADA4888 standard; DNA; 766 BP.
DE Banana gene conferring disease resistance in plants.
PN WO200300906-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.4%; Score 36; DB 9; Length 766;
Best Local Similarity 46.7%; Pred. No. 33;
RESULT 865
ID ABD11412 standard; DNA; 894 BP.
DE Pseudomonas aeruginosa polynucleotide #10016.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.4%; Score 36; DB 11; Length 894;
Best Local Similarity 49.2%; Pred. No. 36;
RESULT 866
ID ABD02947 standard; DNA; 1512 BP.
DE Pseudomonas aeruginosa polynucleotide #1551.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.4%; Score 36; DB 11; Length 1512;
Best Local Similarity 46.4%; Pred. No. 47;
RESULT 867
ID ABD03012 standard; DNA; 1677 BP.
DE Pseudomonas aeruginosa polynucleotide #1616.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.4%; Score 36; DB 11; Length 1677;
Best Local Similarity 46.4%; Pred. No. 49;
RESULT 868
ID ADP44558 standard; cDNA; 2235 BP.
DE Bacterial polynucleotide #19309.
PN US200323675-A1.
PD 18-DEC-2003.
PA (CAOY) CAO Y.
PA (HINK) HINKLE G J.
PA (SLAT) SLATER S C.
PA (CHEN) CHEN X.
PA (GOLD) GOLDMAN B S.
Query Match 2.4%; Score 36; DB 13; Length 2235;
Best Local Similarity 52.7%; Pred. No. 57;
RESULT 869
ID ACA42098 standard; DNA; 3099 BP.
DE Prokaryotic essential gene #23755.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 2.4%; Score 36; DB 8; Length 3099;
Best Local Similarity 50.6%; Pred. No. 67;
RESULT 870
ID AAF16277 standard; cDNA; 3779 BP.
DE Human prostate cancer antigen nucleotide sequence SEQ ID NO:712.

FN WO200055174-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 2.4%; Score 36; DB 3; Length 3779;
Best Local Similarity 51.3%; Pred. No. 74;
RESULT 871
ID AAV63754 standard; cDNA; 4315 BP.
DE Human JAGGED2 cDNA.
PD WO9858958-A2.
PD 30-DEC-1998.
PA (UNIW) UNIV WASHINGTON.
PA (CHIL-) CHILDRENS HOSPITAL PHILADELPHIA.
Query Match 2.4%; Score 36; DB 2; Length 4315;
Best Local Similarity 51.9%; Pred. No. 79;
RESULT 872
ID AD085357 standard; cDNA; 5079 BP.
DE Human tumor-associated antigenic target (TAT) cDNA sequence #2171.
PD WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUDD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 2.4%; Score 36; DB 12; Length 5079;
Best Local Similarity 51.9%; Pred. No. 85;
RESULT 873
ID AAL36491 standard; DNA; 15362 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 2856.
PD WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.4%; Score 36; DB 4; Length 15362;
Best Local Similarity 49.0%; Pred. No. 1.5e+02;
RESULT 874
ID ABX59479 standard; cDNA; 15362 BP.
DE cDNA encoding novel human musculoskeletal system antigen #1823.
PD US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBEN/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.4%; Score 36; DB 8; Length 15362;
Best Local Similarity 49.0%; Pred. No. 1.5e+02;
RESULT 875
ID ADJ30229 standard; DNA; 15362 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2856.
PD US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.4%; Score 36; DB 12; Length 15362;
Best Local Similarity 49.0%; Pred. No. 1.5e+02;
RESULT 876
ID AAG99655 standard; DNA; 19303 BP.
DE Human membrane spanning 4-domain family, subfamily A genomic sequence.
PD WO200262946-A2.
PD 15-AUG-2002.
PA (UYDU-) UNIV DUKE.
Query Match 2.4%; Score 36; DB 6; Length 19303;
Best Local Similarity 43.0%; Pred. No. 1.7e+02;
RESULT 877
ID ADD00956 standard; DNA; 28000 BP.
DE Human jagged 2 encoding DNA SEQ ID NO:11.
PD WO200307848-A2.
PD 25-SEP-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 2.4%; Score 36; DB 10; Length 28000;
Best Local Similarity 51.9%; Pred. No. 2e+02;
RESULT 878
ID ADH62916 standard; DNA; 28000 BP.
DE Human jagged 2 gene.
PD US2003170636-A1.
PD 11-SEP-2003.
PA (ISIS-) ISIS PHARM INC.

Query Match 2.4%; Score 36; DB 10; Length 28000;
Best Local Similarity 51.9%; Pred. No. 2e+02;
RESULT 879
ID ADH57071 standard; DNA; 28000 BP.
DE Genomic human jagged 2 DNA sequence SeqID 11.
PD US2003207839-A1.
PD 06-NOV-2003.
PA (FREIR/) FREIER S M.
Query Match 2.4%; Score 36; DB 10; Length 28000;
Best Local Similarity 51.9%; Pred. No. 2e+02;
RESULT 880
ID ACN44596 standard; DNA; 69090 BP.
DE Mouse genomic sequence mCG2215.
PD WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.4%; Score 36; DB 11; Length 69090;
Best Local Similarity 58.3%; Pred. No. 3.1e+02;
RESULT 881
ID ADL13931 standard; DNA; 180385 BP.
DE Osteoarthritis-associated polymorphic nucleotide #463.
PD WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 2.4%; Score 36; DB 10; Length 180385;
Best Local Similarity 48.1%; Pred. No. 5e+02;
RESULT 882
ID ACN44124 standard; DNA; 189158 BP.
DE Mouse genomic sequence mCG14749.
PD WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.4%; Score 36; DB 11; Length 189158;
Best Local Similarity 48.1%; Pred. No. 5.1e+02;
RESULT 883
ID ACN45150 standard; DNA; 217409 BP.
DE Human genomic sequence hCG34092.
PD WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.4%; Score 36; DB 11; Length 217409;
Best Local Similarity 48.5%; Pred. No. 5.5e+02;
RESULT 884
ID ACH44435 standard; cDNA; 469 BP.
DE Human foetal brain cDNA #5160.
PD US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STRAC/) STRACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 2.4%; Score 35.8; DB 9; Length 469;
Best Local Similarity 61.1%; Pred. No. 30;
RESULT 885
ID ADJ11721 standard; DNA; 561 BP.
DE Rice cDNA modulated by post-transcriptional gene silencing SeqID 357.
PD US2003135888-A1.
PD 17-JUL-2003.
PA (ZHUT/) ZHU T.
PA (WANG/) WANG X.
PA (CHAN/) CHANG H.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KEEP/) KREPS J.
PA (MOUG/) MOUGHAMER T.
PA (PROV/) PROVART N.
PA (RICK/) RICHKE D.
Query Match 2.4%; Score 35.8; DB 11; Length 561;
Best Local Similarity 47.9%; Pred. No. 32;

RESULT 886
ID ADA70499 standard; DNA; 564 BP.
DE Rice gene SEQ ID 3822.
PN WO200300898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.4%; Score 35.8; DB 8; Length 564;
Best Local Similarity 47.9%; Pred. No. 33;
RESULT 887
ID ADA8727 standard; DNA; 564 BP.
DE Rice gene conferring disease resistance in plants.
PN WO200300906-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.4%; Score 35.8; DB 9; Length 564;
Best Local Similarity 47.9%; Pred. No. 33;
RESULT 888
ID ADJ11367 standard; DNA; 564 BP.
DE Rice DNA modulated by post-transcriptional gene silencing SeqID 3.
PN US2003135888-A1.
PD 17-JUL-2003.
PA (ZHUT) ZHU T.
PA (WANG) WANG X.
PA (CHANG) CHANG H.
PA (BRIG) BRIGGS S P.
PA (COOP) COOPER B.
PA (GLAZ) GLAZEBROOK J.
PA (GOLF) GOLF S A.
PA (KATA) KATAGIRI F.
PA (KREP) KREPS J.
PA (MOUG) MOUGHAMER T.
PA (PROV) PROVANT N.
PA (RICK) RICE D.
Query Match 2.4%; Score 35.8; DB 11; Length 564;
Best Local Similarity 47.9%; Pred. No. 33;
RESULT 889
ID ADB59062 standard; DNA; 648 BP.
DE Toxicity-related gene, SEQ ID 4088.
PN WO2003064624-A2.
PD 07-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 2.4%; Score 35.8; DB 10; Length 648;
Best Local Similarity 46.6%; Pred. No. 35;
RESULT 890
ID ADB53815 standard; DNA; 648 BP.
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:4357.
PN WO2003065993-A2.
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 2.4%; Score 35.8; DB 10; Length 648;
Best Local Similarity 46.6%; Pred. No. 35;
RESULT 891
ID ABT12404 standard; DNA; 648 BP.
DE Toxicity modelling related rat gene SEQ ID NO 2106.
PN WO200295000-A2.
PD 28-NOV-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 2.4%; Score 35.8; DB 10; Length 648;
Best Local Similarity 46.6%; Pred. No. 35;
RESULT 892
ID AAZ93365 standard; DNA; 774 BP.
DE Sequence encoding F-box protein FBP-15.
PN WO200012679-A1.
PD 09-MAR-2000.
PA (UNIV) UNIV NEW YORK STATE.
Query Match 2.4%; Score 35.8; DB 3; Length 774;
Best Local Similarity 51.7%; Pred. No. 38;
RESULT 893
ID AA141056 standard; cDNA; 774 BP.
DE cDNA of Human F-box protein FBP15 SEQ ID NO 39.
PN WO20025665-A2.
PD 18-JUL-2002.
PA (UNIV) UNIV NEW YORK STATE.

Query Match 2.4%; Score 35.8; DB 6; Length 774;
Best Local Similarity 51.7%; Pred. No. 38;
RESULT 894
ID ABD08278 standard; DNA; 783 BP.
DE Pseudomonas aeruginosa polynucleotide #6882.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.4%; Score 35.8; DB 11; Length 783;
Best Local Similarity 55.1%; Pred. No. 38;
RESULT 895
ID AAS87609 standard; cDNA; 1074 BP.
DE DNA encoding novel human diagnostic protein #23413.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.4%; Score 35.8; DB 5; Length 1074;
Best Local Similarity 51.6%; Pred. No. 45;
RESULT 896
ID AAI58521 standard; cDNA; 1457 BP.
DE Human polynucleotide SEQ ID NO 724.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.4%; Score 35.8; DB 4; Length 1457;
Best Local Similarity 51.7%; Pred. No. 52;
RESULT 897
ID ADQ98738 standard; cDNA; 1457 BP.
DE DNA encoding human GPCR-like protein seqid 408.
PN US6569662-B1.
PD 27-MAY-2003.
PA (HYSE-) HYSEQ INC.
Query Match 2.4%; Score 35.8; DB 5; Length 1457;
Best Local Similarity 51.7%; Pred. No. 52;
RESULT 898
ID ADB48498 standard; cDNA; 1457 BP.
DE Novel human cDNA SEQ ID NO 408.
PN US2003104529-A1.
PD 05-JUN-2003.
PA (ZHOU) ZHOU P.
PA (TANG) TANG Y T.
PA (LIUC) LIU C.
PA (ASUN) ASUNDI V.
PA (DRMA) DRMANAC R T.
Query Match 2.4%; Score 35.8; DB 9; Length 1457;
Best Local Similarity 51.7%; Pred. No. 52;
RESULT 899
ID ADM01372 standard; cDNA; 2281 BP.
DE Human cDNA of the invention SEQ ID NO:57.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) REAS ASSOC BIOTECHNOLOGY.
Query Match 2.4%; Score 35.8; DB 11; Length 2281;
Best Local Similarity 56.3%; Pred. No. 65;
RESULT 900
ID ADM6961 standard; cDNA; 2394 BP.
DE Human protein encoding cDNA SEQ ID NO:54.
PN WO2004009834-A2.
PD 29-JAN-2004.
PA (NUVE-) NUVELO INC.
Query Match 2.4%; Score 35.8; DB 12; Length 2394;
Best Local Similarity 57.7%; Pred. No. 67;
RESULT 901
ID ADM6960 standard; cDNA; 2490 BP.
DE Human protein encoding cDNA SEQ ID NO:53.
PN WO2004009834-A2.
PD 29-JAN-2004.
PA (NUVE-) NUVELO INC.
Query Match 2.4%; Score 35.8; DB 12; Length 2490;
Best Local Similarity 57.7%; Pred. No. 68;
RESULT 902
ID ADH76501 standard; DNA; 2572 BP.
DE 727 amino acid human neurotransmitter transporter protein encoding DNA.

PN US2003219774-A1.
PD 27-NOV-2003.
PA (SHAR/) SHARMA R.
PA (RAMA/) RAMANATHAN C S.
PA (WEST/) WESTPHAL R.
PA (FEDER/) FEDER J N.
PA (LEEL/) LEE L M.
Query Match
Best Local Similarity 2.4%; Score 35.8; DB 12; Length 2572;
47.2%; Pred. No. 69;
RESULT 903
ID ADU11615 standard; DNA; 2874 BP.
DE Rice DNA modulated by post-transcriptional gene silencing SeqID 251.
PN US2003135888-A1.
PD 17-JUL-2003.
PA (ZHUT/) ZHU T.
PA (WANG/) WANG X.
PA (CHAN/) CHANG H.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KEEP/) KEEPS J.
PA (MOUG/) MOUGHAMER T.
PA (PROV/) PROVART N.
PA (RICK/) RIQUE D.
Query Match
Best Local Similarity 2.4%; Score 35.8; DB 11; Length 2874;
47.9%; Pred. No. 73;
RESULT 904
ID ABX71181 standard; cDNA; 3168 BP.
DE Novel human cDNA sequence #406.
PN WO200281731-A2.
PD 17-OCT-2002.
PA (HYSE-) HYSEQ INC.
PA (GOOD/) GOODRICH R W.
Query Match
Best Local Similarity 2.4%; Score 35.8; DB 8; Length 3168;
47.2%; Pred. No. 77;
RESULT 905
ID AAS72201 standard; cDNA; 3599 BP.
DE DNA encoding novel human diagnostic protein #8005.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 2.4%; Score 35.8; DB 5; Length 3599;
50.3%; Pred. No. 82;
RESULT 906
ID ADS10356 standard; DNA; 3662 BP.
DE Human therapeutic DNA - SEQ ID 593.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match
Best Local Similarity 2.4%; Score 35.8; DB 13; Length 3662;
53.1%; Pred. No. 83;
RESULT 907
ID ACNA40359 standard; cDNA; 3686 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA326477, SEQ ID NO:5089.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.4%; Score 35.8; DB 13; Length 3686;
50.3%; Pred. No. 83;
RESULT 908
ID ADR25659 standard; DNA; 4080 BP.
DE Breast cancer prognosis marker #1520.
PN WO2004065545-A2.
PD 05-AUG-2004.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
PA (NECA-) NETHERLANDS CANCER INST.
Query Match
Best Local Similarity 2.4%; Score 35.8; DB 13; Length 4080;
51.6%; Pred. No. 87;
RESULT 909
ID AAD36022 standard; DNA; 43950 BP.
DE Human kinase genomic DNA.

Query Match
Best Local Similarity 2.4%; Score 35.8; DB 6; Length 43950;
51.6%; Pred. No. 2.8e+02;
RESULT 910
ID ABD33339 standard; DNA; 62658 BP.
DE Human cancer-associated (CA) gene HD07-061.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match
Best Local Similarity 2.4%; Score 35.8; DB 13; Length 62658;
51.6%; Pred. No. 3.4e+02;
RESULT 911
ID ADD97640 standard; DNA; 79731 BP.
DE Mouse cancer associated sequence MD10-020, SEQ ID 617.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match
Best Local Similarity 2.4%; Score 35.8; DB 12; Length 79731;
57.1%; Pred. No. 3.8e+02;
RESULT 912
ID AAA78038 standard; cDNA; 174 BP.
DE cDNA encoding human colon tumour polypeptide, SEQ ID NO:325.
PN WO200037643-A2.
PD 29-JUN-2000.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 2.4%; Score 35.6; DB 3; Length 174;
51.2%; Pred. No. 21;
RESULT 913
ID AAA78081 standard; cDNA; 174 BP.
DE cDNA encoding human colon tumour polypeptide, SEQ ID NO:368.
PN WO200037643-A2.
PD 29-JUN-2000.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 2.4%; Score 35.6; DB 3; Length 174;
51.2%; Pred. No. 21;
RESULT 914
ID AA128776 standard; cDNA; 174 BP.
DE Colon tumour related determined cDNA sequence for clone 25886.
PN WO200149716-A2.
PD 12-JUL-2001.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 2.4%; Score 35.6; DB 4; Length 174;
51.2%; Pred. No. 21;
RESULT 915
ID AA128819 standard; cDNA; 174 BP.
DE Colon tumour related determined cDNA sequence for clone 25934.
PN WO200149716-A2.
PD 12-JUL-2001.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 2.4%; Score 35.6; DB 4; Length 174;
51.2%; Pred. No. 21;
RESULT 916
ID AB233005 standard; cDNA; 174 BP.
DE Human colon tumour cDNA clone 25934 SEQ ID NO:368.
PN WO200283070-A2.
PD 24-OCT-2002.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 2.4%; Score 35.6; DB 8; Length 174;
51.2%; Pred. No. 21;
RESULT 917
ID AB232962 standard; cDNA; 174 BP.
DE Human colon tumour cDNA clone 25886 SEQ ID NO:325.
PN WO200283070-A2.
PD 24-OCT-2002.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 2.4%; Score 35.6; DB 8; Length 174;
51.2%; Pred. No. 21;
RESULT 918
ID AD567683 standard; cDNA; 242 BP.
DE Corn breeding-derived polynucleotide (cpds), SEQ ID 2699.
PN US2003237110-A9.
PD 25-DEC-2003.
PA (INCY-) INCYTE PHARM INC.
Query Match
Best Local Similarity 2.4%; Score 35.6; DB 7; Length 242;

Best Local Similarity	62.2%;	Pred. No. 24;
RESULT 919		
ID	ADA58416 standard; cDNA; 309 BP.	
DE	Maize sucrose synthase EST #60.	
PN	US2003135870-A1.	
PD	17-JUL-2003.	
PA	(CHEI//) CHEIKH N.	
PA	(FISH//) FISHER D K.	
PA	(LIUJ//) LIU J.	
Query Match	2.4%;	Score 35.6; DB 9; Length 309;
Best Local Similarity	58.5%;	Pred. No. 27;
RESULT 920		
ID	ACU19214 standard; DNA; 410 BP.	
DE	DNA clone originating in barley containing SNP encoding sequence #9205.	
PN	WO2003057877-A1.	
PD	17-JUL-2003.	
PA	(UYNI-) UNIV JAPAN OKAYAMA.	
Query Match	2.4%;	Score 35.6; DB 9; Length 410;
Best Local Similarity	47.7%;	Pred. No. 32;
RESULT 921		
ID	ACU51862 standard; cDNA; 458 BP.	
DE	Cotton androecium tissue EST Clone ID: LIB3828-009-Q1-N6-B6, SEQ:6663.	
PN	US2004123340-A1.	
PD	24-JUN-2004.	
PA	(DEIK//) DEIKMAN J.	
PA	(FENG//) FENG P C C.	
PA	(FINC//) FINCHER K L.	
PA	(ZIEG//) ZIEGLER T E.	
Query Match	2.4%;	Score 35.6; DB 13; Length 458;
Best Local Similarity	52.7%;	Pred. No. 33;
RESULT 922		
ID	ACU45185 standard; cDNA; 504 BP.	
DE	Human foetal brain cDNA #5910.	
PN	US2003073623-A1.	
PD	17-APR-2003.	
PA	(DERR//) DERRANC R T.	
PA	(LABA//) LABAT I.	
PA	(STAC//) STACHE-CRAIN B.	
PA	(DICK//) DICKSON M C.	
PA	(JONE//) JONES L W.	
Query Match	2.4%;	Score 35.6; DB 9; Length 504;
Best Local Similarity	58.5%;	Pred. No. 35;
RESULT 923		
ID	AAS65914 standard; cDNA; 558 BP.	
DE	DNA encoding novel human diagnostic protein #1718.	
PN	WO200175067-A2.	
PD	11-OCT-2001.	
PA	(HYSE-) HYSEQ INC.	
Query Match	2.4%;	Score 35.6; DB 5; Length 558;
Best Local Similarity	51.2%;	Pred. No. 37;
RESULT 924		
ID	AA123315 standard; DNA; 575 BP.	
DE	Probe #13248 for gene expression analysis in human cervical cell sample	
PN	WO200157277-A2.	
PD	09-AUG-2001.	
PA	(MOLE-) MOLECULAR DYNAMICS INC.	
Query Match	2.4%;	Score 35.6; DB 4; Length 575;
Best Local Similarity	45.9%;	Pred. No. 37;
RESULT 925		
ID	ABA68422 standard; DNA; 575 BP.	
DE	Human foetal liver single exon nucleic acid probe #16727.	
PN	WO200157277-A2.	
PD	09-AUG-2001.	
PA	(MOLE-) MOLECULAR DYNAMICS INC.	
Query Match	2.4%;	Score 35.6; DB 4; Length 575;
Best Local Similarity	45.9%;	Pred. No. 37;
RESULT 926		
ID	AA148636 standard; DNA; 575 BP.	
DE	Probe #17322 used to measure gene expression in human placenta sample.	
PN	WO200157272-A2.	
PD	09-AUG-2001.	
PA	(MOLE-) MOLECULAR DYNAMICS INC.	
Query Match	2.4%;	Score 35.6; DB 4; Length 575;
Best Local Similarity	45.9%;	Pred. No. 37;
RESULT 927		
ID	AA148636 standard; DNA; 575 BP.	
DE	Probe #17322 used to measure gene expression in human placenta sample.	
PN	WO200157272-A2.	
PD	09-AUG-2001.	
PA	(MOLE-) MOLECULAR DYNAMICS INC.	
Query Match	2.4%;	Score 35.6; DB 4; Length 575;
Best Local Similarity	45.9%;	Pred. No. 37;

Best Local Similarity	45.9%;	Pred. No. 37;
RESULT 927		
ID	ABA50472 standard; DNA; 575 BP.	
DE	Human breast cell single exon nucleic acid probe #9167.	
PN	WO200157271-A2.	
PD	09-AUG-2001.	
PA	(MOLE-) MOLECULAR DYNAMICS INC.	
Query Match	2.4%;	Score 35.6; DB 4; Length 575;
Best Local Similarity	45.9%;	Pred. No. 37;
RESULT 928		
ID	ABA54131 standard; DNA; 575 BP.	
DE	Probe #13879 for gene expression analysis in human heart cell sample.	
PN	WO200157274-A2.	
PD	09-AUG-2001.	
PA	(MOLE-) MOLECULAR DYNAMICS INC.	
Query Match	2.4%;	Score 35.6; DB 4; Length 575;
Best Local Similarity	45.9%;	Pred. No. 37;
RESULT 929		
ID	AAK42567 standard; DNA; 575 BP.	
DE	Human bone marrow expressed single exon probe SEQ ID NO: 17124.	
PN	WO200157276-A2.	
PD	09-AUG-2001.	
PA	(MOLE-) MOLECULAR DYNAMICS INC.	
Query Match	2.4%;	Score 35.6; DB 4; Length 575;
Best Local Similarity	45.9%;	Pred. No. 37;
RESULT 930		
ID	AAK16793 standard; DNA; 575 BP.	
DE	Human brain expressed single exon probe SEQ ID NO: 16784.	
PN	WO200157275-A2.	
PD	09-AUG-2001.	
PA	(MOLE-) MOLECULAR DYNAMICS INC.	
Query Match	2.4%;	Score 35.6; DB 4; Length 575;
Best Local Similarity	45.9%;	Pred. No. 37;
RESULT 931		
ID	ABA542178 standard; DNA; 575 BP.	
DE	Human liver single exon probe, SEQ ID No 17168.	
PN	WO200157273-A2.	
PD	09-AUG-2001.	
PA	(MOLE-) MOLECULAR DYNAMICS INC.	
Query Match	2.4%;	Score 35.6; DB 4; Length 575;
Best Local Similarity	45.9%;	Pred. No. 37;
RESULT 932		
ID	AAI08956 standard; DNA; 575 BP.	
DE	Probe #8947 used to measure gene expression in human breast sample.	
PN	WO200157270-A2.	
PD	09-AUG-2001.	
PA	(MOLE-) MOLECULAR DYNAMICS INC.	
Query Match	2.4%;	Score 35.6; DB 5; Length 575;
Best Local Similarity	45.9%;	Pred. No. 37;
RESULT 933		
ID	ABS116615 standard; DNA; 575 BP.	
DE	Human genome-derived single exon probe ORF from lung SEQ ID No 16606.	
PN	WO200186003-A2.	
PD	15-NOV-2001.	
PA	(MOLE-) MOLECULAR DYNAMICS INC.	
Query Match	2.4%;	Score 35.6; DB 6; Length 687;
Best Local Similarity	45.9%;	Pred. No. 37;
RESULT 934		
ID	ABQ19226 standard; DNA; 687 BP.	
DE	Oligonucleotide for detecting cytosine methylation SEQ ID NO 5817.	
PN	WO200218632-A2.	
PD	07-MAR-2002.	
PA	(EPIC-) EPIDENOMICS AG.	
Query Match	2.4%;	Score 35.6; DB 6; Length 687;
Best Local Similarity	53.7%;	Pred. No. 41;
RESULT 935		
ID	ABQ19227 standard; DNA; 687 BP.	
DE	Oligonucleotide for detecting cytosine methylation SEQ ID NO 5818.	
PN	WO200218632-A2.	
PD	07-MAR-2002.	
PA	(EPIC-) EPIDENOMICS AG.	
Query Match	2.4%;	Score 35.6; DB 6; Length 687;
Best Local Similarity	53.7%;	Pred. No. 41;

RESULT 936
ID ADR46437 standard; DNA; 719 BP.
DE A thaliana caltrectin-like protein coding sequence SEQ ID NO: 3.
PN WO2004070035-A2.
PD 19-AUG-2004.
PA (SUNG-) SONGENE GMBH & CO KGAA.
Query Match
Best Local Similarity 2.4%; Score 35.6; DB 13; Length 719;
RESULT 937
ID ADT42681 standard; cDNA; 747 BP.
DE Bacterial polynucleotide #17432.
PN US200323675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 2.4%; Score 35.6; DB 13; Length 747;
RESULT 938
ID AAC35370 standard; DNA; 760 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 9944.
PN EP1033405-A2.
PD 06-SEP-2000.
PA
Query Match
Best Local Similarity 2.4%; Score 35.6; DB 3; Length 760;
RESULT 939
ID AA160307 standard; cDNA; 1627 BP.
DE Human polynucleotide SEQ ID NO 4296.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSEQ) HYSEQ INC.
Query Match
Best Local Similarity 2.4%; Score 35.6; DB 4; Length 1627;
RESULT 940
ID AAH15073 standard; cDNA; 1790 BP.
DE Human cDNA sequence SEQ ID NO.13081.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match
Best Local Similarity 2.4%; Score 35.6; DB 4; Length 1790;
RESULT 941
ID AAI14105 standard; DNA; 1969 BP.
DE Probe #4038 for gene expression analysis in human cervical cell sample.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 2.4%; Score 35.6; DB 4; Length 1969;
RESULT 942
ID ABA55830 standard; DNA; 1969 BP.
DE Human foetal liver single exon nucleic acid probe #4135.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 2.4%; Score 35.6; DB 4; Length 1969;
RESULT 943
ID AA135486 standard; DNA; 1969 BP.
DE Probe #4172 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 2.4%; Score 35.6; DB 4; Length 1969;
RESULT 944
ID ABA45341 standard; DNA; 1969 BP.
DE Human breast cell single exon nucleic acid probe #4036.
PN WO200157271-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.

Query Match
Best Local Similarity 2.4%; Score 35.6; DB 4; Length 1969;
RESULT 945
ID ABA25506 standard; DNA; 1969 BP.
DE Probe #3972 for gene expression analysis in human heart cell sample.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 2.4%; Score 35.6; DB 4; Length 1969;
RESULT 946
ID AAK29533 standard; DNA; 1969 BP.
DE Human bone marrow expressed single exon probe SEQ ID NO: 4090.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 2.4%; Score 35.6; DB 4; Length 1969;
RESULT 947
ID AAK04048 standard; DNA; 1969 BP.
DE Human brain expressed single exon probe SEQ ID NO: 4039.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 2.4%; Score 35.6; DB 4; Length 1969;
RESULT 948
ID ABS29157 standard; DNA; 1969 BP.
DE Human liver single exon probe, SEQ ID NO 4147.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 2.4%; Score 35.6; DB 4; Length 1969;
RESULT 949
ID AA103958 standard; DNA; 1969 BP.
DE Probe #3949 used to measure gene expression in human breast sample.
PN WO200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 2.4%; Score 35.6; DB 5; Length 1969;
RESULT 950
ID ABS04084 standard; DNA; 1969 BP.
DE Human genome-derived single exon probe from lung SEQ ID NO 4075.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match
Best Local Similarity 2.4%; Score 35.6; DB 6; Length 1969;
RESULT 951
ID AAF59600 standard; cDNA; 2035 BP.
DE Human cell cycle and proliferation protein CCYPR-11 cDNA, SEQ ID NO:65.
PN WO200107471-A2.
PD 01-FEB-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 2.4%; Score 35.6; DB 4; Length 2035;
RESULT 952
ID ADA47789 standard; DNA; 2066 BP.
DE Human NOV45F gene SEQ ID NO:151.
PN WO2001076642-A2.
PD 18-SEP-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 2.4%; Score 35.6; DB 10; Length 2066;
RESULT 953
ID ADH41892 standard; DNA; 2066 BP.
DE Novel human nucleic acid NOV36a.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 2.4%; Score 35.6; DB 12; Length 2066;

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Best Local Similarity 57.0%; Pred. No. 71;
RESULT 954
ID ADJ79059 standard; DNA; 2066 BP.
DE Human NOVX protein Nov45F gene sequence.
PN US2004014053-A1.
PD 22-JAN-2004.
PA (ZERRH/) ZERRHUSEN B D.
PA (PAT/) PATURAJAN M.
PA (KEKU/) KEKUDA R.
PA (MILL/) MILLER C E.
PA (RIEG/) RIEGER D K.
PA (PENNA/) PENNA C B A.
PA (SHIM/) SHIMKETS R A.
PA (LILL/) LI L.
PA (BERG/) BERGHS C.
PA (ZHON/) ZHONG M.
PA (CASM/) CASMAN S J.
PA (VOSS/) VOSS E Z.
PA (BOLD/) BOLDOG F L.
PA (PADI/) PADIGARU M.
PA (SMIT/) SMITHSON G.
PA (JIMW/) JI W.
PA (GORM/) GORMAN L.
PA (VERN/) VERNET C A M.
PA (LEIT/) LEITE M W.
PA (GUOX/) GUO X S.
PA (ANDE/) ANDERSON D W.
PA (SEPT/) SPYTEK K A.
PA (GERL/) GERLACH V.
PA (BURC/) BURGESS C E.
PA (KHRA/) KHRAMTSOV N V.
PA (ORTT/) ORT T.
PA (ELER/) ELERMAN K.
PA (RASF/) RASTELLI L.
PA (AGEE/) AGEE M L.
PA (CHAN/) CHAUDHURI A.
PA (CHAN/) CHANT J S.
PA (DIPI/) DIPIPO V A.
PA (EDIN/) EDINGER S R.
PA (EISE/) EISEN A J.
PA (GANG/) GANGOLLI E A.
PA (GIOT/) GIOT L.
PA (IOIC/) OOI C E.
PA (ROTH/) ROTHENBERG M E.
PA (SPAD/) SPADERNA S K.
PA (HJAL/) HJALT T.
PA (LITX/) LIT X.
PA (TAUP/) TAUPIER R J.
PA (CATT/) CATTERTON E.
PA (SHEN/) SHENOY S G.
Query Match
Best Local Similarity 2.4%; Score 35.6; DB 12; Length 2066;
RESULT 955
ID ADO54827 standard; DNA; 2136 BP.
DE Human macrophage stimulating protein (MSP) DNA SegID 1.
PN KR2003003840-A.
PD 14-JAN-2003.
PA (PANG-) PANGENOMICS CO LTD.
Query Match
Best Local Similarity 2.4%; Score 35.6; DB 11; Length 2136;
RESULT 956
ID AAC48435 standard; DNA; 2173 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 57468.
PN EP1033405-A2.
PD 06-SEP-2000.
PA
Query Match
Best Local Similarity 2.4%; Score 35.6; DB 3; Length 2173;
RESULT 957
ID ADT45831 standard; cDNA; 2205 BP.
DE Bacterial polynucleotide #20582.
PN US200333675-A1.
PD 18-DEC-2003.
PA (CAOV/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 2.4%; Score 35.6; DB 13; Length 2205;
RESULT 958
ID AAT47149 standard; cDNA; 2213 BP.
DE Macrophage stimulating protein C672X deletion variant cDNA.
PN EP750040-A2.
PD 27-DEC-1996.
PA (TOYM) TOYO BOSEKI KK.
Query Match
Best Local Similarity 2.4%; Score 35.6; DB 2; Length 2213;
RESULT 959
ID AAT47145 standard; cDNA; 2216 BP.
DE Macrophage stimulating protein C672X variant cDNA.
PN EP750040-A2.
PD 27-DEC-1996.
PA (TOYM) TOYO BOSEKI KK.
Query Match
Best Local Similarity 2.4%; Score 35.6; DB 2; Length 2216;
RESULT 960
ID AAV72083 standard; cDNA; 2216 BP.
DE Human MSP cDNA.
PN WO9855141-A1.
PD 10-DEC-1998.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
Query Match
Best Local Similarity 2.4%; Score 35.6; DB 2; Length 2216;
RESULT 961
ID ABV75112 standard; cDNA; 2216 BP.
DE Human hepatocyte growth factor-like protein (HGFL) encoding cDNA.
PN WO200283074-A2.
PD 24-OCT-2002.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match
Best Local Similarity 2.4%; Score 35.6; DB 8; Length 2216;
RESULT 962
ID AAO79724 standard; cDNA to mRNA; 2219 BP.
DE Human L5/3 tumour suppressor gene (Phe214 polymorphism).
PN US5315000-A.
PD 24-MAY-1994.
PA (CHIL-) CHILDRENS HOSPITAL MEDICAL CENT.
Query Match
Best Local Similarity 2.4%; Score 35.6; DB 2; Length 2219;
RESULT 963
ID AAO79723 standard; cDNA to mRNA; 2219 BP.
DE Human L5/3 tumour suppressor gene (Cys214 polymorphism).
PN US5315000-A.
PD 24-MAY-1994.
PA (CHIL-) CHILDRENS HOSPITAL MEDICAL CENT.
Query Match
Best Local Similarity 2.4%; Score 35.6; DB 2; Length 2219;
RESULT 964
ID AAT62436 standard; cDNA to mRNA; 2219 BP.
DE Human L5/3 partial clone #33 polymorphism #1.
PN US5606029-A.
PD 25-FEB-1997.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match
Best Local Similarity 2.4%; Score 35.6; DB 2; Length 2219;
RESULT 965
ID AAT62437 standard; cDNA to mRNA; 2219 BP.
DE Human L5/3 partial clone #33 polymorphism #2.
PN US5606029-A.
PD 25-FEB-1997.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match
Best Local Similarity 2.4%; Score 35.6; DB 2; Length 2219;
RESULT 966
ID ABV94342 standard; cDNA; 2219 BP.
DE Breast carcinoma related nucleotide sequence SEQ ID NO:333.
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PN WO200246467-A2.
PD 13-JUN-2002.
PA (IPSO-) IPSOGEN.
Query Match 2.4%; Score 35.6; DB 6; Length 2219;
Best Local Similarity 57.0%; Pred. No. 73;
RESULT 967
ID AD084917 standard; cDNA; 2220 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #1731.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH-) GENENTECH INC.
PA (WOTD/) WU T D.
PA (ZHOY/) ZHOY Y.
Query Match 2.4%; Score 35.6; DB 13; Length 2220;
Best Local Similarity 57.0%; Pred. No. 73;
RESULT 968
ID AA079729 standard; cDNA; 2262 BP.
DE Full-length human l5/3 tumour suppressor gene cDNA.
PN US531500-A.
PD 24-MAY-1994.
PA (CHIL-) CHILDRENS HOSPITAL MEDICAL CENT.
Query Match 2.4%; Score 35.6; DB 2; Length 2262;
Best Local Similarity 57.0%; Pred. No. 74;
RESULT 969
ID AAT62439 standard; cDNA to mRNA; 2262 BP.
DE Human l5/3 construct gene.
PN US5606029-A.
PD 25-FEB-1997.
PA (CHIL-) CHILDRENS HOSPITAL MEDICAL CENT.
Query Match 2.4%; Score 35.6; DB 2; Length 2262;
Best Local Similarity 57.0%; Pred. No. 74;
RESULT 970
ID ADF81916 standard; DNA; 2292 BP.
DE Leukaemia-related DNA sequence #2472.
PN WO2003039443-A2.
PD 15-MAY-2003.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA (HAFR/) HAFERLACH T.
PA (SCHO/) SCHOCH C.
PA (KERN/) KERN W.
Query Match 2.4%; Score 35.6; DB 10; Length 2292;
Best Local Similarity 57.0%; Pred. No. 74;
RESULT 971
ID ACC42371 standard; DNA; 2440 BP.
DE Human extracellular messenger, EXMES-11, coding sequence.
PN WO2003018612-A2.
PD 06-MAR-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 2.4%; Score 35.6; DB 8; Length 2440;
Best Local Similarity 57.0%; Pred. No. 77;
RESULT 972
ID AA159516 standard; cDNA; 2482 BP.
DE Human polynucleotide SEQ ID NO 1719.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.4%; Score 35.6; DB 4; Length 2482;
Best Local Similarity 47.0%; Pred. No. 77;
RESULT 973
ID ACN41133 standard; cDNA; 2493 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:8.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 2.4%; Score 35.6; DB 13; Length 2493;
Best Local Similarity 57.0%; Pred. No. 78;
RESULT 974
ID ACC42370 standard; DNA; 2573 BP.
DE Human extracellular messenger, EXMES-10, coding sequence.
PN WO2003018612-A2.
PD 06-MAR-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 2.4%; Score 35.6; DB 8; Length 2573;
Best Local Similarity 57.0%; Pred. No. 79;
RESULT 975
ID ADS56284 standard; cDNA; 2586 BP.
DE Bacterial polynucleotide #8271.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SIAT/) SIATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 2.4%; Score 35.6; DB 13; Length 2586;
Best Local Similarity 55.7%; Pred. No. 79;
RESULT 976
ID ACN41131 standard; cDNA; 2589 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:6.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 2.4%; Score 35.6; DB 13; Length 2589;
Best Local Similarity 57.0%; Pred. No. 79;
RESULT 977
ID AAL51943 standard; DNA; 2598 BP.
DE Human extracellular messenger gene #1.
PN WO2003002610-A1.
PD 09-JAN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 2.4%; Score 35.6; DB 8; Length 2598;
Best Local Similarity 57.0%; Pred. No. 79;
RESULT 978
ID AAL17666 standard; cDNA; 2666 BP.
DE Human cDNA sequence SEQ ID NO:17576.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 2.4%; Score 35.6; DB 4; Length 2666;
Best Local Similarity 47.0%; Pred. No. 80;
RESULT 979
ID ACC42374 standard; DNA; 2769 BP.
DE Human extracellular messenger, EXMES-14, coding sequence.
PN WO2003018612-A2.
PD 06-MAR-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 2.4%; Score 35.6; DB 8; Length 2769;
Best Local Similarity 57.0%; Pred. No. 82;
RESULT 980
ID ACN41130 standard; cDNA; 3140 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:5.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 2.4%; Score 35.6; DB 13; Length 3140;
Best Local Similarity 57.0%; Pred. No. 87;
RESULT 981
ID AA865913 standard; cDNA; 4029 BP.
DE DNA encoding novel human diagnostic protein #1717.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.4%; Score 35.6; DB 5; Length 4029;
Best Local Similarity 51.2%; Pred. No. 98;
RESULT 982
ID ADD29793 standard; mRNA; 6997 BP.
DE Human tumour suppressor mRNA SEQ ID NO:251.
PN WO2003058201-A2.
PD 17-JUL-2003.
PA (QUAR-) QUARK BIOTECH INC.
PA (CLAV-) CLEVELAND CLINIC FOUND.
Query Match 2.4%; Score 35.6; DB 10; Length 6997;
Best Local Similarity 51.2%; Pred. No. 1.3e+02;
RESULT 983
ID AAQ25975 standard; DNA; 15377 BP.
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DE MH mutant porcine ryanodine receptor cDNA.
PN WO211387-A1.
PD 09-JUL-1992.
PA (UTOR) UNIT TORONTO INNOVATIONS FOUND.
PA (UTG-) UNIT GUELPH.
Query Match 2.4%; Score 35.6; DB 2; Length 15377;
RESULT 984
DE Human cancer-associated (CA) gene sequence SEQ ID NO:1.
PN WO2004058288-A1.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 35.6; DB 12; Length 49087;
RESULT 985
DE Human cancer-associated genomic DNA HD7-023.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 35.6; DB 13; Length 49175;
RESULT 986
DE Human cancer-associated genomic DNA HD7-023.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 35.6; DB 13; Length 73882;
RESULT 987
DE Human cancer-associated sequence HD08-025, SEQ ID 254.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 35.6; DB 12; Length 86149;
RESULT 988
DE Murine cancer-associated (CA) gene MD07-119.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 35.6; DB 13; Length 92219;
RESULT 989
DE Human cancer-associated sequence hCG30014.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 35.6; DB 10; Length 110000;
RESULT 990
DE Human cancer-associated genomic DNA HD17-008.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 35.6; DB 11; Length 118931;
RESULT 992
DE Human cancer-associated genomic DNA HD17-008.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 35.6; DB 13; Length 129381;
RESULT 993
DE Human cancer-associated sequence MD09-009, SEQ ID 503.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 35.6; DB 12; Length 151052;

Best Local Similarity 48.1%; Pred. No. 5.9e+02;
RESULT 994
DE Human DNA differentially expressed in granulocytic cells #139.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 2.4%; Score 35.6; DB 6; Length 201143;
RESULT 995
DE Bovine EST associated with lactation/muscle/fat deposition #4013.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 2.4%; Score 35.4; DB 8; Length 385;
RESULT 996
DE DNA encoding novel human diagnostic protein #26488.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.4%; Score 35.4; DB 5; Length 393;
RESULT 997
DE Bovine EST associated with lactation/muscle/fat deposition #7745.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 2.4%; Score 35.4; DB 8; Length 413;
RESULT 998
DE Bovine EST associated with lactation/muscle/fat deposition #2019.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 2.4%; Score 35.4; DB 8; Length 416;
RESULT 999
DE Pseudomonas aeruginosa polynucleotide #10025.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.4%; Score 35.4; DB 11; Length 423;
RESULT 1000
DE Bovine EST associated with lactation/muscle/fat deposition #2677.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 2.4%; Score 35.4; DB 8; Length 428;
RESULT 1001
DE B napus caltractin-like protein coding sequence SEQ ID NO: 5.
PN WO2004070035-A2.

PD 19-AUG-2004.
PA (SUNG-) SUNGENE GMBH & CO KGAA.
Query Match 2.4%; Score 35.4; DB 13; Length 428;
Best Local Similarity 48.7%; Pred. NO. 37;
RESULT 1002
ID ABX35170 standard; cDNA; 450 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #335.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYATT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 2.4%; Score 35.4; DB 8; Length 450;
Best Local Similarity 47.2%; Pred. NO. 38;
RESULT 1003
ID ACH14525 standard; cDNA; 492 BP.
DE Human adult brain cDNA #1737.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 2.4%; Score 35.4; DB 9; Length 492;
Best Local Similarity 47.2%; Pred. NO. 39;
RESULT 1004
ID ADA69809 standard; DNA; 579 BP.
DE Rice gene, SEQ ID 3132.
PN WO200300898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.4%; Score 35.4; DB 8; Length 579;
Best Local Similarity 48.3%; Pred. NO. 43;
RESULT 1005
ID ADE76270 standard; DNA; 701 BP.
DE Human BSK-36-8 complementary strand DNA.
PN EP1310567-A2.
PD 14-MAY-2003.
PA (OLIG-) OLIGENE GMBH.
Query Match 2.4%; Score 35.4; DB 10; Length 701;
Best Local Similarity 47.2%; Pred. NO. 47;
RESULT 1006
ID ACF04830 standard; DNA; 1008 BP.
DE M lichenicola melithiazol synthesis gene ORF 5.
PN WO2003080828-A2.
PD 02-OCT-2003.
PA (GBFB) GBF GES BIOTECH FORSCHUNG GMBH.
Query Match 2.4%; Score 35.4; DB 10; Length 1008;
Best Local Similarity 49.2%; Pred. NO. 56;
RESULT 1007
ID ADO83950 standard; cDNA; 1525 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #764.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 2.4%; Score 35.4; DB 12; Length 1525;
Best Local Similarity 47.2%; Pred. NO. 69;
RESULT 1008
ID ADO85345 standard; cDNA; 1525 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #2159.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 2.4%; Score 35.4; DB 13; Length 1525;
Best Local Similarity 47.2%; Pred. NO. 69;
RESULT 1009
ID ACF34491 standard; DNA; 1526 BP.

DE Gene encoding angiogenesis protein BN0112.
PN WO2003027285-A1.
PD 03-APR-2003.
PA (BION-) BIONOMICS LTD.
Query Match 2.4%; Score 35.4; DB 8; Length 1526;
Best Local Similarity 47.2%; Pred. NO. 69;
RESULT 1010
ID ACC50093 standard; cDNA; 1526 BP.
DE Breast cancer associated cDNA sequence SEQ ID NO:34.
PN WO2003004989-A2.
PD 16-JAN-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.4%; Score 35.4; DB 8; Length 1526;
Best Local Similarity 47.2%; Pred. NO. 69;
RESULT 1011
ID ADF81420 standard; DNA; 1526 BP.
DE Leukaemia-related DNA sequence #1976.
PN WO2003039443-A2.
PD 15-MAY-2003.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (TYLU-) UNITV LUDWIG MAXIMILIANS.
PA (HAPE/) HAPERLACH T.
PA (SCHO/) SCHOCH C.
PA (KERN/) KERN W.
Query Match 2.4%; Score 35.4; DB 10; Length 1526;
Best Local Similarity 47.2%; Pred. NO. 69;
RESULT 1012
ID ACN39732 standard; cDNA; 1526 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA325923, SEQ ID NO:4063.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 2.4%; Score 35.4; DB 13; Length 1526;
Best Local Similarity 47.2%; Pred. NO. 69;
RESULT 1013
ID AAT91855 standard; cDNA; 1559 BP.
DE DUB-1 enhancer/promoter.
PN WO9706247-A2.
PD 20-FEB-1997.
PA (DAND) DNA PARBER CANCER INST INC.
Query Match 2.4%; Score 35.4; DB 2; Length 1559;
Best Local Similarity 51.6%; Pred. NO. 70;
RESULT 1014
ID ACA39654 standard; DNA; 1770 BP.
DE Prokaryotic essential gene #21311.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 2.4%; Score 35.4; DB 8; Length 1770;
Best Local Similarity 52.3%; Pred. NO. 74;
RESULT 1015
ID ACN92807 standard; DNA; 3535 BP.
DE Breast cancer related marker, seq id 13957.
PN US200309974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.4%; Score 35.4; DB 11; Length 3535;
Best Local Similarity 47.2%; Pred. NO. 1e+02;
RESULT 1016
ID AD124476 standard; cDNA; 3718 BP.
DE Human modifier of Chk1 (MCHK) encoding cDNA SEQ ID NO:26.
PN WO2004004785-A1.
PD 15-JAN-2004.
PA (EXEL-) EXELIXIS INC.
Query Match 2.4%; Score 35.4; DB 12; Length 3718;
Best Local Similarity 47.2%; Pred. NO. 1.1e+02;
RESULT 1017
ID ACC46250 standard; cDNA; 3978 BP.
DE Human dltbp intracellular signalling protein-encoding cDNA.
PN WO200297031-A2.
PD 05-DEC-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 2.4%; Score 35.4; DB 8; Length 3978;

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Best Local Similarity 47.2%; Pred. No. 1.1e+02;
RESULT 1018
ID AAT74034 standard; cDNA; 4621 BP.
DE Mouse male-enhanced antigen-2 encoding cDNA.
PN UF09121869-A.
PD 13-MAY-1997.
PA (ITOH-) ITO HAM KK.
Query Match 2.4%; Score 35.4; DB 2; Length 4621;
Best Local Similarity 51.2%; Pred. No. 1.2e+02;
RESULT 1019
ID AAX04132 standard; cDNA; 4621 BP.
DE Mouse male enhanced antigen 2 encoding cDNA.
PN JP1018622-A.
PD 26-JAN-1999.
PA (ITOH-) ITO HAM KK.
Query Match 2.4%; Score 35.4; DB 2; Length 4621;
Best Local Similarity 51.2%; Pred. No. 1.2e+02;
RESULT 1020
ID ABD32920 standard; cDNA; 5012 BP.
DE Human cancer-associated cDNA HR18-043.9.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 35.4; DB 13; Length 5012;
Best Local Similarity 59.7%; Pred. No. 1.2e+02;
RESULT 1021
ID ABD32918 standard; cDNA; 5099 BP.
DE Human cancer-associated cDNA HR18-043.7.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 35.4; DB 13; Length 5099;
Best Local Similarity 59.7%; Pred. No. 1.3e+02;
RESULT 1022
ID ABD32919 standard; cDNA; 5186 BP.
DE Human cancer-associated cDNA HR18-043.8.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 35.4; DB 13; Length 5186;
Best Local Similarity 59.7%; Pred. No. 1.3e+02;
RESULT 1023
ID ABD33393 standard; DNA; 24318 BP.
DE Human cancer-associated (CA) gene HD07-073.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 35.4; DB 13; Length 24318;
Best Local Similarity 46.2%; Pred. No. 2.7e+02;
RESULT 1024
ID AAD52172 standard; DNA; 26000 BP.
DE Human interferon gamma receptor 1 (IFNGR1) gene.
PN WO200288162-A1.
PD 07-NOV-2002.
PA (ISIS-) ISIS PHARM INC.
Query Match 2.4%; Score 35.4; DB 10; Length 26000;
Best Local Similarity 53.2%; Pred. No. 2.8e+02;
RESULT 1025
ID ADQ97945 standard; DNA; 39414 BP.
DE Mouse cancer associated sequence MD11-027, SEQ ID 922.
PN WO2004060304-A2.
PD 22-JUN-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 35.4; DB 12; Length 39414;
Best Local Similarity 51.6%; Pred. No. 3.5e+02;
RESULT 1026
ID ABD32684 standard; DNA; 41991 BP.
DE Human cancer-associated genomic DNA HD13-117.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 35.4; DB 13; Length 41991;
Best Local Similarity 53.2%; Pred. No. 3.6e+02;

RESULT 1027
ID ACF04818 standard; DNA; 51855 BP.
DE Melitiazol biosynthetic gene cluster.
PN WO2003080828-A2.
PD 02-OCT-2003.
PA (GBRB) GBR GBS BIOTECH FORSCHUNG GMBH.
Query Match 2.4%; Score 35.4; DB 10; Length 51855;
Best Local Similarity 49.2%; Pred. No. 4e+02;
RESULT 1028
ID ABD33551 standard; DNA; 84410 BP.
DE Murine cancer-associated (CA) gene MD07-110.
PN WO2004058146-A2.
PD 15-JUN-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 35.4; DB 13; Length 84410;
Best Local Similarity 54.1%; Pred. No. 5.1e+02;
RESULT 1029
ID ACN44000 standard; DNA; 90026 BP.
DE Mouse genomic sequence mCG12663.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 35.4; DB 11; Length 90026;
Best Local Similarity 47.5%; Pred. No. 5.3e+02;
RESULT 1030
ID ADC85287 standard; DNA; 96596 BP.
DE Mouse fish genomic sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 35.4; DB 10; Length 96596;
Best Local Similarity 51.6%; Pred. No. 5.4e+02;
RESULT 1031
ID ADX02807 standard; DNA; 96597 BP.
DE Mouse fish carcinoma associated gene, SEQ ID NO.1325.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 35.4; DB 9; Length 96597;
Best Local Similarity 51.6%; Pred. No. 5.4e+02;
RESULT 1032
ID ADB72545 standard; DNA; 96597 BP.
DE Mouse fish gene.
PN WO200308583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 35.4; DB 10; Length 96597;
Best Local Similarity 51.6%; Pred. No. 5.4e+02;
RESULT 1033
ID ADM74402 standard; DNA; 96597 BP.
DE Murine carcinoma associated (CA) nucleic acid #37.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR) MORRIS D W.
Query Match 2.4%; Score 35.4; DB 12; Length 96597;
Best Local Similarity 51.6%; Pred. No. 5.4e+02;
RESULT 1034
ID ABX16390 standard; DNA; 659158 BP.
DE Mouse high growth region.
PN US2002155564-A1.
PD 24-OCT-2002.
PA (REGC) UNIV CALIFORNIA.
Query Match 2.4%; Score 35.4; DB 8; Length 110000;
Best Local Similarity 56.4%; Pred. No. 5.8e+02;
RESULT 1035
ID ADG70184 standard; DNA; 379652 BP.
DE DNA of BAC BA236m15-00303.
PN WO2003000727-A2.
PD 03-JUN-2003.
PA (ISIS-) ISIS INNOVATIONS LTD.
Query Match 2.4%; Score 35.4; DB 10; Length 110000;
Best Local Similarity 47.2%; Pred. No. 5.8e+02;
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RESULT 1036
ID AD097050 standard; DNA; 687411 BP.
DE Human cancer associated sequence HD08-001, SEQ ID 26.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 35.4; DB 12; Length 110000;
Best Local Similarity 50.9%; Pred. No. 5.8e+02;
RESULT 1037
Query Match 2.4%; Score 35.4; DB 13; Length 110000;
Best Local Similarity 50.9%; Pred. No. 5.8e+02;
RESULT 1038
ID ABD32911 standard; DNA; 783062 BP.
DE Human cancer-associated genomic DNA HD18-043.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 35.4; DB 13; Length 110000;
Best Local Similarity 59.7%; Pred. No. 5.8e+02;
RESULT 1039
ID ABD32886 standard; DNA; 117328 BP.
DE Mouse cancer-associated genomic DNA MD18-013.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 35.4; DB 13; Length 117328;
Best Local Similarity 55.2%; Pred. No. 6e+02;
RESULT 1040
ID ADP80536 standard; DNA; 118788 BP.
DE Human HPC2/ELAC2 gene SeqID1.
PN JP200416565-A.
PD 17-JUN-2004.
PA (TAKA/) TAKAHASHI H.
PA (WATA/) WATANABE M.
PA (FURU/) FURUSATO M.
PA (HONS) YAKULT HONSHA KK.
Query Match 2.4%; Score 35.4; DB 12; Length 118788;
Best Local Similarity 46.2%; Pred. No. 6e+02;
RESULT 1041
ID ABR63573 standard; cDNA; 130263 BP.
DE Human cDNA differentially expressed in granulocytic cells #144.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 2.4%; Score 35.4; DB 6; Length 130263;
Best Local Similarity 63.5%; Pred. No. 6.3e+02;
RESULT 1042
ID ABR39880 standard; cDNA; 406 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #5045.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARRE/) WARREN W C.
Query Match 2.4%; Score 35.2; DB 8; Length 406;
Best Local Similarity 48.1%; Pred. No. 41;
RESULT 1043
ID ADA48417 standard; DNA; 500 BP.
DE Rice gene conferring disease resistance in plants.
PN WO200300906-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.4%; Score 35.2; DB 9; Length 500;
Best Local Similarity 48.1%; Pred. No. 45;
RESULT 1044
ID ADN73638 standard; cDNA; 510 BP.
DE Thale cress cDNA repressed in E2fs/Dpa expressing plants SeqID 1533.
PN WO2004035798-A2.
PD 29-APR-2004.
PA (CROP-) CROPPESIGN NV.
Query Match 2.4%; Score 35.2; DB 12; Length 510;
Best Local Similarity 48.1%; Pred. No. 46;

RESULT 1045
ID ADA9332 standard; cDNA; 557 BP.
DE Bacterial polynucleotide #4075.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 2.4%; Score 35.2; DB 13; Length 557;
Best Local Similarity 60.4%; Pred. No. 48;
RESULT 1046
ID AAC6937 standard; DNA; 594 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO. 51958.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 2.4%; Score 35.2; DB 3; Length 594;
Best Local Similarity 48.1%; Pred. No. 49;
RESULT 1047
ID ABR98560 standard; cDNA; 615 BP.
DE Rice leaf specific expression label sequence #12.
PN CN1364933-A.
PD 21-AUG-2002.
PA (UYZH-) UNIV ZHEJIANG.
Query Match 2.4%; Score 35.2; DB 8; Length 615;
Best Local Similarity 53.3%; Pred. No. 50;
RESULT 1048
ID ADC75910 standard; DNA; 632 BP.
DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 834.
PN WO2003020905-A2.
PD 13-MAR-2003.
PA (DOMC) DOM CHEM CO.
Query Match 2.4%; Score 35.2; DB 10; Length 632;
Best Local Similarity 52.0%; Pred. No. 51;
RESULT 1049
ID ACU2023 standard; DNA; 674 BP.
DE DNA clone originating in barley containing SNP encoding sequence #10014.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UYNI-) UNIV JAPAN OKAYAMA.
Query Match 2.4%; Score 35.2; DB 9; Length 674;
Best Local Similarity 53.7%; Pred. No. 52;
RESULT 1050
ID ACI20017 standard; DNA; 708 BP.
DE DNA clone originating in barley containing SNP encoding sequence #10008.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UYNI-) UNIV JAPAN OKAYAMA.
Query Match 2.4%; Score 35.2; DB 9; Length 708;
Best Local Similarity 53.7%; Pred. No. 54;
RESULT 1051
ID ABR62083 standard; cDNA; 1010 BP.
DE Human cDNA encoding novel secreted protein LP218.
PN WO200214358-A2.
PD 21-FEB-2002.
PA (ELIL) ELIL & CO ELI.
Query Match 2.4%; Score 35.2; DB 6; Length 1010;
Best Local Similarity 50.0%; Pred. No. 64;
RESULT 1052
ID AAF61042 standard; DNA; 2250 BP.
DE P. putida KT2440-associated DNA ORF06553.
PN DE19935086-A1.
PD 01-FEB-2001.
PA (TIGR-) TIGR INST GENOMIC RES.
PA (QUIA-) QUIAGEN GMBH.
PA (GBFZ-) GBS BIOTECHNOLOGISCHE FORSCHUNG MBH.
PA (MEDT-) MEDIZINISCHE HOCHSCHULE HANNOVER.
Query Match 2.4%; Score 35.2; DB 4; Length 2250;
Best Local Similarity 49.0%; Pred. No. 95;
RESULT 1053
ID ADA02845 standard; cDNA; 2403 BP.

DE Mouse Fgf13 carcinoma associated coding sequence, SEQ ID NO:1363.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.4%; Score 35.2; DB 9; Length 2403;
Best Local Similarity 51.2%; Pred. No. 98;
RESULT 1054
ID ADB72583 standard; cDNA; 2403 BP.
DE Mouse Fgf13 cDNA.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.4%; Score 35.2; DB 10; Length 2403;
Best Local Similarity 51.2%; Pred. No. 98;
RESULT 1055
ID ADC85324 standard; DNA; 2403 BP.
DE Mouse Fgf13 mRNA sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.4%; Score 35.2; DB 10; Length 2403;
Best Local Similarity 51.2%; Pred. No. 98;
RESULT 1056
ID ADM74440 standard; DNA; 2403 BP.
DE Murine carcinoma associated (CA) nucleic acid #57.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR/) MORRIS D W.
PA (ENGEL/) ENGELHARD E K.
Query Match 2.4%; Score 35.2; DB 12; Length 2403;
Best Local Similarity 51.2%; Pred. No. 98;
RESULT 1057
ID AAZ09484 standard; DNA; 2606 BP.
DE Bovine retina 1h ion channel DNA fragment.
PN WO9942574-A1.
PD 26-AUG-1999.
PA (KERJ) FORSCHUNGSZENTRUM JUELICH GMBH.
Query Match 2.4%; Score 35.2; DB 2; Length 2606;
Best Local Similarity 57.1%; Pred. No. 1e+02;
RESULT 1058
ID ADK0684 standard; DNA; 2692 BP.
DE HOMO protein encoding sequence #31.
PN WO2004014946-A1.
PD 19-FEB-2004.
PA (NEWO-) NEWORGEN LTD.
Query Match 2.4%; Score 35.2; DB 12; Length 2692;
Best Local Similarity 48.1%; Pred. No. 1e+02;
RESULT 1059
ID ADA02844 standard; cDNA; 2887 BP.
DE Mouse Fgf13 carcinoma associated cDNA, SEQ ID NO:1362.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.4%; Score 35.2; DB 9; Length 2887;
Best Local Similarity 51.2%; Pred. No. 1.1e+02;
RESULT 1060
ID ADB72582 standard; mRNA; 2887 BP.
DE Mouse Fgf13 mRNA.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.4%; Score 35.2; DB 10; Length 2887;
Best Local Similarity 51.2%; Pred. No. 1.1e+02;
RESULT 1061
ID ADC85323 standard; DNA; 2887 BP.
DE Mouse Fgf13 genomic sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.4%; Score 35.2; DB 10; Length 2887;
Best Local Similarity 51.2%; Pred. No. 1.1e+02;
RESULT 1062
ID ADM74439 standard; DNA; 2887 BP.

DE Murine carcinoma associated (CA) nucleic acid #56.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR/) MORRIS D W.
PA (ENGEL/) ENGELHARD E K.
Query Match 2.4%; Score 35.2; DB 12; Length 2887;
Best Local Similarity 51.2%; Pred. No. 1.1e+02;
RESULT 1063
ID AAZ09487 standard; DNA; 2922 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 13216.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PKRE) PE CORP NY.
Query Match 2.4%; Score 35.2; DB 2; Length 2922;
Best Local Similarity 57.1%; Pred. No. 1.1e+02;
RESULT 1064
ID ABL20581 standard; DNA; 3318 BP.
DE Mouse fibroblast growth factor receptor 3 (FGFR3) mutant cDNA.
PN WO200171042-A2.
PD 24-JUL-2001.
PA (VEDA) YEDA RES & DEV CO LTD.
PA (PROCC-) PROCHON BIOTECH LTD.
Query Match 2.4%; Score 35.2; DB 5; Length 3083;
Best Local Similarity 51.2%; Pred. No. 1.8e+02;
RESULT 1065
ID AAD34802 standard; cDNA; 8083 BP.
DE Mouse fibroblast growth factor receptor 3 (FGFR3) mutant cDNA.
PN US6256532-B1.
PD 24-JUL-2001.
PA (VEDA) YEDA RES & DEV CO LTD.
PA (PROCC-) PROCHON BIOTECH LTD.
Query Match 2.4%; Score 35.2; DB 6; Length 17934;
Best Local Similarity 50.9%; Pred. No. 2.7e+02;
RESULT 1067
ID ADE6967 standard; DNA; 34571 BP.
DE Mouse cancer associated gene genomic sequence SEQ ID NO:13.
PN WO2004074321-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 35.2; DB 13; Length 34571;
Best Local Similarity 54.7%; Pred. No. 3.7e+02;
RESULT 1068
ID ACN44230 standard; DNA; 66973 BP.
DE Human genomic sequence hCG21559.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.4%; Score 35.2; DB 11; Length 66973;
Best Local Similarity 52.0%; Pred. No. 5.2e+02;
RESULT 1070
ID ADS73531 standard; cDNA; 73882 BP.
DE tcp gene cluster.
Query Match 2.4%; Score 35.2; DB 13; Length 73882;
Best Local Similarity 52.0%; Pred. No. 5.4e+02;
RESULT 1071
ID ACN44380 standard; DNA; 76846 BP.
DE Mouse genomic sequence mCG18525.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.4%; Score 35.2; DB 11; Length 76846;
Best Local Similarity 58.7%; Pred. No. 5.5e+02;
RESULT 1072

ID ADC86916 standard; DNA; 349989 BP.
DE Human GPCR gene SEQ ID NO:1369.
PN EPI270724-A2.
PD 02-JAN-2003.
PA (NACD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ABSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 2.4%; Score 35.2; DB 10; Length 349989;
Best Local Similarity 65.0%; Pred. No. 1.1e+03;
RESULT 1073

ID ADA58745 standard; cDNA; 224 BP.
DE Maize sucrose synthase EST #389.
PN US2003135870-A1.
PD 17-JUL-2003.
PA (CHEI/) CHEIKH N.
PA (FISH/) FISHER D K.
PA (LIU/) LIU J.
Query Match 2.4%; Score 35; DB 9; Length 224;
Best Local Similarity 55.3%; Pred. No. 34;
RESULT 1074

ID ADA58686 standard; cDNA; 235 BP.
DE Maize sucrose synthase EST #330.
PN US2003135870-A1.
PD 17-JUL-2003.
PA (CHEI/) CHEIKH N.
PA (FISH/) FISHER D K.
PA (LIU/) LIU J.
Query Match 2.4%; Score 35; DB 9; Length 235;
Best Local Similarity 55.3%; Pred. No. 35;
RESULT 1075

ID ADA58541 standard; cDNA; 270 BP.
DE Maize sucrose synthase EST #185.
PN US2003135870-A1.
PD 17-JUL-2003.
PA (CHEI/) CHEIKH N.
PA (FISH/) FISHER D K.
PA (LIU/) LIU J.
Query Match 2.4%; Score 35; DB 9; Length 270;
Best Local Similarity 55.3%; Pred. No. 38;
RESULT 1076

ID ADA49273 standard; DNA; 339 BP.
DE Maize gene conferring disease resistance in plants.
PN WO2003000906-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.4%; Score 35; DB 9; Length 339;
Best Local Similarity 48.7%; Pred. No. 42;
RESULT 1077

ID ABX40527 standard; cDNA; 344 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #5692.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARB/) WARREN W C.
Query Match 2.4%; Score 35; DB 8; Length 344;
Best Local Similarity 45.5%; Pred. No. 43;
RESULT 1078

ID ADO19577 standard; DNA; 393 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2396.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.4%; Score 35; DB 12; Length 393;
Best Local Similarity 50.3%; Pred. No. 45;
RESULT 1079

ID ACH44942 standard; cDNA; 487 BP.
DE Human foetal brain cDNA #5667.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.

PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 2.4%; Score 35; DB 9; Length 487;
Best Local Similarity 61.5%; Pred. No. 51;
RESULT 1080

ID AAH10073 standard; cDNA; 547 BP.
DE Human cDNA clone (3'-primer) SEQ ID NO:6908.
PN EPI074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 2.4%; Score 35; DB 4; Length 547;
Best Local Similarity 50.9%; Pred. No. 54;
RESULT 1081

ID ACH72546 standard; DNA; 598 BP.
DE Human genome derived single exon probe #5741.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 2.4%; Score 35; DB 12; Length 598;
Best Local Similarity 59.6%; Pred. No. 56;
RESULT 1082

ID ADA68731 standard; DNA; 805 BP.
DE Rice gene, SEQ ID 2054.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.4%; Score 35; DB 8; Length 805;
Best Local Similarity 47.8%; Pred. No. 65;
RESULT 1083

ID AAS44974 standard; cDNA; 814 BP.
DE cDNA encoding novel human secretory protein, Seq ID No 55.
PN WO200166689-A2.
PD 13-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.4%; Score 35; DB 5; Length 814;
Best Local Similarity 46.2%; Pred. No. 65;
RESULT 1084

ID ADY43885 standard; cDNA; 870 BP.
DE Bacterial polynucleotide #18636.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOV/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 2.4%; Score 35; DB 13; Length 870;
Best Local Similarity 48.7%; Pred. No. 68;
RESULT 1085

ID ADP28033 standard; DNA; 1176 BP.
DE Human secreted protein encoding sequence SEQ ID #31.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 2.4%; Score 35; DB 12; Length 1176;
Best Local Similarity 61.5%; Pred. No. 78;
RESULT 1086

ID ADM47892 standard; DNA; 1216 BP.
DE Polynucleotide sequence #310 useful in producing transgenic plants.
PN US2003233670-A1.
PD 18-DEC-2003.
PA (EDGE/) EDGERTON M D.
PA (CHOM/) CHOMET P S.
PA (LACC/) LACCETTI L B.
Query Match 2.4%; Score 35; DB 12; Length 1216;
Best Local Similarity 47.5%; Pred. No. 80;
RESULT 1087

ID ABD08729 standard; DNA; 1488 BP.
DE Pseudomonas aeruginosa polynucleotide #7333.
PN US6551795-B1.
PD 22-APR-2003.

PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.4%; Score 35; DB 11; Length 1488;
Best Local Similarity 50.3%; Pred. No. 88;
RESULT 1088
ID ADE76934 standard; cDNA; 1498 BP.
DE Human cDNA differentially expressed in a liver disorder #71.
PN US200310871-A1.
PD 12-JUN-2003.
PA (KASE/) KASER M R.
Query Match 2.4%; Score 35; DB 12; Length 1498;
Best Local Similarity 61.5%; Pred. No. 88;
RESULT 1089
ID AA190669 standard; cDNA; 1520 BP.
DE Human polynucleotide SEQ ID NO 10729.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.4%; Score 35; DB 4; Length 1520;
Best Local Similarity 59.6%; Pred. No. 89;
RESULT 1090
ID ABD08808 standard; DNA; 1593 BP.
DE Pseudomonas aeruginosa polynucleotide #7412.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.4%; Score 35; DB 11; Length 1593;
Best Local Similarity 50.3%; Pred. No. 91;
RESULT 1091
ID ADP28053 standard; DNA; 1692 BP.
DE Human secreted protein encoding sequence SEQ ID #51.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 2.4%; Score 35; DB 12; Length 1692;
Best Local Similarity 61.5%; Pred. No. 94;
RESULT 1092
ID ADP28010 standard; DNA; 1692 BP.
DE Human secreted protein encoding sequence SEQ ID #8.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 2.4%; Score 35; DB 12; Length 1692;
Best Local Similarity 61.5%; Pred. No. 94;
RESULT 1093
ID ADE47787 standard; DNA; 1698 BP.
DE Human NOV45e gene SEQ ID NO:149.
PN WO2003076642-A2.
PD 18-SEP-2003.
PA (CURA-) CURAGEN CORP.
Query Match 2.4%; Score 35; DB 10; Length 1698;
Best Local Similarity 56.5%; Pred. No. 94;
RESULT 1094
ID ADH41894 standard; DNA; 1698 BP.
DE Novel human nucleic acid NOV36b.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 2.4%; Score 35; DB 12; Length 1698;
Best Local Similarity 56.5%; Pred. No. 94;
RESULT 1095
ID ADJ79057 standard; DNA; 1698 BP.
DE Human NOVX protein NOV45E gene sequence.
PN US2004014053-A1.
PD 22-JAN-2004.
PA (ZERRH/) ZERRHUSEN B D.
PA (PAT/) PATURAJAN M.
PA (KEKU/) KEKUDA R.
PA (MILL/) MILLER C E.
PA (RIEG/) RIEGER D K.
PA (PENNA/) PENNA C E A.
PA (SHIM/) SHIMKETS R A.
PA (LILL/) LI L.
PA (BERG/) BERGHS C.

PA (ZHON/) ZHONG M.
PA (CASW/) CASMAN S J.
PA (VOSS/) VOSS E Z.
PA (BOLD/) BOLDOG F L.
PA (PADI/) PADIGARU M.
PA (SMIT/) SMITHSON G.
PA (JIMW/) JI W.
PA (GORM/) GORMAN L.
PA (VERN/) VERNET C A M.
PA (LEIT/) LEITE M W.
PA (GUOX/) GUO X S.
PA (ANDE/) ANDERSON D W.
PA (SPYT/) SPYTEK K A.
PA (GERL/) GERLACH V.
PA (BURG/) BURGESS C E.
PA (KIRA/) KIRAMTSOV N V.
PA (ORTY/) ORT T.
PA (ELLE/) ELLERMAN K.
PA (RAST/) RASTELLI L.
PA (AGEE/) AGE E M L.
PA (CHAU/) CHAUDHURI A.
PA (CHAN/) CHANT J S.
PA (DIP/) DIPPO V A.
PA (EDIN/) EDINGER S R.
PA (EISE/) EISEN A J.
PA (GANG/) GANGOLI E A.
PA (GIOT/) GIOT L.
PA (OOIC/) OOI C E.
PA (ROTH/) ROTHENBERG M E.
PA (SPAD/) SPADERNA S K.
PA (HJAL/) HJALT T.
PA (LIUX/) LIU X.
PA (TAUP/) TAUPFER R J.
PA (CAT/) CATTERTON E.
PA (SHEN/) SHENOY S G.
Query Match 2.4%; Score 35; DB 12; Length 1698;
Best Local Similarity 56.5%; Pred. No. 94;
RESULT 1096
ID AAH17389 standard; cDNA; 1851 BP.
DE Human cDNA sequence SEQ ID NO:16827.
PN EP074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 2.4%; Score 35; DB 4; Length 1851;
Best Local Similarity 50.3%; Pred. No. 98;
RESULT 1097
ID ABA08292 standard; cDNA; 1890 BP.
DE Human equine herpesvirus p24 homologue-encoding cDNA, SEQ ID NO:68.
PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.4%; Score 35; DB 4; Length 1890;
Best Local Similarity 49.7%; Pred. No. 99;
RESULT 1098
ID ABR08324 standard; DNA; 2011 BP.
DE Human NOV7 gene sequence.
PN WO200246408-A2.
PD 13-JUN-2002.
PA (CURA-) CURAGEN CORP.
Query Match 2.4%; Score 35; DB 6; Length 2011;
Best Local Similarity 61.5%; Pred. No. 1e+02;
RESULT 1099
ID ABS59330 standard; DNA; 2011 BP.
DE Human macrophage stimulating protein precursor-like gene.
PN WO200233087-A2.
PD 25-APR-2002.
PA (CURA-) CURAGEN CORP.
Query Match 2.4%; Score 35; DB 6; Length 2011;
Best Local Similarity 61.5%; Pred. No. 1e+02;
RESULT 1100
ID ADJ38433 standard; cDNA; 2011 BP.
DE Human cDNA encoding protein NOV5.
PN US2003212256-A1.

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PD 13-NOV-2003.
PA (EDIN/) EDINGER S R.
PA (GERL/) GERLACH V.
PA (MACD/) MACDOUGALL J R.
PA (MALY/) MALYANKAR U M.
PA (SMIT/) SMITHSON G.
PA (MILL/) MILLER I.
PA (PEYM/) PEYMAN J A.
PA (STON/) STONE D J.
PA (GUNT/) GUNTHER E.
PA (ELLE/) ELLERMAN K.
PA (SHIM/) SHIMKETS R A.
PA (PADI/) PADIGARU M.
PA (GUOX/) GUO X.
PA (PATP/) PATTURAJAN M.
PA (TAUP/) TAUPIER R J.
PA (BURG/) BURGESS C E.
PA (ZERR/) ZERRHUSEN B D.
PA (KERU/) KERUDA R.
PA (SPYT/) SPYTEK K A.
PA (GANG/) GANGOLLI E A.
PA (FERN/) FERNANDES E R.
PA (GORM/) GORMAN L.
Query Match
Best Local Similarity 2.4%; Score 35; DB 10; Length 2011;
RESULT 1101
ID AAS83813 standard; cDNA; 2052 BP.
DE DNA encoding novel human diagnostic protein #19617.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 2.4%; Score 35; DB 5; Length 2052;
RESULT 1102
ID AD74313 standard; cDNA; 2139 BP.
DE Bacterial polynucleotide #18064.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 2.4%; Score 35; DB 13; Length 2139;
RESULT 1103
ID ABR92065 standard; DNA; 2200 BP.
DE DNA encoding novel hepatocyte growth factor-like protein #2.
PN WO200229058-A2.
PD 11-APR-2002.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 2.4%; Score 35; DB 6; Length 2200;
RESULT 1104
ID ABR92064 standard; DNA; 2200 BP.
DE DNA encoding novel hepatocyte growth factor-like protein #1.
PN WO200229058-A2.
PD 11-APR-2002.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 2.4%; Score 35; DB 6; Length 2200;
RESULT 1105
ID AAD26582 standard; cDNA; 2200 BP.
DE Human MSP precursor-like protein, POLY13 encoding cDNA.
PN WO200185767-A2.
PD 15-NOV-2001.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 2.4%; Score 35; DB 6; Length 2200;
RESULT 1106
ID ADE47779 standard; DNA; 2200 BP.
DE Human NOV45a gene SEQ ID NO:141.
PN WO2003076642-A2.

PD 18-SEP-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 2.4%; Score 35; DB 10; Length 2200;
RESULT 1107
ID ADH41896 standard; DNA; 2200 BP.
DE Novel human nucleic acid NOV36C.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 2.4%; Score 35; DB 12; Length 2200;
RESULT 1108
ID ADJ79049 standard; DNA; 2200 BP.
DE Human NOVX protein NOV45A gene sequence.
PN US2004014053-A1.
PD 22-JAN-2004.
PA (ZERR/) ZERRHUSEN B D.
PA (PATP/) PATTURAJAN M.
PA (KERU/) KERUDA R.
PA (MILL/) MILLER C E.
PA (RIEG/) RIEGER D K.
PA (PENA/) PENNA C E A.
PA (SHIM/) SHIMKETS R A.
PA (LITL/) LI L.
PA (BERG/) BERGHS C.
PA (ZHON/) ZHONG M.
PA (CASM/) CASHMAN S J.
PA (VOSS/) VOSS E Z.
PA (BOLD/) BOLDOG F L.
PA (PADI/) PADIGARU M.
PA (SMIT/) SMITHSON G.
PA (JITW/) JI W.
PA (GORM/) GORMAN L.
PA (VERN/) VERNET C A M.
PA (LEIT/) LEITE M W.
PA (GUOX/) GUO X S.
PA (ANDE/) ANDERSON D W.
PA (SPYT/) SPYTEK K A.
PA (GERL/) GERLACH V.
PA (BURG/) BURGESS C E.
PA (KERA/) KHRAMTSOV N V.
PA (ORRT/) ORT T.
PA (ELLE/) ELLERMAN K.
PA (RAST/) RASTBILI L.
PA (AGEE/) AGEE M L.
PA (CHAU/) CHAUDHURI A.
PA (CHAN/) CHANT J S.
PA (DIPJ/) DIPIPPO V A.
PA (EDIN/) EDINGER S R.
PA (EISE/) EISEN A J.
PA (GANG/) GANGOLLI E A.
PA (GIOT/) GIOT L.
PA (OOIC/) OOI C E.
PA (ROTH/) ROTHENBERG M E.
PA (SPAD/) SPADERNA S K.
PA (HUAL/) HUALT T.
PA (LITX/) LIU X.
PA (TAUP/) TAUPIER R J.
PA (CATP/) CATERTON E.
PA (SHEN/) SHENOY S G.
Query Match
Best Local Similarity 2.4%; Score 35; DB 12; Length 2200;
RESULT 1109
ID AAS83814 standard; cDNA; 2296 BP.
DE DNA encoding novel human diagnostic protein #19618.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 2.4%; Score 35; DB 5; Length 2296;
RESULT 1110
ID ACN41132 standard; cDNA; 2533 BP.
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DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:7.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 2.4%; Score 35; DB 13; Length 2533;
Best Local Similarity 61.5%; Pred. No. 1.1e+02;
RESULT 1111
ID ADQ25501 standard; DNA; 2768 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 8321.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.4%; Score 35; DB 12; Length 2768;
Best Local Similarity 44.3%; Pred. No. 1.2e+02;
RESULT 1112
ID ADK18361 standard; DNA; 3570 BP.
DE Human NOVX protein encoding gene #8.
PN WO2003057854-A2.
PD 17-JUL-2003.
PA (CURA-) CURAGEN CORP.
Query Match 2.4%; Score 35; DB 10; Length 3570;
Best Local Similarity 55.3%; Pred. No. 1.4e+02;
RESULT 1113
ID ADK18363 standard; DNA; 4775 BP.
DE Human NOVX protein encoding gene #9.
PN WO2003057854-A2.
PD 17-JUL-2003.
PA (CURA-) CURAGEN CORP.
Query Match 2.4%; Score 35; DB 10; Length 4775;
Best Local Similarity 55.3%; Pred. No. 1.6e+02;
RESULT 1114
ID AAS83815 standard; cDNA; 5635 BP.
DE DNA encoding novel human diagnostic protein #19619.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HISE-) HISEQ INC.
Query Match 2.4%; Score 35; DB 5; Length 5635;
Best Local Similarity 61.5%; Pred. No. 1.7e+02;
RESULT 1115
ID ADK18365 standard; DNA; 5760 BP.
DE Human NOVX protein encoding gene #10.
PN WO2003057854-A2.
PD 17-JUL-2003.
PA (CURA-) CURAGEN CORP.
Query Match 2.4%; Score 35; DB 10; Length 5760;
Best Local Similarity 55.3%; Pred. No. 1.7e+02;
RESULT 1116
ID ADK18367 standard; DNA; 6008 BP.
DE Human NOVX protein encoding gene #11.
PN WO2003057854-A2.
PD 17-JUL-2003.
PA (CURA-) CURAGEN CORP.
Query Match 2.4%; Score 35; DB 10; Length 6008;
Best Local Similarity 55.3%; Pred. No. 1.8e+02;
RESULT 1117
ID ADP13461 standard; DNA; 6008 BP.
DE Renal cell carcinoma differentially expressed gene #197.
PN WO2004048933-A2.
PD 10-JUN-2004.
PA (AMHP-) WYETH.
PA (TWIN-) TWINE N C.
PA (BURC-) BURCZYNSKI M E.
PA (TREP-) TREPICCHIO W L.
PA (DORN-) DORNER A.
PA (STOV-) STOVER U A.
PA (SLON-) SLONI D K.
Query Match 2.4%; Score 35; DB 12; Length 6008;
Best Local Similarity 55.3%; Pred. No. 1.8e+02;
RESULT 1118
ID ADC86968 standard; DNA; 6269 BP.
DE Human GPCR gene SEQ ID NO:1421.
PN EP1270724-A2.
PD 02-JAN-2003.

PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 2.4%; Score 35; DB 10; Length 6269;
Best Local Similarity 46.8%; Pred. No. 1.8e+02;
RESULT 1119
ID AA105754 standard; DNA; 6647 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8442.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.4%; Score 35; DB 4; Length 6647;
Best Local Similarity 59.6%; Pred. No. 1.9e+02;
RESULT 1120
ID ABA20362 standard; DNA; 6647 BP.
DE Human nervous system related polynucleotide SEQ ID NO 12693.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.4%; Score 35; DB 5; Length 6647;
Best Local Similarity 59.6%; Pred. No. 1.9e+02;
RESULT 1121
ID ADS52723 standard; DNA; 6957 BP.
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3265.
PN WO2003065993-A2.
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 2.4%; Score 35; DB 10; Length 6957;
Best Local Similarity 51.6%; Pred. No. 1.9e+02;
RESULT 1122
ID ADC86850 standard; DNA; 8360 BP.
DE Human GPCR gene SEQ ID NO:1303.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 2.4%; Score 35; DB 10; Length 8360;
Best Local Similarity 48.7%; Pred. No. 2.1e+02;
RESULT 1123
ID ADQ91701 standard; DNA; 10287 BP.
DE Polypeptide synthase ORF11, SEQ ID 24.
PN WO2004065401-A1.
PD 05-AUG-2004.
PA (ECOP-) ECOP1A BIOSCIENCES INC.
Query Match 2.4%; Score 35; DB 13; Length 10287;
Best Local Similarity 57.9%; Pred. No. 2.3e+02;
RESULT 1124
ID AA105755 standard; DNA; 16579 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8443.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.4%; Score 35; DB 4; Length 16579;
Best Local Similarity 59.6%; Pred. No. 2.9e+02;
RESULT 1125
ID ABA20363 standard; DNA; 16579 BP.
DE Human nervous system related polynucleotide SEQ ID NO 12694.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.4%; Score 35; DB 5; Length 16579;
Best Local Similarity 59.6%; Pred. No. 2.9e+02;
RESULT 1126
ID ACN44588 standard; DNA; 33454 BP.
DE Mouse genomic sequence mCG22056.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.4%; Score 35; DB 11; Length 33454;
Best Local Similarity 52.4%; Pred. No. 4.1e+02;
RESULT 1128

ID AAK83781 standard; DNA; 37664 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38593.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCT INC.
Query Match 2.4%; Score 35; DB 4; Length 37664;
Best Local Similarity 54.2%; Pred. No. 4.4e+02;
RESULT 1129
ID ACN44064 standard; DNA; 44748 BP.
DE Mouse genomic sequence MCG13520.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.4%; Score 35; DB 11; Length 44748;
Best Local Similarity 47.9%; Pred. No. 4.8e+02;
RESULT 1130
ID ACN44456 standard; DNA; 56258 BP.
DE Mouse genomic sequence MCG19337.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.4%; Score 35; DB 11; Length 56258;
Best Local Similarity 54.2%; Pred. No. 5.4e+02;
RESULT 1131
ID AAK83782 standard; DNA; 61710 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38594.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCT INC.
Query Match 2.4%; Score 35; DB 4; Length 61710;
Best Local Similarity 54.2%; Pred. No. 5.6e+02;
RESULT 1132
ID ADA02747 standard; DNA; 96599 BP.
DE Mouse Irf2 carcinoma associated gene, SEQ ID NO:1265.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.4%; Score 35; DB 9; Length 96599;
Best Local Similarity 54.2%; Pred. No. 7e+02;
RESULT 1133
ID ADB72485 standard; DNA; 96599 BP.
DE Mouse Irf2 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.4%; Score 35; DB 10; Length 96599;
Best Local Similarity 54.2%; Pred. No. 7e+02;
RESULT 1134
ID ADC85227 standard; DNA; 96599 BP.
DE Mouse Irf2 genomic sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.4%; Score 35; DB 10; Length 96599;
Best Local Similarity 54.2%; Pred. No. 7e+02;
RESULT 1135
ID ADM74342 standard; DNA; 96599 BP.
DE Murine carcinoma associated (CA) nucleic acid #7.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR/) MORRIS D W.
PA (ENGE/) ENGELHARD E K.
Query Match 2.4%; Score 35; DB 12; Length 96599;
Best Local Similarity 54.2%; Pred. No. 7e+02;
RESULT 1136
ID ADN30326 standard; DNA; 121434 BP.
DE Human Notch2 genomic DNA region #1.
PN US2004101847-A1.
PD 27-MAY-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match 2.4%; Score 35; DB 12; Length 121434;
Best Local Similarity 52.4%; Pred. No. 7.8e+02;
RESULT 1137

ID ADQ59431 standard; DNA; 154504 BP.
DE Human cancer-associated (CA) gene sequence SEQ ID NO:67.
PN WO2004058288-A1.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 35; DB 12; Length 154504;
Best Local Similarity 52.4%; Pred. No. 8.8e+02;
RESULT 1138
ID ADQ97891 standard; DNA; 155083 BP.
DE Mouse cancer associated sequence MD11-020, SEQ ID 868.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 35; DB 12; Length 155083;
Best Local Similarity 57.9%; Pred. No. 8.8e+02;
RESULT 1139
ID ADQ91695 standard; DNA; 164051 BP.
DE Polyketide synthase related DNA config 2, SEQ ID 18.
PN WO2004065401-A1.
PD 05-AUG-2004.
PA (ECOP-) ECOPHA BIOSCIENCES INC.
Query Match 2.4%; Score 35; DB 13; Length 164051;
Best Local Similarity 57.9%; Pred. No. 9e+02;
RESULT 1140
ID ADQ97362 standard; DNA; 215126 BP.
DE Mouse cancer associated sequence MD08-038, SEQ ID 339.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.4%; Score 35; DB 12; Length 215126;
Best Local Similarity 30.6%; Pred. No. 1e+03;
RESULT 1141
ID ADA70687 standard; DNA; 410 BP.
DE Rice gene, SEQ ID 4010.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.3%; Score 34.8; DB 8; Length 410;
Best Local Similarity 48.9%; Pred. No. 53;
RESULT 1142
ID AA182119 standard; cDNA; 415 BP.
DE Human polynucleotide SEQ ID NO 2179.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.3%; Score 34.8; DB 4; Length 415;
Best Local Similarity 48.9%; Pred. No. 53;
RESULT 1143
ID AAC10054 standard; cDNA; 530 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 14129.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 2.3%; Score 34.8; DB 3; Length 530;
Best Local Similarity 42.0%; Pred. No. 60;
RESULT 1144
ID ABX56967 standard; DNA; 568 BP.
DE Arabidopsis thaliana polynucleotide #319.
PN US2002040489-A1.
PD 04-APR-2002.
PA (GORL/) GORLACH J.
PA (ANYV/) AN Y.
PA (HAMT/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (RAIN/) RAINES T M.
PA (YUYV/) YU Y.
PA (RAME/) RAMEKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHEW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.

PA (KRIC/) KRICKER M.
PA (SLAT/) SLATER T.
PA (DAVI/) DAVIS K R.
PA (ALLE/) ALLEN K.
PA (HOFF/) HOFFMAN N.
PA (HURB/) HURBAN P.
Query Match
Best Local Similarity 2.3%; Score 34.8; DB 10; Length 568;
RESULT 1145
ID ADL12630 standard; cDNA; 694 BP.
DE Human steroid-induced C3A liver cell cDNA #359.
PN US6673549-B1.
PD 06-JUN-2004.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 2.3%; Score 34.8; DB 12; Length 694;
RESULT 1146
ID ADJ42637 standard; cDNA; 747 BP.
DE Plant cDNA #3637.
PN US2004016025-A1.
PD 22-JUN-2004.
PA (BUDW/) BUDWORTH P.
PA (MORG/) MORGANER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KRER/) KREPS J.
PA (PROV/) PROVANT N.
PA (RICK/) RICE D.
PA (ZHUT/) ZHU T.
Query Match
Best Local Similarity 2.3%; Score 34.8; DB 12; Length 747;
RESULT 1147
ID AAC39827 standard; DNA; 751 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 26049.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 2.3%; Score 34.8; DB 3; Length 751;
RESULT 1148
ID ABL13473 standard; cDNA; 935 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 34901.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 2.3%; Score 34.8; DB 4; Length 935;
RESULT 1149
ID AAT70982 standard; cDNA; 1176 BP.
DE Rat histamine H4 receptor cDNA.
PN WO200192485-A1.
PD 06-DEC-2001.
PA (ORTH) ORTHO-MCNEIL PHARM INC.
Query Match
Best Local Similarity 2.3%; Score 34.8; DB 6; Length 1176;
RESULT 1150
ID ADA49077 standard; DNA; 1290 BP.
DE Wheat gene conferring disease resistance in plants.
PN WO2000300906-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match
Best Local Similarity 2.3%; Score 34.8; DB 9; Length 1290;
RESULT 1151
ID AAX90405 standard; DNA; 1375 BP.
DE Actinomadura sp. DSM43186 35 kDa xylanase encoding DNA.
PN US935836-A.
PD 10-AUG-1999.
PA (ROHG) ROEHM ENZYME FINLAND OY.
Query Match
Best Local Similarity 2.3%; Score 34.8; DB 2; Length 1375;
PA (SLAT/) SLATER S C.

RESULT 1152
ID AAT64930 standard; DNA; 1375 BP.
DE Actinomadura flexuosa 35 kDa (AM35) xylanase encoding DNA.
PN WO9727306-A1.
PD 31-JUL-1997.
PA (ALKO-) ALKO GROUP LTD.
Query Match
Best Local Similarity 2.3%; Score 34.8; DB 2; Length 1375;
RESULT 1153
ID AAC59256 standard; cDNA; 1607 BP.
DE Human secreted protein cDNA sequence #42.
PN WO200055199-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 2.3%; Score 34.8; DB 3; Length 1607;
RESULT 1154
ID ACA27405 standard; DNA; 1837 BP.
DE Prokaryotic essential gene #9062.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 2.3%; Score 34.8; DB 8; Length 1837;
RESULT 1155
ID ADQ35997 standard; DNA; 1956 BP.
DE Novel mouse gene sequence #670.
PN WO2004046310-A2.
PD 03-JUN-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match
Best Local Similarity 2.3%; Score 34.8; DB 12; Length 1956;
RESULT 1156
ID AAS68016 standard; cDNA; 1999 BP.
DE DNA encoding novel human diagnostic protein #3820.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 2.3%; Score 34.8; DB 5; Length 1999;
RESULT 1157
ID ACA27342 standard; DNA; 2028 BP.
DE Prokaryotic essential gene #8999.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 2.3%; Score 34.8; DB 8; Length 2028;
RESULT 1158
ID ADB63067 standard; cDNA; 2077 BP.
DE Human cDNA encoding clone SMINT20007470.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match
Best Local Similarity 2.3%; Score 34.8; DB 10; Length 2077;
RESULT 1159
ID AAS83500 standard; cDNA; 2484 BP.
DE Bacterial polynucleotide #19304.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 2.3%; Score 34.8; DB 5; Length 2484;
RESULT 1160
ID AOT45909 standard; cDNA; 2484 BP.
DE Bacterial polynucleotide #20660.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.

PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 2.3%; Score 34.8; DB 13; Length 2484;
Best Local Similarity 49.5%; Pred. No. 1.3e+02;
RESULT 1161
ID AAS56030 standard; DNA; 2679 BP.
DE Salmonella typhi DNA for cellular proliferation protein #63.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 2.3%; Score 34.8; DB 4; Length 2679;
Best Local Similarity 58.8%; Pred. No. 1.3e+02;
RESULT 1162
ID ACAS1586 standard; DNA; 2679 BP.
DE Prokaryotic essential gene #33243.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 2.3%; Score 34.8; DB 8; Length 2679;
Best Local Similarity 58.8%; Pred. No. 1.3e+02;
RESULT 1163
ID ABZ23911 standard; DNA; 3108 BP.
DE Human 3OST4 polypeptide encoding DNA.
PN WO200292849-A2.
PD 21-NOV-2002.
PA (ASTR-) ASTRAZENCA UK LTD.
Query Match 2.3%; Score 34.8; DB 8; Length 3108;
Best Local Similarity 53.7%; Pred. No. 1.4e+02;
RESULT 1164
ID ACF04819 standard; DNA; 3153 BP.
DE Mlichenicola melithiazol synthesis gene Mel B.
PN WO2003080828-A2.
PD 02-OCT-2003.
PA (GFPB) GFP GES BIOTECH FORSCHUNG GMBH.
Query Match 2.3%; Score 34.8; DB 10; Length 3153;
Best Local Similarity 50.6%; Pred. No. 1.5e+02;
RESULT 1165
ID ADS47373 standard; cDNA; 3237 BP.
DE Bacterial polynucleotide #2116.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HTNK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 2.3%; Score 34.8; DB 13; Length 3237;
Best Local Similarity 52.0%; Pred. No. 1.5e+02;
RESULT 1166
ID AAX37250 standard; DNA; 3658 BP.
DE Human 3-OST-4 encoding DNA.
PN WO9922005-A2.
PD 06-MAY-1999.
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
Query Match 2.3%; Score 34.8; DB 2; Length 3658;
Best Local Similarity 53.7%; Pred. No. 1.6e+02;
RESULT 1167
ID ABA15504 standard; DNA; 4034 BP.
DE Human nervous system related polynucleotide SEQ ID NO 7835.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.3%; Score 34.8; DB 5; Length 4034;
Best Local Similarity 54.8%; Pred. No. 1.6e+02;
RESULT 1168
ID ABA16206 standard; DNA; 4034 BP.
DE Human nervous system related polynucleotide SEQ ID NO 8537.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.3%; Score 34.8; DB 5; Length 4034;
Best Local Similarity 54.8%; Pred. No. 1.6e+02;
RESULT 1169
ID AAX37251 standard; DNA; 4045 BP.
DE Human 3-OST-4 5' promoter and exon sequence.
PN WO9922005-A2.
PD 06-MAY-1999.
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
Query Match 2.3%; Score 34.8; DB 2; Length 4045;
Best Local Similarity 53.7%; Pred. No. 1.6e+02;
RESULT 1170
ID AAS28590 standard; DNA; 4172 BP.
DE Genomic sequence #430 encoding for novel human respiratory antigen.
PN WO200155448-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.3%; Score 34.8; DB 4; Length 4172;
Best Local Similarity 57.3%; Pred. No. 1.7e+02;
RESULT 1171
ID ADG41786 standard; DNA; 4172 BP.
DE Human respiratory system associated genomic DNA seq id 1024.
PN US2003215893-A1.
PD 20-NOV-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.3%; Score 34.8; DB 10; Length 4172;
Best Local Similarity 57.3%; Pred. No. 1.7e+02;
RESULT 1172
ID ADI97560 standard; DNA; 4172 BP.
DE Human respiratory system associated polypeptide-related DNA SeqID1024.
PN US200307704-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.3%; Score 34.8; DB 11; Length 4172;
Best Local Similarity 57.3%; Pred. No. 1.7e+02;
RESULT 1173
ID AAI10263 standard; DNA; 11883 BP.
DE Bordetella pertussis filamentous haemagglutinin gene, fHAB.
PN US6036960-A.
PD 14-MAR-2000.
PA (RELM/) RELMAN D A.
PA (DOME/) DOMENIGHINI M.
PA (RAIP/) RAPPUOLI R.
PA (FALK/) FALKOW S.
Query Match 2.3%; Score 34.8; DB 3; Length 11883;
Best Local Similarity 49.5%; Pred. No. 2.8e+02;
RESULT 1174
ID AAQ04668 standard; DNA; 12036 BP.
DE FHA structural gene, fHAB.
PN WO9904641-A.
PD 03-MAY-1990.
PA (STRD) UNIV IELAND STANFORD JUNIOR.
PA (ISTS) SCLAVO SPA.
Query Match 2.3%; Score 34.8; DB 2; Length 12036;
Best Local Similarity 49.5%; Pred. No. 2.8e+02;
RESULT 1175
ID ABZ23912 standard; DNA; 12277 BP.
DE Human 3OST4 genomic DNA fragment.
PN WO200292849-A2.
PD 21-NOV-2002.
PA (ASTR-) ASTRAZENCA UK LTD.
Query Match 2.3%; Score 34.8; DB 8; Length 12277;
Best Local Similarity 53.7%; Pred. No. 2.9e+02;
RESULT 1176
ID AEN97984 standard; DNA; 13695 BP.
DE FMR2 coding sequence.
PN WO9967395-A1.
PD 29-DEC-1999.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
Query Match 2.3%; Score 34.8; DB 3; Length 13695;
Best Local Similarity 48.3%; Pred. No. 3e+02;
RESULT 1177
ID AAK89020 standard; DNA; 32152 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 2596.
PN WO200155314-A2.

PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.3%; Score 34.8; DB 4; Length 32152;
Best Local Similarity 55.9%; Pred. No. 4.6e+02;
RESULT 1178
ID AAK91534 standard; DNA; 32152 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 5110.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.3%; Score 34.8; DB 4; Length 32152;
Best Local Similarity 55.9%; Pred. No. 4.6e+02;
RESULT 1179
ID AAI57791 standard; DNA; 32152 BP.
DE Human colorectal cancer antigen coding sequence SEQ ID NO: 328.
PN WO200155350-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.3%; Score 34.8; DB 4; Length 32152;
Best Local Similarity 55.9%; Pred. No. 4.6e+02;
RESULT 1180
ID AAS39621 standard; DNA; 32152 BP.
DE Genomic sequence #40 encoding human colon associated polypeptide.
PN WO200155302-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.3%; Score 34.8; DB 5; Length 32152;
Best Local Similarity 55.9%; Pred. No. 4.6e+02;
RESULT 1181
ID ABS99968 standard; DNA; 32152 BP.
DE Genomic DNA #172 encoding human colorectal cancer related protein.
PN US2002119919-A1.
PD 29-AUG-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.3%; Score 34.8; DB 6; Length 32152;
Best Local Similarity 55.9%; Pred. No. 4.6e+02;
RESULT 1182
ID ADB32561 standard; DNA; 32152 BP.
DE Human novel colon related polypeptide DNA SEQ ID NO 518.
PN US2003050231-A1.
PD 13-MAR-2003.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.3%; Score 34.8; DB 9; Length 32152;
Best Local Similarity 55.9%; Pred. No. 4.6e+02;
RESULT 1183
ID ADB93121 standard; DNA; 32152 BP.
DE Human colorectal cancer related polypeptide DNA #172.
PN US2003054420-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.3%; Score 34.8; DB 10; Length 32152;
Best Local Similarity 55.9%; Pred. No. 4.6e+02;
RESULT 1184
ID AAK66362 standard; DNA; 36933 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21174.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.3%; Score 34.8; DB 4; Length 36933;
Best Local Similarity 55.9%; Pred. No. 5e+02;
RESULT 1185
ID AAX23520 standard; DNA; 45546 BP.
DE Human kidney aminopeptidase P genomic DNA fragment 4.
PN WO9911799-A2.
PD 11-MAR-1999.
PA (MEDI-) MEDICAL COLLEGE GEORGIA RES INST.
Query Match 2.3%; Score 34.8; DB 2; Length 45546;
Best Local Similarity 54.8%; Pred. No. 5.5e+02;
RESULT 1186

ID ACF04818 standard; DNA; 51855 BP.
DE Melithiazol biosynthetic gene cluster.
PN WO2003080828-A2.
PD 02-OCT-2003.
PA (GBFB) GBF GRS BIOTECH FORSCHUNG GMBH.
Query Match 2.3%; Score 34.8; DB 10; Length 51855;
Best Local Similarity 50.6%; Pred. No. 5.9e+02;
RESULT 1187
ID ADQ97340 standard; DNA; 60202 BP.
DE Mouse cancer associated sequence MD08-035, SEQ ID 317.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.3%; Score 34.8; DB 12; Length 60202;
Best Local Similarity 46.1%; Pred. No. 6.3e+02;
RESULT 1188
ID ACN44284 standard; DNA; 71678 BP.
DE Mouse genomic sequence mCG16994.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.3%; Score 34.8; DB 11; Length 71678;
Best Local Similarity 54.8%; Pred. No. 6.9e+02;
RESULT 1189
ID ACN44560 standard; DNA; 94672 BP.
DE Mouse genomic sequence mCG21419.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.3%; Score 34.8; DB 11; Length 94672;
Best Local Similarity 53.7%; Pred. No. 7.9e+02;
RESULT 1190
ID ACN43984 standard; DNA; 493631 BP.
DE Mouse genomic sequence mCG12182.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.3%; Score 34.8; DB 11; Length 110000;
Best Local Similarity 55.9%; Pred. No. 8.5e+02;
RESULT 1191
Query Match 2.3%; Score 34.8; DB 13; Length 110000;
Best Local Similarity 48.1%; Pred. No. 8.5e+02;
RESULT 1192
Query Match 2.3%; Score 34.8; DB 13; Length 110000;
Best Local Similarity 48.1%; Pred. No. 8.5e+02;
RESULT 1193
ID ADQ17592 standard; DNA; 116561 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 409.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.3%; Score 34.8; DB 12; Length 116561;
Best Local Similarity 54.8%; Pred. No. 8.7e+02;
RESULT 1194
ID ABD33312 standard; DNA; 138115 BP.
DE Murine cancer-associated (CA) gene MD07-056.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.3%; Score 34.8; DB 13; Length 138115;
Best Local Similarity 52.0%; Pred. No. 9.4e+02;
RESULT 1195
ID ADL13775 standard; DNA; 173805 BP.
DE Osteoarthritis-associated polymorphic nucleotide #307.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 2.3%; Score 34.8; DB 10; Length 173805;
Best Local Similarity 53.7%; Pred. No. 1.1e+03;
RESULT 1196
ID ACN44002 standard; DNA; 228139 BP.
DE Human genomic sequence hCG37533.
PN WO2003073826-A2.

PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.3%; Score 34.8; DB 11; Length 228139;
Best Local Similarity 48.1%; Pred. No. 1.2e+03;
RESULT 1197
ID AAR43643 standard; cDNA; 267 BP.
DE SSG #9.
PN WO200175169-A2.
PD 11-OCT-2001.
PA (DIAD-) DIADEXUS INC.
Query Match 2.3%; Score 34.6; DB 4; Length 267;
Best Local Similarity 53.3%; Pred. No. 49;
RESULT 1198
ID AAI13112 standard; DNA; 422 BP.
DE Probe #3045 for gene expression analysis in human cervical cell sample.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.3%; Score 34.6; DB 4; Length 422;
Best Local Similarity 64.2%; Pred. No. 61;
RESULT 1199
ID ABA54811 standard; DNA; 422 BP.
DE Human foetal liver single exon nucleic acid probe #3116.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.3%; Score 34.6; DB 4; Length 422;
Best Local Similarity 64.2%; Pred. No. 61;
RESULT 1200
ID AAI34463 standard; DNA; 422 BP.
DE Probe #3149 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.3%; Score 34.6; DB 4; Length 422;
Best Local Similarity 64.2%; Pred. No. 61;
RESULT 1201
ID ABA44357 standard; DNA; 422 BP.
DE Human breast cell single exon nucleic acid probe #3052.
PN WO200157271-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.3%; Score 34.6; DB 4; Length 422;
Best Local Similarity 64.2%; Pred. No. 61;
RESULT 1202
ID ABA24575 standard; DNA; 422 BP.
DE Probe #3041 for gene expression analysis in human heart cell sample.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.3%; Score 34.6; DB 4; Length 422;
Best Local Similarity 64.2%; Pred. No. 61;
RESULT 1203
ID AAK28539 standard; DNA; 422 BP.
DE Human bone marrow expressed single exon probe SEQ ID NO: 3096.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.3%; Score 34.6; DB 4; Length 422;
Best Local Similarity 64.2%; Pred. No. 61;
RESULT 1204
ID AAK03087 standard; DNA; 422 BP.
DE Human brain expressed single exon probe SEQ ID NO: 3078.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.3%; Score 34.6; DB 4; Length 422;
Best Local Similarity 64.2%; Pred. No. 61;
RESULT 1205
ID ABA28139 standard; DNA; 422 BP.
DE Human liver single exon probe, SEQ ID NO 3129.
PN WO200157273-A2.
PD 09-AUG-2001.

PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.3%; Score 34.6; DB 4; Length 422;
Best Local Similarity 64.2%; Pred. No. 61;
RESULT 1206
ID AAI03015 standard; DNA; 422 BP.
DE Probe #3006 used to measure gene expression in human breast sample.
PN WO200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.3%; Score 34.6; DB 5; Length 422;
Best Local Similarity 64.2%; Pred. No. 61;
RESULT 1207
ID ABS03051 standard; DNA; 422 BP.
DE Human genome-derived single exon probe from lung SEQ ID No 3042.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.3%; Score 34.6; DB 6; Length 422;
Best Local Similarity 64.2%; Pred. No. 61;
RESULT 1208
ID AAC35781 standard; DNA; 497 BP.
DE Zea mays DNA fragment SEQ ID NO: 11399.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 2.3%; Score 34.6; DB 3; Length 497;
Best Local Similarity 53.3%; Pred. No. 66;
RESULT 1209
ID ADA71021 standard; DNA; 500 BP.
DE Rice gene, SEQ ID 4344.
PN WO200300898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.3%; Score 34.6; DB 8; Length 500;
Best Local Similarity 47.1%; Pred. No. 66;
RESULT 1210
ID ABA22262 standard; DNA; 615 BP.
DE Schwann cell specific enhancer consensus SCE1 nucleotide sequence #2.
PN WO200288352-A2.
PD 07-NOV-2002.
PA (UTMC-) UNIV MCGILL.
Query Match 2.3%; Score 34.6; DB 8; Length 615;
Best Local Similarity 18.9%; Pred. No. 73;
RESULT 1211
ID ADA42630 standard; cDNA; 740 BP.
DE Plant cDNA #3630.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOF/) GOF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RIQUE D.
PA (ZHUT/) ZHU T.
Query Match 2.3%; Score 34.6; DB 12; Length 740;
Best Local Similarity 48.3%; Pred. No. 81;
RESULT 1212
ID ADC12755 standard; DNA; 933 BP.
DE Human GPCR gene, SEQ ID No 87.
PN WO200300893-A2.
PD 03-JAN-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 2.3%; Score 34.6; DB 10; Length 933;
Best Local Similarity 53.3%; Pred. No. 90;
RESULT 1213
ID ABD03694 standard; DNA; 984 BP.
DE Pseudomonas aeruginosa polynucleotide #2298.
PN US651795-B1.
PD 22-APR-2003.

PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.3%; Score 34.6; DB 11; Length 984;
Best Local Similarity 49.7%; Pred. No. 93;
RESULT 1214
ID ABZ22275 standard; DNA; 997 BP.
DE Mouse and human consensus SCE1 nucleotide sequence #2.
PN WO200288352-A2.
PD 07-NOV-2002.
PA (UYWC-) UNIV MCGILL.
Query Match 2.3%; Score 34.6; DB 8; Length 997;
Best Local Similarity 18.9%; Pred. No. 93;
RESULT 1215
ID ADRI8583 standard; cDNA; 1083 BP.
DE Human GPCR 14273 coding sequence, SEQ ID 2.
PN WO2004065960-A1.
PD 05-AUG-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 2.3%; Score 34.6; DB 13; Length 1083;
Best Local Similarity 53.3%; Pred. No. 97;
RESULT 1216
ID ABT04869 standard; cDNA; 1086 BP.
DE Human G protein coupled receptor hRUP31 coding sequence.
PN WO200242461-A2.
PD 30-MAY-2002.
PA (AREN-) ARENA PHARM INC.
Query Match 2.3%; Score 34.6; DB 6; Length 1086;
Best Local Similarity 53.3%; Pred. No. 98;
RESULT 1217
ID ABST73399 standard; DNA; 1086 BP.
DE DNA encoding human GPCR HF1948 mutant E135N.
PN WO200268600-A2.
PD 06-SEP-2002.
PA (AREN-) ARENA PHARM INC.
Query Match 2.3%; Score 34.6; DB 6; Length 1086;
Best Local Similarity 53.3%; Pred. No. 98;
RESULT 1218
ID ABST73343 standard; cDNA; 1086 BP.
DE cDNA encoding human GPCR HF1948.
PN WO200268600-A2.
PD 06-SEP-2002.
PA (AREN-) ARENA PHARM INC.
Query Match 2.3%; Score 34.6; DB 6; Length 1086;
Best Local Similarity 53.3%; Pred. No. 98;
RESULT 1219
ID AC60998 standard; cDNA; 1086 BP.
DE cDNA encoding novel human G protein coupled receptor HGPRMY18.
PN US2003022186-A1.
PD 30-JAN-2003.
PA (FEDE/) FEDER J N.
PA (MINT/) MINTIER G.
PA (RAMA/) RAMANATHAN C S.
Query Match 2.3%; Score 34.6; DB 8; Length 1086;
Best Local Similarity 53.3%; Pred. No. 98;
RESULT 1220
ID ADB47641 standard; cDNA; 1086 BP.
DE Human cDNA encoding GPCR, HGPRMY18.
PN US2003129653-A1.
PD 10-JUL-2003.
PA (FEDE/) FEDER J N.
PA (MINT/) MINTIER G.
PA (RAMA/) RAMANATHAN C S.
PA (HAWK/) HAWKEN D R.
Query Match 2.3%; Score 34.6; DB 9; Length 1086;
Best Local Similarity 53.3%; Pred. No. 98;
RESULT 1221
ID ADR40535 standard; cDNA; 1086 BP.
DE Human G-protein coupled receptor HGPRMY18 cDNA.
PN US2004161823-A1.
PD 19-AUG-2004.
PA (FEDE/) FEDER J N.
PA (MINT/) MINTIER G.
PA (RAMA/) RAMANATHAN C S.
PA (HAWK/) HAWKEN D R.

Query Match 2.3%; Score 34.6; DB 13; Length 1086;
Best Local Similarity 53.3%; Pred. No. 98;
RESULT 1222
ID ABX10627 standard; DNA; 1160 BP.
DE DNA encoding human orphan SNORF49 receptor.
PN US2002151705-A1.
PD 17-OCT-2002.
PA (SMIT/) SMITH K E.
PA (OUAN/) OUAN Y.
Query Match 2.3%; Score 34.6; DB 8; Length 1160;
Best Local Similarity 53.3%; Pred. No. 1e+02;
RESULT 1223
ID ADT46979 standard; cDNA; 1278 BP.
DE Bacterial polynucleotide #21730.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 2.3%; Score 34.6; DB 13; Length 1278;
Best Local Similarity 45.2%; Pred. No. 1.1e+02;
RESULT 1224
ID AAD08854 standard; cDNA; 1321 BP.
DE Human G-protein coupled receptor-20 (GCREC-20) cDNA.
PN WO200142288-A2.
PD 14-JUN-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 2.3%; Score 34.6; DB 4; Length 1321;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1225
ID ADT44390 standard; cDNA; 1368 BP.
DE Bacterial polynucleotide #19141.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 2.3%; Score 34.6; DB 13; Length 1368;
Best Local Similarity 49.2%; Pred. No. 1.1e+02;
RESULT 1226
ID ADC87380 standard; DNA; 1372 BP.
DE Human GPCR gene SEQ ID NO:1833.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 2.3%; Score 34.6; DB 10; Length 1372;
Best Local Similarity 46.5%; Pred. No. 1.1e+02;
RESULT 1227
ID AA166039 standard; cDNA; 1458 BP.
DE Human G protein-coupled receptor encoding cDNA SEQ ID NO 2.
PN JP2001211885-A.
PD 07-AUG-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 2.3%; Score 34.6; DB 4; Length 1458;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1228
ID ADR01275 standard; DNA; 1599 BP.
DE Farnesyl dibenzodiazepinone biosynthetic ORF32 protein HOYH DNA.
PN WO2004065591-A1.
PD 05-AUG-2004.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Query Match 2.3%; Score 34.6; DB 13; Length 1599;
Best Local Similarity 52.4%; Pred. No. 1.2e+02;
RESULT 1229
ID AA64346 standard; DNA; 1743 BP.
DE DNA encoding a human G-protein coupled receptor designated 14273.
PN WO200050596-A2.
PD 31-AUG-2000.

PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.3%; Score 34.6; DB 3; Length 1743;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1230
ID ABQ81226 standard; cDNA, 1743 BP.
DE Human 14273 nucleic acid, associated with metabolic disorder.
PN WO200267868-A2.
PD 06-SEP-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.3%; Score 34.6; DB 6; Length 1743;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1231
ID ADF70511 standard; DNA, 1800 BP.
DE Orphan receptor ligand-related human protein gene SeqID134.
PN WO2003071272-A1.
PD 28-AUG-2003.
PA (TAKE) TAKEEDA CHEM IND LTD.
Query Match 2.3%; Score 34.6; DB 10; Length 1800;
Best Local Similarity 53.3%; Pred. No. 1.3e+02;
RESULT 1232
ID ADB58993 standard; DNA, 2034 BP.
DE Toxicity-related gene, SEQ ID 4019.
PN WO2003064624-A2.
PD 07-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 2.3%; Score 34.6; DB 10; Length 2034;
Best Local Similarity 51.6%; Pred. No. 1.3e+02;
RESULT 1233
ID ADB53747 standard; DNA, 2034 BP.
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:4289.
PN WO2003065993-A2.
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 2.3%; Score 34.6; DB 10; Length 2034;
Best Local Similarity 51.6%; Pred. No. 1.3e+02;
RESULT 1234
ID ABD1675 standard; DNA, 2073 BP.
DE Pseudomonas aeruginosa polynucleotide #10279.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.3%; Score 34.6; DB 11; Length 2073;
Best Local Similarity 47.8%; Pred. No. 1.3e+02;
RESULT 1235
ID ADO28989 standard; cDNA, 2081 BP.
DE Human novel GPCR PGR4 polynucleotide, SEQ ID NO:88.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 2.3%; Score 34.6; DB 12; Length 2081;
Best Local Similarity 53.3%; Pred. No. 1.3e+02;
RESULT 1236
ID ADA70561 standard; DNA, 2145 BP.
DE Rice gene, SEQ ID 3884.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.3%; Score 34.6; DB 8; Length 2145;
Best Local Similarity 49.2%; Pred. No. 1.4e+02;
RESULT 1237
ID ACA50840 standard; DNA, 2355 BP.
DE Prokaryotic essential gene #32497.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 2.3%; Score 34.6; DB 8; Length 2355;
Best Local Similarity 46.5%; Pred. No. 1.4e+02;
RESULT 1238
ID ADB63556 standard; cDNA, 2650 BP.
DE Human cDNA encoding clone TEST120287760.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.

PA (REAS-) REAS ASSOC BIOTECHNOLOGY.
Query Match 2.3%; Score 34.6; DB 10; Length 2650;
Best Local Similarity 56.6%; Pred. No. 1.5e+02;
RESULT 1239
ID ABD1973 standard; DNA, 2772 BP.
DE Pseudomonas aeruginosa polynucleotide #10577.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.3%; Score 34.6; DB 11; Length 2772;
Best Local Similarity 47.8%; Pred. No. 1.6e+02;
RESULT 1240
ID AAF62205 standard; DNA, 2890 BP.
DE Melon ethylene receptor gene promoter.
PN JP2001037484-A.
PD 13-FEB-2001.
PA (IBAR-) IBARAKI PREFECTURE.
Query Match 2.3%; Score 34.6; DB 5; Length 2890;
Best Local Similarity 56.6%; Pred. No. 1.6e+02;
RESULT 1241
ID AAL51205 standard; DNA, 3083 BP.
DE Human gene sequence #3.
PN WO20029103-A1.
PD 12-DEC-2002.
PA (KAZU-) KAZUSA DNA RES INST FOUND.
Query Match 2.3%; Score 34.6; DB 8; Length 3083;
Best Local Similarity 55.4%; Pred. No. 1.6e+02;
RESULT 1242
ID ADQ23587 standard; DNA, 3141 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6407.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.3%; Score 34.6; DB 12; Length 3141;
Best Local Similarity 55.4%; Pred. No. 1.7e+02;
RESULT 1243
ID AAL51404 standard; cDNA, 3537 BP.
DE Human secreted protein coding sequence, SEQ ID NO 1.
PN WO200292621-A1.
PD 21-NOV-2002.
PA (PEKE) PE CORP NY.
PA (SHAO/) SHAO W.
PA (GONG/) GONG F.
PA (DPRR/) DI FRANCESCO V.
PA (BEAS/) BEASLEY E M.
Query Match 2.3%; Score 34.6; DB 8; Length 3537;
Best Local Similarity 55.4%; Pred. No. 1.8e+02;
RESULT 1244
ID AAF62217 standard; DNA, 3797 BP.
DE Melon ethylene receptor gene promoter-related sequence.
PN JP2001037484-A.
PD 13-FEB-2001.
PA (IBAR-) IBARAKI PREFECTURE.
Query Match 2.3%; Score 34.6; DB 5; Length 3797;
Best Local Similarity 56.6%; Pred. No. 1.8e+02;
RESULT 1245
ID ADR01273 standard; DNA, 5960 BP.
DE Farnesyl dibenzodiazepinone biosynthetic locus Contig 2, SEQ ID 64.
PN WO2004065591-A1.
PD 05-AUG-2004.
PA (ECOP-) ECOPITA BIOSCIENCES INC.
Query Match 2.3%; Score 34.6; DB 13; Length 5960;
Best Local Similarity 52.4%; Pred. No. 2.3e+02;
RESULT 1246
ID AAA10594 standard; DNA, 10732 BP.
DE Gene encoding a subunit of cellulose synthase.
PN JP2000060568-A.
PD 29-FEB-2000.
PA (MIZU/) MIZUNO K.
PA (OJIP) OJI PAPER CO.
Query Match 2.3%; Score 34.6; DB 3; Length 10732;
Best Local Similarity 13.4%; Pred. No. 3e+02;

RESULT 1247
ID AAS59569 standard; DNA; 29139 BP.
DE Propionibacterium acnes immunogenic protein encoding DNA #64.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 2.3%; Score 34.6; DB 4; Length 29139;
Best Local Similarity 51.6%; Pred. No. 5e+02;
RESULT 1248
ID AC644498 standard; DNA; 29139 BP.
DE Propionibacterium acnes DNA contig sequence #64.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 2.3%; Score 34.6; DB 8; Length 29139;
Best Local Similarity 51.6%; Pred. No. 5e+02;
RESULT 1249
ID ABD32614 standard; DNA; 34245 BP.
DE Mouse cancer-associated genomic DNA MD12-027.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.3%; Score 34.6; DB 13; Length 34245;
Best Local Similarity 54.3%; Pred. No. 5.4e+02;
RESULT 1250
ID ADP31997 standard; DNA; 39949 BP.
DE Full length cosmid 2A7.
PN WO2003099993-A2.
PD 04-DEC-2003.
PA (AVERT-) AVERTIS PHARM INC.
Query Match 2.3%; Score 34.6; DB 12; Length 39949;
Best Local Similarity 54.3%; Pred. No. 5.9e+02;
RESULT 1251
ID ADF31998 standard; DNA; 48200 BP.
DE Cosmid 2A7.
PN WO2003099993-A2.
PD 04-DEC-2003.
PA (AVERT-) AVERTIS PHARM INC.
Query Match 2.3%; Score 34.6; DB 12; Length 48200;
Best Local Similarity 54.3%; Pred. No. 6.4e+02;
RESULT 1252
ID ABD33307 standard; DNA; 53828 BP.
DE Murine cancer-associated (CA) gene MD07-055.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.3%; Score 34.6; DB 13; Length 53828;
Best Local Similarity 50.9%; Pred. No. 6.8e+02;
RESULT 1253
ID ABN87364 standard; cDNA; 55155 BP.
DE Human lipase encoding gene sequence SEQ ID NO:3.
PN US2002052034-A1.
PD 02-MAY-2002.
PA (GUEG/) GUEGLER K.
PA (WEBB/) WEBSTER M.
PA (KERC/) KETCHUM K A.
PA (DPR/) DI FRANCESCO V.
PA (BRAS/) BRASLEY E M.
Query Match 2.3%; Score 34.6; DB 6; Length 55155;
Best Local Similarity 61.8%; Pred. No. 6.9e+02;
RESULT 1254
ID ADQ97700 standard; DNA; 86804 BP.
DE Mouse cancer associated sequence MD10-031, SEQ ID 677.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.3%; Score 34.6; DB 12; Length 86804;
Best Local Similarity 50.9%; Pred. No. 8.6e+02;
RESULT 1255
ID AAH88704 standard; DNA; 160755 BP.
DE Human DNA sequence SEQ ID 544.
PN WO200151659-A2.
PD 19-JUL-2001.

PA (GERT-) GENSET.
Query Match 2.3%; Score 34.6; DB 4; Length 160755;
Best Local Similarity 55.4%; Pred. No. 1.2e+03;
RESULT 1256
ID ACN44110 standard; DNA; 223556 BP.
DE Human genomic sequence hCG38337.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.3%; Score 34.6; DB 11; Length 223556;
Best Local Similarity 53.3%; Pred. No. 1.3e+03;
RESULT 1257
ID ACN44068 standard; DNA; 295096 BP.
DE Mouse genomic sequence mCG13636.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.3%; Score 34.6; DB 11; Length 295096;
Best Local Similarity 48.7%; Pred. No. 1.5e+03;
RESULT 1258
ID ADQ48726 standard; DNA; 316 BP.
DE Novel canine microarray-related DNA sequence SeqID28.
PN WO2004063324-A2.
PD 29-JUL-2004.
PA (GENE-) GENE LOGIC INC.
PA (PRIZ-) PRIZER PROD INC.
Query Match 2.3%; Score 34.4; DB 13; Length 316;
Best Local Similarity 56.8%; Pred. No. 60;
RESULT 1259
ID AAD03892 standard; DNA; 340 BP.
DE Human target of methylation-induced silencing-1 (TMS1) exon1 DNA.
PN WO200129235-A2.
PD 26-APR-2001.
PA (UYEM-) UNIV EMORY.
Query Match 2.3%; Score 34.4; DB 4; Length 340;
Best Local Similarity 46.0%; Pred. No. 62;
RESULT 1260
ID AAS90909 standard; cDNA; 379 BP.
DE DNA encoding novel human diagnostic protein #26713.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.3%; Score 34.4; DB 5; Length 379;
Best Local Similarity 47.6%; Pred. No. 66;
RESULT 1261
ID AAS75428 standard; cDNA; 379 BP.
DE DNA encoding novel human diagnostic protein #11232.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.3%; Score 34.4; DB 5; Length 379;
Best Local Similarity 47.6%; Pred. No. 66;
RESULT 1262
ID ADB09716 standard; DNA; 379 BP.
DE Novel DNA-related contig nucleotide sequence #438.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 2.3%; Score 34.4; DB 10; Length 379;
Best Local Similarity 47.6%; Pred. No. 66;
RESULT 1263
ID AAD03907 standard; cDNA; 405 BP.
DE Alternatively spliced form of human TMS1 cDNA (lacking exon3).
PN WO200129235-A2.
PD 26-APR-2001.
PA (UYEM-) UNIV EMORY.
Query Match 2.3%; Score 34.4; DB 4; Length 405;
Best Local Similarity 46.0%; Pred. No. 68;
RESULT 1264
ID AAC98638 standard; cDNA; 432 BP.
DE Human colon cancer antigen nucleotide sequence SEQ ID NO:648.
PN WO200055351-A1.
PD 21-SEP-2000.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.3%; Score 34.4; DB 3; Length 432;
Best Local Similarity 46.0%; Pred. No. 70;
RESULT 1265
ID ABX37280 standard; cDNA; 434 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #2445.
PN US200237139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 2.3%; Score 34.4; DB 8; Length 434;
Best Local Similarity 46.0%; Pred. No. 70;
RESULT 1266
ID AAC36571 standard; DNA; 449 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 14294.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 2.3%; Score 34.4; DB 3; Length 449;
Best Local Similarity 53.8%; Pred. No. 71;
RESULT 1267
ID AAD03891 standard; DNA; 626 BP.
DE Cpg island of human TMS1 gene.
PN WO200129235-A2.
PD 26-APR-2001.
PA (UYEM-) UNIV EMORY.
Query Match 2.3%; Score 34.4; DB 4; Length 626;
Best Local Similarity 46.0%; Pred. No. 84;
RESULT 1268
ID AAD03906 standard; cDNA; 713 BP.
DE Alternatively spliced form of human TMS1 cDNA (lacking exon2).
PN WO200129235-A2.
PD 26-APR-2001.
PA (UYEM-) UNIV EMORY.
Query Match 2.3%; Score 34.4; DB 4; Length 713;
Best Local Similarity 46.0%; Pred. No. 90;
RESULT 1269
ID AAR30007 standard; cDNA; 740 BP.
DE Human CARD-5 cDNA.
PN WO200100826-A2.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.3%; Score 34.4; DB 4; Length 740;
Best Local Similarity 46.0%; Pred. No. 92;
RESULT 1270
ID ABR87966 standard; cDNA; 740 BP.
DE Human caspase recruitment domain-5 (CARD-5) cDNA.
PN WO200244354-A2.
PD 06-JUN-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.3%; Score 34.4; DB 6; Length 740;
Best Local Similarity 46.0%; Pred. No. 92;
RESULT 1271
ID ABR87967 standard; DNA; 740 BP.
DE Human caspase recruitment domain-5 (CARD-5) cDNA complementary strand.
PN WO200244354-A2.
PD 06-JUN-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.3%; Score 34.4; DB 6; Length 740;
Best Local Similarity 46.0%; Pred. No. 92;
RESULT 1272
ID ABS56032 standard; cDNA; 740 BP.
DE cDNA encoding human caspase recruitment domain-5 (CARD-5).
PN US2002128198-A1.
PD 12-SEP-2002.
PA (BERT/) BERTIN J.
Query Match 2.3%; Score 34.4; DB 8; Length 740;
Best Local Similarity 46.0%; Pred. No. 92;
RESULT 1273
ID AAS59817 standard; cDNA; 745 BP.
DE Human novel cytokine encoding cDNA 790CIP2B_1 #1.
PN WO200175093-A1.

PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.3%; Score 34.4; DB 4; Length 745;
Best Local Similarity 46.0%; Pred. No. 92;
RESULT 1274
ID AAD03890 standard; cDNA; 770 BP.
DE Human target of methylation-induced silencing-1 (TMS1) cDNA.
PN WO200129235-A2.
PD 26-APR-2001.
PA (UYEM-) UNIV EMORY.
Query Match 2.3%; Score 34.4; DB 4; Length 770;
Best Local Similarity 46.0%; Pred. No. 93;
RESULT 1275
ID AA233631 standard; cDNA; 779 BP.
DE Human breast tumour-associated EST 21.
PN DE19813839-A1.
PD 23-SEP-1999.
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
Query Match 2.3%; Score 34.4; DB 2; Length 779;
Best Local Similarity 46.0%; Pred. No. 94;
RESULT 1276
ID AA47126 standard; DNA; 782 BP.
DE Pyrin domain containing protein Pycard coding sequence.
PN WO200240668-A2.
PD 23-MAY-2002.
PA (APOT-) APOTTECH RES & DEV LTD.
Query Match 2.3%; Score 34.4; DB 6; Length 782;
Best Local Similarity 46.0%; Pred. No. 94;
RESULT 1277
ID ADF90785 standard; DNA; 796 BP.
DE Human hepatic-fibrosis disease marker SEQ ID 247.
PN JP2003259877-A.
PD 16-SEP-2003.
PA (SOMU) SOMITOMO SEIYAKU KK.
Query Match 2.3%; Score 34.4; DB 10; Length 796;
Best Local Similarity 46.0%; Pred. No. 95;
RESULT 1278
ID AAH34052 standard; cDNA; 806 BP.
DE Human colon cancer antigen encoding cDNA SEQ ID NO:1134.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.3%; Score 34.4; DB 4; Length 806;
Best Local Similarity 46.0%; Pred. No. 96;
RESULT 1279
ID AAC77884 standard; cDNA; 811 BP.
DE Human cancer associated gene sequence SEQ ID NO:278.
PN WO200055350-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.3%; Score 34.4; DB 3; Length 811;
Best Local Similarity 46.0%; Pred. No. 96;
RESULT 1280
ID ADR01252 standard; DNA; 825 BP.
DE Farnesyl dibenzodiazepinone biosynthetic ORF21 protein ALDB DNA.
PN WO2004065591-A1.
PD 05-AUG-2004.
PA (ECOP-) ECOPHA BIOSCIENCES INC.
Query Match 2.3%; Score 34.4; DB 13; Length 825;
Best Local Similarity 54.8%; Pred. No. 97;
RESULT 1281
ID ADN05025 standard; cDNA; 936 BP.
DE Antiproliferative cDNA sequence #727.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 2.3%; Score 34.4; DB 12; Length 936;
Best Local Similarity 46.0%; Pred. No. 1e+02;
RESULT 1282
ID ADP07316 standard; DNA; 936 BP.
DE Human TMS1 DNA.
PN DE10255104-A1.
PD 11-MAR-2004.

PA (EPIC-) EPIGENOMICS AG.
Query Match 2.3%; Score 34.4; DB 12; Length 936;
Best Local Similarity 46.0%; Pred. No. 1e+02;
RESULT 1283
ID ADP56277 standard; cDNA; 936 BP.
DE Human PRO cDNA sequence SEQ ID NO:2253.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GENTH) GENTECH INC.
Query Match 2.3%; Score 34.4; DB 13; Length 936;
Best Local Similarity 46.0%; Pred. No. 1e+02;
RESULT 1284
ID AAI97783 standard; cDNA; 1049 BP.
DE Human neuroblastoma expressed polynucleotide SEQ ID NO 3858.
PN WO200166719-A1.
PD 13-SEP-2001.
PA (CHIB-) CHIBA PREPCTURE.
PA (HISM) HISAMITSU PHARM CO. LTD.
Query Match 2.3%; Score 34.4; DB 4; Length 1049;
Best Local Similarity 46.7%; Pred. No. 1.1e+02;
RESULT 1285
ID ADT46829 standard; cDNA; 1164 BP.
DE Bacterial polynucleotide #21580.
PN US200323675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATTER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 2.3%; Score 34.4; DB 13; Length 1164;
Best Local Similarity 53.8%; Pred. No. 1.1e+02;
RESULT 1286
ID AAS54218 standard; DNA; 1470 BP.
DE Pseudomonas aeruginosa DNA for cellular proliferation protein #349.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELITRA) ELITRA PHARM INC.
Query Match 2.3%; Score 34.4; DB 4; Length 1470;
Best Local Similarity 46.0%; Pred. No. 1.3e+02;
RESULT 1287
ID AAS27365 standard; cDNA; 1619 BP.
DE cDNA encoding novel signal transduction pathway protein, Seq ID 400.
PN WO200154733-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.3%; Score 34.4; DB 4; Length 1619;
Best Local Similarity 50.6%; Pred. No. 1.4e+02;
RESULT 1288
ID AAS34830 standard; cDNA; 1619 BP.
DE cDNA encoding novel human neoplastic disease associated polypeptide #64.
PN WO200155163-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.3%; Score 34.4; DB 4; Length 1619;
Best Local Similarity 50.6%; Pred. No. 1.4e+02;
RESULT 1289
ID ADB93543 standard; cDNA; 1619 BP.
DE Human cDNA encoding a novel protein #390.
PN US2002168711-A1.
PD 14-NOV-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.3%; Score 34.4; DB 10; Length 1619;
Best Local Similarity 50.6%; Pred. No. 1.4e+02;
RESULT 1290
ID ADC45988 standard; cDNA; 1619 BP.
DE Human neoplastic disease-associated gene 64 cDNA #1.
PN US2003082758-A1.
PD 01-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.3%; Score 34.4; DB 10; Length 1619;
Best Local Similarity 50.6%; Pred. No. 1.4e+02;
RESULT 1291
ID ADF30323 standard; cDNA; 2525 BP.
DE Human cancer suppressing protein PPI0443-encoding cDNA, SEQ.10 and 12.
PN CN1368508-A.
PD 11-SEP-2002.
PA (SHAN-) SHANGHAI INST ONCOLOGY.
Query Match 2.3%; Score 34.4; DB 10; Length 2525;
Best Local Similarity 52.9%; Pred. No. 1.7e+02;
RESULT 1292
ID AAS27013 standard; cDNA; 2686 BP.
DE cDNA encoding novel signal transduction pathway protein, Seq ID 48.
PN WO200154733-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.3%; Score 34.4; DB 4; Length 2686;
Best Local Similarity 50.6%; Pred. No. 1.7e+02;
RESULT 1293
ID ADB93191 standard; cDNA; 2686 BP.
DE Human cDNA encoding a novel protein #38.
PN US2002168711-A1.
PD 14-NOV-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.3%; Score 34.4; DB 10; Length 2686;
Best Local Similarity 50.6%; Pred. No. 1.7e+02;
RESULT 1294
ID ADU50974 standard; cDNA; 2768 BP.
DE Human cDNA encoding NOV15a.
PN US2004030096-A1.
PD 12-FEB-2004.
PA (GORM/) GORMAN L.
PA (ZERR/) ZERRHUSEN B D.
PA (EDIN/) EDINGER S R.
PA (PADI/) PADIGARU M.
PA (GUOX/) GUO X.
PA (KEKU/) KEKUDA R.
PA (ZHON/) ZHONG M.
PA (PATY/) PATTRALAN M.
PA (MITL/) MITLER C E.
PA (JTWI/) JI W.
PA (PENNA/) PENNA C E A.
PA (BURG/) BURGESS C E.
PA (SCIO/) SCIORE P.
PA (STON/) STONE D J.
PA (TAUP/) TAUPETER R J.
PA (CASM/) CASMAN S J.
PA (ROTH/) ROTHENBERG M E.
PA (MALY/) MALYANKAR U M.
PA (BOLD/) BOLDOG F L.
Query Match 2.3%; Score 34.4; DB 12; Length 2768;
Best Local Similarity 50.6%; Pred. No. 1.8e+02;
RESULT 1295
ID AAD03889 standard; DNA; 2821 BP.
DE Human target of methylation-induced silencing-1 (TWG1) genomic DNA.
PN WO200129235-A2.
PD 26-APR-2001.
PA (UTEM-) UNIV EMORY.
Query Match 2.3%; Score 34.4; DB 4; Length 2821;
Best Local Similarity 46.0%; Pred. No. 1.8e+02;
RESULT 1296
ID AAS44718 standard; DNA; 3321 BP.
DE Human full-length polynucleotide sequence #143.
PN WO200164834-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.3%; Score 34.4; DB 4; Length 3321;
Best Local Similarity 50.6%; Pred. No. 1.9e+02;
RESULT 1297
ID ABX14762 standard; cDNA; 3380 BP.
DE cDNA encoding novel human ras-like protein.
PN US2002132291-A1.

PD 19-SEP-2002.
PA (YELU/) YE J.
DE (KETCHUM K A.
PA (DFRA/) DI FRANCESCO V.
PA (BRAS/) BRASLEY E M.
Query Match 2.3%; Score 34.4; DB 8; Length 3380;
Best Local Similarity 50.6%; Pred. No. 2e+02;
RESULT 1298
ID AAL26787 standard; cDNA; 3399 BP.
DE Human breast cancer expressed polynucleotide 19244.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.3%; Score 34.4; DB 4; Length 3399;
Best Local Similarity 52.9%; Pred. No. 2e+02;
RESULT 1299
ID ACN88722 standard; DNA; 3411 BP.
DE Breast cancer related marker, seq id 9872.
PN US200309974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.3%; Score 34.4; DB 11; Length 3411;
Best Local Similarity 52.9%; Pred. No. 2e+02;
RESULT 1300
ID ADH61306 standard; DNA; 3420 BP.
DE INTSIG encoding DNA 7512389CB1, SEQ ID 23.
PN WO2004001005-A2.
PD 31-DEC-2003.
PA (INCY-) INCYTE CORP.
Query Match 2.3%; Score 34.4; DB 12; Length 3420;
Best Local Similarity 49.4%; Pred. No. 2e+02;
RESULT 1301
ID ADK65790 standard; DNA; 3438 BP.
DE Angiogenesis-differentially expressed gene ANH0423.
PN WO2003066831-A2.
PD 14-AUG-2003.
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
Query Match 2.3%; Score 34.4; DB 10; Length 3438;
Best Local Similarity 50.6%; Pred. No. 2e+02;
RESULT 1302
ID AAV15181 standard; cDNA to mRNA; 3955 BP.
DE Human serrate 2 encoding cDNA.
PN WO9802458-A1.
PD 22-JAN-1998.
PA (ASAH) ASAH KASEI KOGYO KK.
Query Match 2.3%; Score 34.4; DB 2; Length 3955;
Best Local Similarity 51.3%; Pred. No. 2.1e+02;
RESULT 1303
ID ADR24345 standard; DNA; 4670 BP.
DE Breast cancer prognosis marker #206.
PN WO200406545-A2.
PD 05-AUG-2004.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
PA (NECA-) NETHERLANDS CANCER INST.
Query Match 2.3%; Score 34.4; DB 13; Length 4670;
Best Local Similarity 50.6%; Pred. No. 2.3e+02;
RESULT 1304
ID ABR95047 standard; DNA; 4702 BP.
DE Gene #1545 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 2.3%; Score 34.4; DB 6; Length 4702;
Best Local Similarity 51.3%; Pred. No. 2.3e+02;
RESULT 1305
ID AAL06946 standard; DNA; 12232 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 9634.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.3%; Score 34.4; DB 4; Length 12232;
Best Local Similarity 59.0%; Pred. No. 3.7e+02;
RESULT 1306

ID AAX83006 standard; DNA; 16442 BP.
DE Partial mouse WRN genomic sequence #2.
PN WO9724435-A1.
PD 10-JUL-1997.
PA (DARW-) DARWIN MOLECULAR CORP.
Query Match 2.3%; Score 34.4; DB 2; Length 16442;
Best Local Similarity 47.6%; Pred. No. 4.3e+02;
RESULT 1307
ID ABD31201 standard; DNA; 36312 BP.
DE Murine cancer-associated (CA) gene MD07-031.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.3%; Score 34.4; DB 13; Length 36312;
Best Local Similarity 44.2%; Pred. No. 6.4e+02;
RESULT 1308
ID ADR01210 standard; DNA; 36602 BP.
DE Farnesyl dibenzodiazephone biosynthetic locus Contlg 1, SEQ ID 1.
PN WO2004065591-A1.
PD 05-AUG-2004.
PA (ECOP-) ECOPHA BIOSCIENCES INC.
Query Match 2.3%; Score 34.4; DB 13; Length 36602;
Best Local Similarity 54.8%; Pred. No. 6.4e+02;
RESULT 1309
ID ACN45024 standard; DNA; 68370 BP.
DE Mouse genomic sequence mCG7008.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.3%; Score 34.4; DB 11; Length 68370;
Best Local Similarity 55.0%; Pred. No. 8.7e+02;
RESULT 1310
ID ACN44818 standard; DNA; 116704 BP.
DE Human genomic sequence hCG30155.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.3%; Score 34.4; DB 11; Length 116704;
Best Local Similarity 54.8%; Pred. No. 1.1e+03;
RESULT 1311
ID ADQ97651 standard; DNA; 127943 BP.
DE Human cancer associated sequence HD10-021, SEQ ID 628.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.3%; Score 34.4; DB 12; Length 127943;
Best Local Similarity 54.8%; Pred. No. 1.2e+03;
RESULT 1312
ID AAH41223 standard; DNA; 349980 BP.
DE Pyrococcus abyssi genomic fragment #2.
PN FR2792651-A1.
PD 27-OCT-2000.
PA (CNRS) CNRS CENT NAT RECH SCI.
PA (IFRE-) IFREMER INST FR RECH EXPL MER.
Query Match 2.3%; Score 34.4; DB 5; Length 349980;
Best Local Similarity 53.8%; Pred. No. 1.9e+03;
RESULT 1313
ID ADC86916 standard; DNA; 349989 BP.
DE Human GPCR gene SEQ ID NO:1369.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 2.3%; Score 34.4; DB 10; Length 349989;
Best Local Similarity 57.4%; Pred. No. 1.9e+03;
RESULT 1314
ID ADS67678 standard; cDNA; 238 BP.
DE Corn seedling-derived polynucleotide (cpds), SEQ ID 2694.
PN US2003237110-A9.
PD 25-DEC-2003.
PA (INCY-) INCYTE PHARM INC.
Query Match 2.3%; Score 34.2; DB 7; Length 238;
Best Local Similarity 60.0%; Pred. No. 59;

RESULT 1315
ID ADP94454 standard; cDNA; 283 BP.
DE Cotton expressed sequence tag, EST, #3465.
PN US200412338-A1.
PD 24-JUN-2004.
PA (FINC/) FINCHER K L.
Query Match 2.3%; Score 34.2; DB 12; Length 283;
Best Local Similarity 46.2%; Pred. No. 65;
RESULT 1316
ID ABV38474 standard; cDNA; 398 BP.
DE Human prostate expression marker cDNA 38465.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.3%; Score 34.2; DB 5; Length 398;
Best Local Similarity 55.5%; Pred. No. 77;
RESULT 1317
ID ABT07648 standard; cDNA; 420 BP.
DE Human breast cancer associated coding sequence SEQ ID NO: 127.
PN WO200264611-A1.
PD 22-AUG-2002.
PA (DIDAD-) DIDADUS INC.
Query Match 2.3%; Score 34.2; DB 6; Length 420;
Best Local Similarity 52.4%; Pred. No. 79;
RESULT 1318
ID AAF07736 standard; cDNA; 567 BP.
DE Fusarium venenatum EST SEQ ID NO:259.
PN WO200056762-A2.
PD 28-SEP-2000.
PA (NOVO) NOVO NORDISK BIOTECH INC.
Query Match 2.3%; Score 34.2; DB 3; Length 567;
Best Local Similarity 47.4%; Pred. No. 91;
RESULT 1319
ID AAH42837 standard; cDNA; 645 BP.
DE Nucleotide sequence of a human metastasis associated 1 gene.
PN WO200153524-A2.
PD 26-JUL-2001.
PA (UNIV-) UNIV NOTTINGHAM TRENT.
Query Match 2.3%; Score 34.2; DB 5; Length 645;
Best Local Similarity 53.8%; Pred. No. 97;
RESULT 1320
ID ABU87669 standard; cDNA; 695 BP.
DE Human ovarian cancer related cDNA clone SEQ ID NO:10647.
PN WO200192581-A2.
PD 06-DEC-2001.
PA (CORI-) CORIXA CORP.
Query Match 2.3%; Score 34.2; DB 6; Length 695;
Best Local Similarity 61.4%; Pred. No. 1e+02;
RESULT 1321
ID AAS69547 standard; cDNA; 708 BP.
DE DNA encoding novel human diagnostic protein #5351.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSB-) HYSBQ INC.
Query Match 2.3%; Score 34.2; DB 5; Length 708;
Best Local Similarity 44.7%; Pred. No. 1e+02;
RESULT 1322
ID AAS75461 standard; cDNA; 708 BP.
DE DNA encoding novel human diagnostic protein #11265.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSB-) HYSBQ INC.
Query Match 2.3%; Score 34.2; DB 5; Length 708;
Best Local Similarity 44.7%; Pred. No. 1e+02;
RESULT 1323
ID ADA69917 standard; DNA; 978 BP.
DE Rice gene, SEQ ID 3240.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.3%; Score 34.2; DB 8; Length 978;
Best Local Similarity 54.3%; Pred. No. 1.2e+02;

RESULT 1324
ID AAQ67210 standard; DNA; 1423 BP.
DE Human corticosteroid binding globulin cDNA.
PN CA2111656-A.
PD 17-JUN-1994.
PA (ALIX) ALLELIX BIOPHARMACEUTICALS INC.
Query Match 2.3%; Score 34.2; DB 2; Length 1423;
Best Local Similarity 47.6%; Pred. No. 1.4e+02;
RESULT 1325
ID AAX22095 standard; DNA; 1767 BP.
DE Cellobiohydrolase CBH B coding sequence.
PN WO9906574-A1.
PD 11-FEB-1999.
PA (KONN) GIST-BROCADES BV.
Query Match 2.3%; Score 34.2; DB 2; Length 1767;
Best Local Similarity 54.3%; Pred. No. 1.6e+02;
RESULT 1326
ID ADT48680 standard; cDNA; 2226 BP.
DE Bacterial polynucleotide #23431.
PN US200323675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 2.3%; Score 34.2; DB 13; Length 2226;
Best Local Similarity 47.4%; Pred. No. 1.8e+02;
RESULT 1327
ID AAH72766 standard; cDNA; 3371 BP.
DE Human cervical cancer marker nucleic acid 4040.
PN WO200142467-A2.
PD 14-JUN-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.3%; Score 34.2; DB 4; Length 3371;
Best Local Similarity 53.3%; Pred. No. 2.2e+02;
RESULT 1328
ID ADP25090 standard; cDNA; 3674 BP.
DE PRO polypeptide encoding cDNA SEQ ID NO:2268.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GERTH) GENTECH INC.
Query Match 2.3%; Score 34.2; DB 13; Length 3674;
Best Local Similarity 52.4%; Pred. No. 2.3e+02;
RESULT 1329
ID ADR83544 standard; DNA; 6999 BP.
DE Human sidekick homologue 1 DNA, target gene of miRNA.
PN WO2004076622-A2.
PD 10-SEP-2004.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
Query Match 2.3%; Score 34.2; DB 13; Length 6999;
Best Local Similarity 56.8%; Pred. No. 3.2e+02;
RESULT 1330
ID ADC26983 standard; DNA; 11358 BP.
DE Sorangium cellulosum tmbA gene cluster tmbC DNA.
PN US2003054547-A1.
PD 20-MAR-2003.
PA (JULI/) JULIEN B.
Query Match 2.3%; Score 34.2; DB 10; Length 11358;
Best Local Similarity 56.8%; Pred. No. 4.1e+02;
RESULT 1331
ID AAK69400 standard; DNA; 11456 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24212.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.3%; Score 34.2; DB 4; Length 11456;
Best Local Similarity 52.4%; Pred. No. 4.1e+02;
RESULT 1332
ID AAX66357 standard; DNA; 16009 BP.
DE Rat smooth muscle myosin heavy chain gene sequence.
PN WO936101-A1.
PD 22-JUL-1999.

PA (UVVI-) UNIV VIRGINIA PATENT FOUND.
Query Match 2.3%; Score 34.2; DB 2; Length 16009;
Best Local Similarity 56.8%; Pred. No. 4.8e+02;
RESULT 1333
ID ABB84504 standard; DNA; 16011 BP.
DE Rat smooth muscle myosin heavy chain gene (-4216 to +11795).
PN WO200259270-A2.
PD 01-AUG-2002.
PA (OWEN/) OWENS G K.
PA (MANA/) MANABE I.
Query Match 2.3%; Score 34.2; DB 6; Length 16011;
Best Local Similarity 56.8%; Pred. No. 4.8e+02;
RESULT 1334
ID ACA60861 standard; DNA; 16011 BP.
DE Rat smooth muscle myosin heavy chain gene fragment.
PN US2003017549-A1.
PD 23-JAN-2003.
PA (OWEN/) OWENS G K.
Query Match 2.3%; Score 34.2; DB 6; Length 16011;
Best Local Similarity 56.8%; Pred. No. 4.8e+02;
RESULT 1335
ID ACN37218 standard; DNA; 20001 BP.
DE Human periodontal disease related gene PTGDS SEQ ID NO:128.
PN WO2004042054-A1.
PD 21-MAY-2004.
PA (HUBI-) HUBIT GENOMIX INC.
PA (KMOI/) KAMOI K.
Query Match 2.3%; Score 34.2; DB 13; Length 20001;
Best Local Similarity 60.0%; Pred. No. 5.4e+02;
RESULT 1336
ID ADC26981 standard; DNA; 20922 BP.
DE Sorangium cellulosum tmbA gene cluster tmbB DNA.
PN US2003054547-A1.
PD 20-MAR-2003.
PA (JULI/) JULIEN B.
Query Match 2.3%; Score 34.2; DB 10; Length 20922;
Best Local Similarity 56.8%; Pred. No. 5.5e+02;
RESULT 1337
ID AAQ10190 standard; DNA; 23666 BP.
DE Cephalosporin antibiotic biosynthetic genes.
PN JP02291274-A.
PD 03-DEC-1990.
PA (TAKE) TAKEIDA CHEM IND LTD.
Query Match 2.3%; Score 34.2; DB 2; Length 23666;
Best Local Similarity 45.6%; Pred. No. 5.8e+02;
RESULT 1338
ID ACN44414 standard; DNA; 24492 BP.
DE Human genomic sequence hCG1780827.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.3%; Score 34.2; DB 11; Length 24492;
Best Local Similarity 60.0%; Pred. No. 5.9e+02;
RESULT 1339
ID AAF88314 standard; DNA; 25360 BP.
DE S. spinoza DNA fragment SEQ ID 3.
PN DE19957268-A1.
PD 08-MAR-2001.
PA (FARB) BAYER AG.
Query Match 2.3%; Score 34.2; DB 4; Length 25360;
Best Local Similarity 47.8%; Pred. No. 6e+02;
RESULT 1340
ID AAF88317 standard; DNA; 29736 BP.
DE S. spinoza DNA fragment SEQ ID 6.
PN DE19957268-A1.
PD 08-MAR-2001.
PA (FARB) BAYER AG.
Query Match 2.3%; Score 34.2; DB 4; Length 29736;
Best Local Similarity 47.8%; Pred. No. 6.5e+02;
RESULT 1341
ID AAD56078 standard; DNA; 32069 BP.
DE Mouse Map3k6 carcinoma associated (CA) gene.
PN WO2003035637-A2.
PD 01-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.3%; Score 34.2; DB 8; Length 32069;
Best Local Similarity 46.4%; Pred. No. 6.8e+02;
RESULT 1342
ID ADA02440 standard; DNA; 32069 BP.
DE Mouse Map3k6 carcinoma associated gene, SEQ ID NO:959.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.3%; Score 34.2; DB 9; Length 32069;
Best Local Similarity 46.4%; Pred. No. 6.8e+02;
RESULT 1343
ID ADB72179 standard; DNA; 32069 BP.
DE Mouse Map3k6 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.3%; Score 34.2; DB 10; Length 32069;
Best Local Similarity 46.4%; Pred. No. 6.8e+02;
RESULT 1344
ID AAS17367 standard; DNA; 33529 BP.
DE DNA sequence of S. cellulosum polyketide synthase cosmId. PKOS28-26.
PN US6280999-B1.
PD 28-AUG-2001.
PA (KOSA-) KOSAN BIOSCIENCE.
Query Match 2.3%; Score 34.2; DB 5; Length 33529;
Best Local Similarity 56.8%; Pred. No. 6.9e+02;
RESULT 1345
ID AAS12439 standard; DNA; 37590 BP.
DE DNA encoding l-aminocyclopropane carboxylate synthase #10.
PN WO200168879-A2.
PD 20-SEP-2001.
PA (FARB) BAYER AG.
Query Match 2.3%; Score 34.2; DB 4; Length 37590;
Best Local Similarity 52.4%; Pred. No. 7.4e+02;
RESULT 1346
ID ADQ97084 standard; DNA; 38690 BP.
DE Human cancer associated sequence HD10-004, SEQ ID 60.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 2.3%; Score 34.2; DB 12; Length 38690;
Best Local Similarity 54.3%; Pred. No. 7.5e+02;
RESULT 1347
ID ADA37416 standard; DNA; 41907 BP.
DE Human rDNA repeat unit.
PN US2003108914-A1.
PD 12-JUN-2003.
PA (HADL/) HADLACZKY G.
Query Match 2.3%; Score 34.2; DB 9; Length 41907;
Best Local Similarity 47.4%; Pred. No. 7.8e+02;
RESULT 1348
ID ACN45116 standard; DNA; 42772 BP.
DE Mouse genomic sequence mCG6527.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.3%; Score 34.2; DB 11; Length 42772;
Best Local Similarity 48.7%; Pred. No. 7.8e+02;
RESULT 1349
ID ADA14747 standard; DNA; 42998 BP.
DE Human ribosomal DNA complete repeating unit.
PN US2002160970-A1.
PD 31-OCT-2002.
PA (HADL/) HADLACZKY G.
PA (SZAL/) SZALAY A A.
Query Match 2.3%; Score 34.2; DB 8; Length 42998;
Best Local Similarity 47.4%; Pred. No. 7.9e+02;
RESULT 1350
ID ABB65032 standard; DNA; 42999 BP.
DE Invertebrate foraging behaviour associated human DNA sequence #12.
PN WO200259370-A2.

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PD 01-AUG-2002.
PA (NEUR-) NEUROSCIENCES RES FOUND INC.
Query Match
Best Local Similarity 2.3%; Score 34.2; DB 6; Length 42999;
RESULT 1351
ID AAD61411 standard; DNA; 42999 BP.
DE Human ribosomal DNA (rDNA) repeat region.
PN US2003101480-A1.
PD 29-MAY-2003.
PA (HADL/) HADJACZKY G.
PA (SZAL/) SZALAY A A.
Query Match
Best Local Similarity 2.3%; Score 34.2; DB 10; Length 42999;
RESULT 1352
ID ADRA3949 standard; DNA; 42999 BP.
DE Human ribosomal DNA complete repeating unit.
PN US2004163147-A1.
PD 19-AUG-2004.
PA (HADL/) HADJACZKY G.
Query Match
Best Local Similarity 2.3%; Score 34.2; DB 13; Length 42999;
RESULT 1353
ID ADPA4151 standard; DNA; 57082 BP.
DE Human CA125 genomic DNA amino terminal sequence SegID 1.
PN WO2004045553-A2.
PD 03-JUN-2004.
PA (UYAR-) UNIV ARKANSAS.
Query Match
Best Local Similarity 2.3%; Score 34.2; DB 12; Length 57082;
RESULT 1354
ID ADQ97534 standard; DNA; 58687 BP.
DE Mouse cancer associated sequence MD09-010, SEQ ID 511.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match
Best Local Similarity 2.3%; Score 34.2; DB 12; Length 58687;
RESULT 1355
ID ADC26995 standard; DNA; 67251 BP.
DE Sorangium cellulosum tmbA gene cluster.
PN US2003054547-A1.
PD 20-MAR-2003.
PA (JULI/) JULIEN B.
Query Match
Best Local Similarity 2.3%; Score 34.2; DB 10; Length 67251;
RESULT 1356
ID ABD32576 standard; DNA; 80423 BP.
DE Mouse cancer-associated genomic DNA MD7-205.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match
Best Local Similarity 2.3%; Score 34.2; DB 13; Length 80423;
RESULT 1357
ID ABX14763 standard; DNA; 88191 BP.
DE Genomic DNA encoding novel human ras-like protein.
PN US2002132291-A1.
PD 19-SEP-2002.
PA (YEJU/) YE J.
PA (KETC/) KETCHUM K A.
PA (DPRA/) DI FRANCESCO V.
PA (BEAS/) BEASLEY E M.
Query Match
Best Local Similarity 2.3%; Score 34.2; DB 8; Length 88191;
RESULT 1358
ID ADA03083 standard; DNA; 93483 BP.
DE Mouse mCG17918 carcinoma associated gene, SEQ ID NO:1601.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match
Best Local Similarity 2.3%; Score 34.2; DB 9; Length 93483;
RESULT 1359
ID ADA63657 standard; DNA; 93483 BP.
DE Mouse mCG17918 gene genomic DNA sequence.
PN WO2003053224-A2.
PD 03-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match
Best Local Similarity 2.3%; Score 34.2; DB 9; Length 93483;
RESULT 1360
ID ADB72821 standard; DNA; 93483 BP.
DE Mouse mCG17918 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match
Best Local Similarity 2.3%; Score 34.2; DB 10; Length 93483;
RESULT 1361
ID ADL27161 standard; DNA; 93483 BP.
DE Mouse genomic sequence for mCG17918.
PN US2003216558-A1.
PD 20-NOV-2003.
PA (MORR/) MORRIS D W.
PA (ENGEL/) ENGELHARD E K.
Query Match
Best Local Similarity 2.3%; Score 34.2; DB 11; Length 93483;
RESULT 1362
ID ABD33157 standard; DNA; 109559 BP.
DE Murine cancer-associated (CA) gene MD07-021.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match
Best Local Similarity 2.3%; Score 34.2; DB 13; Length 109559;
RESULT 1363
ID ABR95044 standard; DNA; 110096 BP.
DE Gene #1542 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match
Best Local Similarity 2.3%; Score 34.2; DB 6; Length 110096;
RESULT 1364
ID ABR95044 standard; DNA; 110096 BP.
DE Gene #1542 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match
Best Local Similarity 2.3%; Score 34.2; DB 6; Length 110096;
RESULT 1365
ID ADL13512 standard; DNA; 178870 BP.
DE Osteoarthritis-associated polymorphic nucleotide #44.
PN WO2003058166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 2.3%; Score 34.2; DB 10; Length 178870;
RESULT 1366
ID ABD32841 standard; DNA; 227448 BP.
DE Mouse cancer-associated genomic DNA MD17-014.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match
Best Local Similarity 2.3%; Score 34.2; DB 13; Length 227448;
RESULT 1367
ID ADF51132 standard; DNA; 243428 BP.
DE Human P-Rex1 genomic DNA sequence.
PN WO2003080664-A1.
PD 02-OCT-2003.
PA (BAHR-) BARAHAM INST.
Query Match
Best Local Similarity 2.3%; Score 34.2; DB 12; Length 243428;
RESULT 1368
ID ADP75180 standard; DNA; 304905 BP.
DE Human Endophilin 2 gene.
PN WO2003031594-A2.
PD 17-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
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Query Match 2.3%; Score 34; DB 11; Length 304905;
Best Local Similarity 55.5%; Pred. No. 2e+03;
RESULT 1369
ID AAG08244 standard; cDNA to mRNA; 234 BP.
DE Exon 4 of rice pyruvate orthophosphate dikinase gene.
FN JP01184657-A.
PD 25-JUL-1995.
PA (NITRA-) JAPAN TAFU GURASU KK.
Query Match 2.3%; Score 34; DB 2; Length 234;
Best Local Similarity 61.1%; Pred. No. 67;
RESULT 1370
ID ADG99503 standard; DNA; 280 BP.
DE Kidney disease-associated gene-related mouse DNA sequence SeqID633.
FN WO2003091427-A1.
PD 06-NOV-2003.
PA (KANS-) KANSAS TECHNOLOGY LICENSING ORG CO LTD.
Query Match 2.3%; Score 34; DB 12; Length 280;
Best Local Similarity 47.2%; Pred. No. 73;
RESULT 1371
ID ADI45208 standard; cDNA; 378 BP.
DE Rice isoprenoid biosynthesis-associated cDNA #70.
FN US2004010815-A1.
PD 15-JAN-2004.
PA (LANG/) LANGSE B M.
PA (GHAS/) GHASSEMIAN M.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOLF/) GOLF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (MOUG/) MOUGHAMER T.
PA (PROV/) PROVART N.
PA (RICK/) RICKS D.
PA (ZHUT/) ZHU T.
Query Match 2.3%; Score 34; DB 12; Length 378;
Best Local Similarity 60.5%; Pred. No. 85;
RESULT 1372
ID AAS69541 standard; cDNA; 390 BP.
DE DNA encoding novel human diagnostic protein #5345.
FN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.3%; Score 34; DB 5; Length 390;
Best Local Similarity 47.6%; Pred. No. 86;
RESULT 1373
ID AA184784 standard; cDNA; 400 BP.
DE Human polynucleotide SEQ ID NO 4844.
FN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.3%; Score 34; DB 4; Length 400;
Best Local Similarity 47.6%; Pred. No. 87;
RESULT 1374
ID ABD16714 standard; DNA; 429 BP.
DE Pseudomonas aeruginosa polynucleotide #15318.
FN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.3%; Score 34; DB 11; Length 429;
Best Local Similarity 49.4%; Pred. No. 90;
RESULT 1375
ID ABR6216 standard; cDNA; 455 BP.
DE cDNA sequence #607 encoding novel human secreted protein.
FN WO200177289-A2.
PD 18-OCT-2001.
PA (GEMY) GENETICS INST INC.
Query Match 2.3%; Score 34; DB 6; Length 455;
Best Local Similarity 52.0%; Pred. No. 93;
RESULT 1376
ID ACH73361 standard; DNA; 510 BP.
DE Human genome derived single exon probe #6556.
FN US2003194704-A1.

PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 2.3%; Score 34; DB 12; Length 510;
Best Local Similarity 50.0%; Pred. No. 98;
RESULT 1377
ID ADB83517 standard; DNA; 521 BP.
DE Rat gene AA799755, SEQ ID NO 11114.
FN WO2003016475-A2.
PD 27-FEB-2003.
PA (GERO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 2.3%; Score 34; DB 10; Length 521;
Best Local Similarity 52.9%; Pred. No. 1e+02;
RESULT 1378
ID ABD16760 standard; DNA; 726 BP.
DE Pseudomonas aeruginosa polynucleotide #15364.
FN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.3%; Score 34; DB 11; Length 726;
Best Local Similarity 49.4%; Pred. No. 1.2e+02;
RESULT 1379
ID ABV06518 standard; cDNA; 793 BP.
DE Human prostate expression marker cDNA 6509.
FN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.3%; Score 34; DB 5; Length 793;
Best Local Similarity 46.6%; Pred. No. 1.2e+02;
RESULT 1380
ID ADR46465 standard; DNA; 895 BP.
DE Tobacco caltractin-like protein coding sequence SEQ ID NO: 31.
FN WO2004070035-A2.
PD 19-AUG-2004.
PA (SUNG-) SUNGENE GMBH & CO KGAA.
Query Match 2.3%; Score 34; DB 13; Length 895;
Best Local Similarity 46.9%; Pred. No. 1.3e+02;
RESULT 1381
ID AAS90702 standard; cDNA; 1167 BP.
DE DNA encoding novel human diagnostic protein #26506.
FN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.3%; Score 34; DB 5; Length 1167;
Best Local Similarity 46.3%; Pred. No. 1.5e+02;
RESULT 1382
ID ABD16865 standard; DNA; 1383 BP.
DE Pseudomonas aeruginosa polynucleotide #15469.
FN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.3%; Score 34; DB 11; Length 1383;
Best Local Similarity 49.4%; Pred. No. 1.6e+02;
RESULT 1383
ID ABD16805 standard; DNA; 1503 BP.
DE Pseudomonas aeruginosa polynucleotide #15409.
FN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.3%; Score 34; DB 11; Length 1503;
Best Local Similarity 49.4%; Pred. No. 1.7e+02;
RESULT 1384
ID AAK52313 standard; cDNA; 1627 BP.
DE Human polynucleotide SEQ ID NO 858.
FN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.3%; Score 34; DB 4; Length 1627;
Best Local Similarity 57.5%; Pred. No. 1.8e+02;
RESULT 1385
ID ABX05202 standard; cDNA; 2154 BP.

DE Human novel polynucleotide #217.
PN WO200274961-A1.
PD 26-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match 2.3%; Score 34; DB 8; Length 2154;
Best Local Similarity 54.9%; Pred. No. 2e+02;
RESULT 1386
ID ADO87317 standard; cDNA; 2192 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #4194.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 2.3%; Score 34; DB 13; Length 2192;
Best Local Similarity 54.9%; Pred. No. 2e+02;
RESULT 1387
ID ADO87554 standard; cDNA; 2192 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #4432.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Query Match 2.3%; Score 34; DB 13; Length 2192;
Best Local Similarity 54.9%; Pred. No. 2e+02;
RESULT 1388
ID ADA53499 standard; cDNA; 2338 BP.
DE Human coding sequence, SEQ ID 1067.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 2.3%; Score 34; DB 10; Length 2338;
Best Local Similarity 52.1%; Pred. No. 2.1e+02;
RESULT 1389
ID ADM03650 standard; cDNA; 2404 BP.
DE Human cDNA of the invention SEQ ID NO:2335.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 2.3%; Score 34; DB 11; Length 2404;
Best Local Similarity 57.5%; Pred. No. 2.1e+02;
RESULT 1390
ID AAT35233 standard; cDNA; 2823 BP.
DE Natural killer lytic associated protein cDNA.
PN WO9626744-A1.
PD 06-SEP-1996.
PA (UYAR-) UNIV ARKANSAS.
Query Match 2.3%; Score 34; DB 2; Length 2823;
Best Local Similarity 50.0%; Pred. No. 2.3e+02;
RESULT 1391
ID ADO36980 standard; DNA; 2844 BP.
DE Cell proliferation-related nucleic acid sequence #70.
PN WO2004061122-A2.
PD 22-JUL-2004.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.3%; Score 34; DB 12; Length 2844;
Best Local Similarity 61.1%; Pred. No. 2.3e+02;
RESULT 1392
ID ADQ15650 standard; DNA; 2844 BP.
DE Rice stress-related protein coding sequence #30.
PN WO2004061080-A2.
PD 22-JUL-2004.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.3%; Score 34; DB 12; Length 2844;
Best Local Similarity 61.1%; Pred. No. 2.3e+02;
RESULT 1393
ID AAL04774 standard; DNA; 3051 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 7462.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 2.3%; Score 34; DB 4; Length 3051;
Best Local Similarity 48.0%; Pred. No. 2.4e+02;
RESULT 1394
ID AAK95303 standard; cDNA; 3809 BP.
DE Human prostate specific gene sequence DEX0283_68.
PN WO200242329-A2.
PD 30-MAY-2002.
PA (DIAD-) DIADEXUS INC.
Query Match 2.3%; Score 34; DB 6; Length 3809;
Best Local Similarity 47.2%; Pred. No. 2.7e+02;
RESULT 1395
ID ADS48518 standard; cDNA; 3851 BP.
DE Bacterial polynucleotide #3261.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 2.3%; Score 34; DB 13; Length 3851;
Best Local Similarity 63.4%; Pred. No. 2.7e+02;
RESULT 1396
ID AAC64438 standard; DNA; 3896 BP.
DE Arabidopsis thaliana PDAT genomic DNA SEQ ID NO:11.
PN WO20060095-A2.
PD 12-OCT-2000.
PA (BADI) BASF PLANT SCI GMBH.
Query Match 2.3%; Score 34; DB 3; Length 3896;
Best Local Similarity 52.9%; Pred. No. 2.7e+02;
RESULT 1397
ID AAC64448 standard; DNA; 3896 BP.
DE Arabidopsis thaliana PDAT genomic DNA SEQ ID NO:10b.
PN WO20060095-A2.
PD 12-OCT-2000.
PA (BADI) BASF PLANT SCI GMBH.
Query Match 2.3%; Score 34; DB 3; Length 3896;
Best Local Similarity 52.9%; Pred. No. 2.7e+02;
RESULT 1398
ID AAR26524 standard; cDNA; 4182 BP.
DE Human protein/oligonucleotide transporter hPHT2 gene intron 1.
PN WO200160854-A1.
PD 23-AUG-2001.
PA (REGC) UNIV CALIFORNIA.
Query Match 2.3%; Score 34; DB 4; Length 4182;
Best Local Similarity 50.0%; Pred. No. 2.8e+02;
RESULT 1399
ID AAQ98237 standard; DNA; 8626 BP.
DE Partial rice pyruvate orthophosphate dikinase gene.
PN JP07184657-A.
PD 25-JUL-1995.
PA (NITA-) JAPAN TAFU GURASU KK.
Query Match 2.3%; Score 34; DB 2; Length 8626;
Best Local Similarity 61.1%; Pred. No. 4e+02;
RESULT 1400
ID ACC4896 standard; DNA; 8766 BP.
DE Rhodococcus ruber eth gene cluster involved in ETEB degradation.
PN EP1270722-A1.
PD 02-JAN-2003.
PA (INSE) INST PASTEUR.
PA (INSE) INST FRANCAIS DU PETROLE.
Query Match 2.3%; Score 34; DB 8; Length 8766;
Best Local Similarity 51.5%; Pred. No. 4.1e+02;
RESULT 1401
ID ABI15220 standard; cDNA; 10479 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 40142.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 2.3%; Score 34; DB 4; Length 10479;
Best Local Similarity 45.5%; Pred. No. 4.4e+02;
RESULT 1402
ID ACC48895 standard; DNA; 12342 BP.

DE Rhodococcus ruber eth gene cluster deleted region.
PN EPI270722-A1.
PD 02-JAN-2003.
PA (INSP) INST PASTEUR.
PA (INSP) INST FRANCAIS DU PETROLE.
Query Match 2.3%; Score 34; DB 8; Length 12342;
Best Local Similarity 51.5%; Pred. No. 4.8e+02;
RESULT 1403
ID AB074539 standard; DNA; 19321 BP.
DE Human transglutaminase-A gene sequence SEQ ID NO:4.
PN WO20029285-A2.
PD 01-AUG-2002.
PA (DECO-) DECODE GENETICS INC.
Query Match 2.3%; Score 34; DB 6; Length 19321;
Best Local Similarity 63.4%; Pred. No. 6e+02;
RESULT 1404
ID ADA14746 standard; DNA; 22118 BP.
DE Mouse 45S rRNA gene.
PN US2002160970-A1.
PD 31-OCT-2002.
PA (HADI/) HADIACZKY G.
PA (SZAL/) SZALAY A A.
Query Match 2.3%; Score 34; DB 8; Length 22118;
Best Local Similarity 56.0%; Pred. No. 6.4e+02;
RESULT 1405
ID ADA37415 standard; DNA; 22118 BP.
DE Origin of replication DNA.
PN US2003108914-A1.
PD 12-JUN-2003.
PA (HADI/) HADIACZKY G.
Query Match 2.3%; Score 34; DB 9; Length 22118;
Best Local Similarity 56.0%; Pred. No. 6.4e+02;
RESULT 1406
ID AAD61410 standard; DNA; 22118 BP.
DE Mouse ribosomal DNA (rDNA) repeat region.
PN US2003101480-A1.
PD 29-MAY-2003.
PA (HADI/) HADIACZKY G.
PA (SZAL/) SZALAY A A.
Query Match 2.3%; Score 34; DB 10; Length 22118;
Best Local Similarity 56.0%; Pred. No. 6.4e+02;
RESULT 1407
ID ADP10518 standard; DNA; 22118 BP.
DE Mouse ribosomal RNA gene repeat unit.
PN WO2003093469-A2.
PD 13-NOV-2003.
PA (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
Query Match 2.3%; Score 34; DB 10; Length 22118;
Best Local Similarity 56.0%; Pred. No. 6.4e+02;
RESULT 1408
ID ACC44629 standard; DNA; 22118 BP.
DE Mouse ribosomal RNA gene (rDNA) nucleotide sequence SEQ ID NO:18.
PN WO200297059-A2.
PD 05-DEC-2002.
PA (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
Query Match 2.3%; Score 34; DB 10; Length 22118;
Best Local Similarity 56.0%; Pred. No. 6.4e+02;
RESULT 1409
ID ADR43948 standard; DNA; 22118 BP.
DE Mouse pre rRNA gene.
PN US2004163147-A1.
PD 19-AUG-2004.
PA (HADI/) HADIACZKY G.
Query Match 2.3%; Score 34; DB 13; Length 22118;
Best Local Similarity 56.0%; Pred. No. 6.4e+02;
RESULT 1410
ID ACC48894 standard; DNA; 23656 BP.
DE Rhodococcus ruber eth gene region involved in ETBE degradation.
PN EPI270722-A1.
PD 02-JAN-2003.
PA (INSP) INST PASTEUR.
PA (INSP) INST FRANCAIS DU PETROLE.
Query Match 2.3%; Score 34; DB 8; Length 23656;
Best Local Similarity 51.5%; Pred. No. 6.6e+02;
RESULT 1411
ID AAK90279 standard; DNA; 25423 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 3855.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.3%; Score 34; DB 4; Length 25423;
Best Local Similarity 57.5%; Pred. No. 6.9e+02;
RESULT 1412
ID AA157656 standard; DNA; 25423 BP.
DE Human colorectal cancer antigen coding sequence SEQ ID NO: 193.
PN WO200155350-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.3%; Score 34; DB 4; Length 25423;
Best Local Similarity 57.5%; Pred. No. 6.9e+02;
RESULT 1413
ID ABS9833 standard; DNA; 25423 BP.
DE Genomic DNA #37 encoding human colorectal cancer related protein.
PN US2002119919-A1.
PD 29-AUG-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.3%; Score 34; DB 6; Length 25423;
Best Local Similarity 57.5%; Pred. No. 6.9e+02;
RESULT 1414
ID ADB92986 standard; DNA; 25423 BP.
DE Human colorectal cancer related polypeptide DNA #37.
PN US2003054420-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.3%; Score 34; DB 10; Length 25423;
Best Local Similarity 57.5%; Pred. No. 6.9e+02;
RESULT 1415
ID AAK90280 standard; DNA; 25424 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 3856.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.3%; Score 34; DB 4; Length 25424;
Best Local Similarity 57.5%; Pred. No. 6.9e+02;
RESULT 1416
ID AA157657 standard; DNA; 25424 BP.
DE Human colorectal cancer antigen coding sequence SEQ ID NO: 194.
PN WO200155350-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.3%; Score 34; DB 4; Length 25424;
Best Local Similarity 57.5%; Pred. No. 6.9e+02;
RESULT 1417
ID ABS99834 standard; DNA; 25424 BP.
DE Genomic DNA #38 encoding human colorectal cancer related protein.
PN US2002119919-A1.
PD 29-AUG-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.3%; Score 34; DB 6; Length 25424;
Best Local Similarity 57.5%; Pred. No. 6.9e+02;
RESULT 1418
ID ADB92987 standard; DNA; 25424 BP.
DE Human colorectal cancer related polypeptide DNA #38.
PN US2003054420-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.3%; Score 34; DB 10; Length 25424;
Best Local Similarity 57.5%; Pred. No. 6.9e+02;
RESULT 1419
ID AAK68605 standard; DNA; 26555 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23417.
PN WO200157182-A2.

PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCT INC.
Query Match 2.3%; Score 34; DB 4; Length 26555;
Best Local Similarity 50.0%; Pred. No. 7e+02;
RESULT 1420
ID AAK6372 standard; DNA; 26555 BP.
DE Human Immune/haematopoietic antigen genomic sequence SEQ ID NO:23184.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCT INC.
Query Match 2.3%; Score 34; DB 4; Length 26555;
Best Local Similarity 50.0%; Pred. No. 7e+02;
RESULT 1421
ID AAI62833 standard; DNA; 26555 BP.
DE Human genomic DNA SEQ ID NO 161.
PN WO200155449-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCT INC.
Query Match 2.3%; Score 34; DB 4; Length 26555;
Best Local Similarity 50.0%; Pred. No. 7e+02;
RESULT 1422
ID AAL56704 standard; DNA; 36604 BP.
DE Chimpanzee adenovirus serotype Pan6 genomic DNA.
PN WO2003046124-A2.
PD 05-JUN-2003.
PA (UTPE-) UNIV PENNSYLVANIA.
Query Match 2.3%; Score 34; DB 8; Length 36604;
Best Local Similarity 50.0%; Pred. No. 8.3e+02;
RESULT 1423
ID ACN44568 standard; DNA; 43799 BP.
DE Mouse genomic sequence MCC21498.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.3%; Score 34; DB 11; Length 43799;
Best Local Similarity 22.4%; Pred. No. 9e+02;
RESULT 1424
ID AAD36070 standard; DNA; 45993 BP.
DE Human liver glucokinase genomic DNA.
PN WO200224741-A2.
PD 28-MAR-2002.
PA (RYAN/) RYAN J W.
Query Match 2.3%; Score 34; DB 6; Length 45993;
Best Local Similarity 46.3%; Pred. No. 9.2e+02;
RESULT 1425
ID ADA02729 standard; DNA; 50396 BP.
DE Mouse Gnb1 carcinoma associated gene, SEQ ID NO:1247.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.3%; Score 34; DB 9; Length 50396;
Best Local Similarity 54.9%; Pred. No. 9.7e+02;
RESULT 1426
ID ADA02732 standard; DNA; 50396 BP.
DE Human GNB1 carcinoma associated gene, SEQ ID NO:1250.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.3%; Score 34; DB 9; Length 50396;
Best Local Similarity 54.9%; Pred. No. 9.7e+02;
RESULT 1427
ID ADB72470 standard; DNA; 50396 BP.
DE Human GNB1 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.3%; Score 34; DB 10; Length 50396;
Best Local Similarity 54.9%; Pred. No. 9.7e+02;
RESULT 1428
ID ADB72467 standard; DNA; 50396 BP.
DE Mouse Gnb1 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.

PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.3%; Score 34; DB 10; Length 50396;
Best Local Similarity 54.9%; Pred. No. 9.7e+02;
RESULT 1429
ID ADE95977 standard; DNA; 50396 BP.
DE Mouse Gnb1 gene genomic DNA sequence.
PN WO2003039484-A2.
PD 15-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.3%; Score 34; DB 10; Length 50396;
Best Local Similarity 54.9%; Pred. No. 9.7e+02;
RESULT 1430
ID ADE95980 standard; DNA; 50396 BP.
DE Human GNB1 gene genomic DNA sequence.
PN WO2003039484-A2.
PD 15-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.3%; Score 34; DB 10; Length 50396;
Best Local Similarity 54.9%; Pred. No. 9.7e+02;
RESULT 1431
ID ADPE4454 standard; DNA; 76994 BP.
DE Sorangium cellulosum discorazole polyketide synthase gene cluster DNA.
PN WO2004053065-A2.
PD 24-JUN-2004.
PA (KOSA-) KOSAN BIOSCIENCES INC.
Query Match 2.3%; Score 34; DB 12; Length 76994;
Best Local Similarity 59.2%; Pred. No. 1.2e+03;
RESULT 1432
ID ACN44076 standard; DNA; 77834 BP.
DE Mouse genomic sequence MCC14020.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.3%; Score 34; DB 11; Length 77834;
Best Local Similarity 52.1%; Pred. No. 1.2e+03;
RESULT 1433
ID ABX09143 standard; DNA; 86114 BP.
DE Mycobacterium tuberculosis H37Rv BAC clone BAC-RV265.
PN WO200274803-A2.
PD 26-SEP-2002.
PA (INSP) INST PASTEUR.
Query Match 2.3%; Score 34; DB 6; Length 86114;
Best Local Similarity 48.0%; Pred. No. 1.3e+03;
RESULT 1434
ID ADO17634 standard; DNA; 96276 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 451.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.3%; Score 34; DB 12; Length 96276;
Best Local Similarity 54.9%; Pred. No. 1.3e+03;
RESULT 1435
ID ADA02501 standard; DNA; 96597 BP.
DE Mouse Bach2 carcinoma associated gene, SEQ ID NO:1019.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.3%; Score 34; DB 9; Length 96597;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
RESULT 1436
ID ADB72239 standard; DNA; 96597 BP.
DE Mouse Bach2 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 2.3%; Score 34; DB 10; Length 96597;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
RESULT 1437
ID ADE95749 standard; DNA; 96597 BP.
DE Mouse Bach2 gene genomic DNA sequence.
PN WO2003039484-A2.
PD 15-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.

Query Match 2.3%; Score 34; DB 10; Length 96597;
 DE Best Local Similarity 50.0%; Pred. No. 1.3e+03;
 RESULT 1438
 Query Match 2.3%; Score 34; DB 4; Length 110000;
 DE Best Local Similarity 48.0%; Pred. No. 1.4e+03;
 RESULT 1439
 Query Match 2.3%; Score 34; DB 4; Length 110000;
 DE Best Local Similarity 48.0%; Pred. No. 1.4e+03;
 RESULT 1440
 Query Match 2.3%; Score 34; DB 6; Length 110000;
 DE Best Local Similarity 52.1%; Pred. No. 1.4e+03;
 RESULT 1441
 Query Match 2.3%; Score 34; DB 6; Length 110000;
 DE Best Local Similarity 52.1%; Pred. No. 1.4e+03;
 RESULT 1442
 Query Match 2.3%; Score 34; DB 12; Length 110000;
 DE Best Local Similarity 52.1%; Pred. No. 1.4e+03;
 RESULT 1443
 Query Match 2.3%; Score 34; DB 12; Length 110000;
 DE Best Local Similarity 52.1%; Pred. No. 1.4e+03;
 RESULT 1444
 Query Match 2.3%; Score 34; DB 12; Length 110000;
 DE Best Local Similarity 52.1%; Pred. No. 1.4e+03;
 RESULT 1445
 Query Match 2.3%; Score 34; DB 12; Length 110000;
 DE Best Local Similarity 52.1%; Pred. No. 1.4e+03;
 RESULT 1446
 Query Match 2.3%; Score 34; DB 12; Length 110000;
 DE Best Local Similarity 52.1%; Pred. No. 1.4e+03;
 RESULT 1447
 Query Match 2.3%; Score 34; DB 12; Length 110000;
 DE Best Local Similarity 52.1%; Pred. No. 1.4e+03;
 RESULT 1448
 Query Match 2.3%; Score 34; DB 12; Length 110000;
 DE Best Local Similarity 52.1%; Pred. No. 1.4e+03;
 RESULT 1449
 ID AAK53491 standard; DNA; 114955 BP.
 DE Human adenosine A1 receptor antisense oligonucleotide fragment.
 PN WO9913886-A1.
 PD 25-MAR-1999.
 PA (UTEC-) UNIV EAST CAROLINA.
 Query Match 2.3%; Score 34; DB 13; Length 110000;
 DE Best Local Similarity 47.2%; Pred. No. 1.4e+03;
 RESULT 1450
 ID ABR35015 standard; cDNA; 136328 BP.
 DE Human gene expression profile polynucleotide SEQ ID NO 127.
 PN WO200274979-A2.
 PD 26-SEP-2002.
 PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
 Query Match 2.3%; Score 34; DB 6; Length 136328;
 DE Best Local Similarity 50.0%; Pred. No. 1.6e+03;
 RESULT 1451
 ID ADO59449 standard; DNA; 153740 BP.
 DE Human cancer-associated (CA) gene sequence SEQ ID NO:85.
 PN WO2004058288-A1.
 PD 15-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 2.3%; Score 34; DB 12; Length 153740;
 DE Best Local Similarity 52.1%; Pred. No. 1.6e+03;
 RESULT 1452
 ID ADI13501 standard; DNA; 167932 BP.
 DE Osteoarthritis-associated polymorphic nucleotide #33.
 PN WO2003054166-A2.
 PD 03-JUL-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 2.3%; Score 34; DB 10; Length 167932;
 DE Best Local Similarity 57.5%; Pred. No. 1.7e+03;
 RESULT 1453

ID ADO97146 standard; DNA; 348101 BP.
 DE Human cancer associated sequence HD08-007, SEQ ID 122.
 PN WO2004060304-A2.
 PD 22-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 2.3%; Score 34; DB 12; Length 348101;
 DE Best Local Similarity 47.2%; Pred. No. 2.3e+03;
 RESULT 1454
 ID ADA58561 standard; cDNA; 270 BP.
 DE Maize sucrose synthase EST #225.
 PN US2003135870-A1.
 PD 17-JUL-2003.
 PA (CHEI/) CHEIKH N.
 PA (FISH/) FISHER D K.
 PA (LITU/) LITU J.
 Query Match 2.3%; Score 33.8; DB 9; Length 270;
 DE Best Local Similarity 58.4%; Pred. No. 82;
 RESULT 1455
 ID ACN87596 standard; DNA; 383 BP.
 DE Breast cancer related marker, seq id 8746.
 PN US200309974-A1.
 PD 29-MAY-2003.
 PA (MILL-) MILLENNium PHARM INC.
 Query Match 2.3%; Score 33.8; DB 11; Length 383;
 DE Best Local Similarity 48.7%; Pred. No. 97;
 RESULT 1456
 ID ABR34899 standard; cDNA; 409 BP.
 DE Human cDNA encoding secreted protein #37.
 PN WO20017288-A2.
 PD 18-OCT-2001.
 PA (GENV) GENETICS INST INC.
 Query Match 2.3%; Score 33.8; DB 6; Length 409;
 DE Best Local Similarity 54.4%; Pred. No. 1e+02;
 RESULT 1457
 ID ABR37415 standard; cDNA; 415 BP.
 DE Bovine EST associated with lactation/muscle/fat deposition #2580.
 PN US2002137139-A1.
 PD 26-SEP-2002.
 PA (BYATT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARW/) WARREN W C.
 Query Match 2.3%; Score 33.8; DB 8; Length 415;
 DE Best Local Similarity 48.7%; Pred. No. 1e+02;
 RESULT 1458
 ID ABD16662 standard; DNA; 438 BP.
 DE Pseudomonas aeruginosa polynucleotide #15266.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 2.3%; Score 33.8; DB 11; Length 438;
 DE Best Local Similarity 49.7%; Pred. No. 1e+02;
 RESULT 1459
 ID ABA59121 standard; DNA; 454 BP.
 DE Human foetal liver single exon nucleic acid probe #7426.
 PN WO200157277-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Query Match 2.3%; Score 33.8; DB 4; Length 454;
 DE Best Local Similarity 50.3%; Pred. No. 1.1e+02;
 RESULT 1460
 ID AA138867 standard; DNA; 454 BP.
 DE Probe #7553 used to measure gene expression in human placenta sample.
 PN WO200157272-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Query Match 2.3%; Score 33.8; DB 4; Length 454;
 DE Best Local Similarity 50.3%; Pred. No. 1.1e+02;
 RESULT 1461
 ID AAK33067 standard; DNA; 454 BP.
 DE Human bone marrow expressed single exon probe SEQ ID NO: 7624.
 PN WO200157276-A2.
 PD 09-AUG-2001.

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PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.3%; Score 33.8; DB 4; Length 454;
Best Local Similarity 50.3%; Pred. No. 1.1e+02;
RESULT 1462
ID AAK07302 standard; DNA; 454 BP.
DE Human brain expressed single exon probe SEQ ID NO: 7293.
PN WO200157275-A2.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.3%; Score 33.8; DB 4; Length 454;
Best Local Similarity 50.3%; Pred. No. 1.1e+02;
RESULT 1463
ID ABS32802 standard; DNA; 454 BP.
DE Human liver single exon probe, SEQ ID NO 7792.
PN WO200157273-A2.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.3%; Score 33.8; DB 4; Length 454;
Best Local Similarity 50.3%; Pred. No. 1.1e+02;
RESULT 1464
ID ABS07882 standard; DNA; 454 BP.
DE Human genome-derived single exon probe from lung SEQ ID NO 7873.
PN WO200186003-A2.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 2.3%; Score 33.8; DB 6; Length 454;
Best Local Similarity 50.3%; Pred. No. 1.1e+02;
RESULT 1465
ID ACH15828 standard; cDNA; 473 BP.
DE Human adult heart cDNA #142.
PN US2003073623-A1.
PA (DNA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 2.3%; Score 33.8; DB 9; Length 473;
Best Local Similarity 46.7%; Pred. No. 1.1e+02;
RESULT 1466
ID AAI88625 standard; cDNA; 512 BP.
DE Human polynucleotide SEQ ID NO 8685.
PN WO200164835-A2.
PA (HYSE-) HYSEQ INC.
Query Match 2.3%; Score 33.8; DB 4; Length 512;
Best Local Similarity 54.4%; Pred. No. 1.1e+02;
RESULT 1467
ID ADD16019 standard; cDNA; 517 BP.
DE cDNA (SeqID 87) that confers an altered visual phenotype in plants.
PN WO2003020741-A1.
PA (DOMC-) DOW CHEM CO.
PA (DOMC-) DOW AGROSCIENCES LLC.
Query Match 2.3%; Score 33.8; DB 10; Length 517;
Best Local Similarity 53.4%; Pred. No. 1.1e+02;
RESULT 1468
ID ADL45106 standard; DNA; 531 BP.
DE Human ovarian cancer DNA marker #18996.
PN WO200170979-A2.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.3%; Score 33.8; DB 5; Length 531;
Best Local Similarity 46.7%; Pred. No. 1.1e+02;
RESULT 1469
ID AAH1011 standard; cDNA; 572 BP.
DE Human cDNA clone (3'-primer) SEQ ID NO:7846.
PN EP1074617-A2.
PA (HELI-) HELIX RES INST.
Query Match 2.3%; Score 33.8; DB 4; Length 572;
Best Local Similarity 46.0%; Pred. No. 1.2e+02;
RESULT 1470
ID ABR89970 standard; cDNA; 619 BP.
DE Expressed sequence tag (EST) #5 encoding human alanine aminotransferase.
PN WO200255712-A2.
PA (FARB-) BAYER AG.
Query Match 2.3%; Score 33.8; DB 6; Length 619;
Best Local Similarity 53.4%; Pred. No. 1.2e+02;
RESULT 1471
ID ABR89969 standard; cDNA; 631 BP.
DE Expressed sequence tag (EST) #4 encoding human alanine aminotransferase.
PN WO200255712-A2.
PA (FARB-) BAYER AG.
Query Match 2.3%; Score 33.8; DB 6; Length 631;
Best Local Similarity 53.4%; Pred. No. 1.2e+02;
RESULT 1472
ID ABO65930 standard; DNA; 654 BP.
DE Arabidopsis thaliana polynucleotide SEQ ID NO 507.
PN US2002059663-A1.
PA (ANY/) ANY Y.
PA (GORL/) GORLACH J.
PA (HAMT/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (RAIN/) RAINES T M.
PA (YUY/) YU Y.
PA (PAGE/) PAGE A.
PA (MATH/) MATHEW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
PA (KRIC/) KRICKER M.
PA (SIAT/) SIATER T.
PA (DAVI/) DAVIS K R.
PA (ALLE/) ALLEN K.
PA (HOFF/) HOFFMAN N.
PA (HURB/) HURBAN P.
Query Match 2.3%; Score 33.8; DB 6; Length 654;
Best Local Similarity 47.4%; Pred. No. 1.3e+02;
RESULT 1473
ID ABD17092 standard; DNA; 672 BP.
DE Pseudomonas aeruginosa polynucleotide #15696.
PN US6551795-B1.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 2.3%; Score 33.8; DB 11; Length 672;
Best Local Similarity 46.4%; Pred. No. 1.3e+02;
RESULT 1474
ID AAC38557 standard; DNA; 716 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 21405.
PN EP1033405-A2.
PA (RITA-) RITAGAKU KENKYUSHO.
Query Match 2.3%; Score 33.8; DB 3; Length 716;
Best Local Similarity 47.4%; Pred. No. 1.3e+02;
RESULT 1475
ID AAV15437 standard; DNA; 753 BP.
DE Human gene fragment D13C10 causing carboxydehydrogenase activity.
PN JP10057062-A.
PA (RITA-) RITAGAKU KENKYUSHO.
Query Match 2.3%; Score 33.8; DB 2; Length 753;
Best Local Similarity 50.3%; Pred. No. 1.4e+02;
RESULT 1476
ID AAH03867 standard; cDNA; 765 BP.
DE Human cDNA clone (5'-primer) SEQ ID NO:702.
PN EP1074617-A2.
PA (HELI-) HELIX RES INST.
Query Match 2.3%; Score 33.8; DB 4; Length 765;
Best Local Similarity 52.5%; Pred. No. 1.4e+02;
RESULT 1477
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ID AAc4956 standard; DNA; 774 BP.
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 44762.
 PN EPI033405-A2.
 PD 06-SEP-2000.
 Query Match
 Best Local Similarity 2.3%; Score 33.8; DB 3; Length 774;
 47.4%; Pred. No. 1.4e+02;
 RESULT 1478
 ID ABR99115 standard; DNA; 777 BP.
 DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 883.
 PN US2002023281-A1.
 PD 21-FEB-2002.
 PA (GORL/) GORLACH J.
 PA (ANY/) AN Y.
 PA (HAM/) HAMILTON C M.
 PA (PRIC/) PRICE J L.
 PA (RAIN/) RAINES T M.
 PA (YUY/) YU Y.
 PA (RAME/) RAMEAKA J G.
 PA (PAGE/) PAGE A.
 PA (MATH/) MATHW A V.
 PA (LEDF/) LEDFORD B L.
 PA (MOES/) MOESSNER J P.
 PA (HNAS/) HNAS W D.
 PA (GARC/) GARCIA C A.
 PA (KRIC/) KRICKER M.
 PA (SLAT/) SLATER T.
 PA (DAVI/) DAVIS K R.
 PA (ALLE/) ALLEN K.
 PA (HOFF/) HOFFMAN N.
 PA (HURB/) HURBAN P.
 Query Match
 Best Local Similarity 2.3%; Score 33.8; DB 6; Length 777;
 49.2%; Pred. No. 1.4e+02;
 RESULT 1479
 ID ADI42806 standard; DNA; 820 BP.
 DE Plant transcription factor polynucleotide #811.
 PN US2004019927-A1.
 PD 29-JAN-2004.
 PA (SHER/) SHERMAN B K.
 PA (RIEC/) RIECHMANN J L.
 PA (JIAN/) JIANG C.
 PA (HEAR/) HEARD J E.
 PA (HNAK/) HNAKE V.
 PA (CREE/) CREELMAN R A.
 PA (RATC/) RATCLIFFE O.
 PA (ADAM/) ADAM L J.
 PA (REUB/) REUBER T L.
 PA (KEDD/) KEDDIE J.
 PA (BROU/) BROUN P E.
 PA (PILG/) PILGRIM M L.
 PA (DUBE/) DUBELL A N.
 PA (PINE/) PINEDA O.
 PA (YUGG/) YU G.
 Query Match
 Best Local Similarity 2.3%; Score 33.8; DB 12; Length 820;
 48.2%; Pred. No. 1.4e+02;
 RESULT 1480
 ID ADO03013 standard; cDNA; 820 BP.
 DE Corn orthologue of Thalecress transcription factor, cDNA #124.
 PN US2004045049-A1.
 PD 04-MAR-2004.
 PA (ZHAN/) ZHANG J.
 PA (FROM/) FROM M E.
 PA (HEAR/) HEARD J E.
 PA (RIEC/) RIECHMANN J L.
 PA (ADAM/) ADAM L J.
 PA (BROU/) BROUN P E.
 PA (PINE/) PINEDA O.
 PA (REUB/) REUBER T L.
 PA (KEDD/) KEDDIE J S.
 PA (YUGG/) YU G.
 PA (JIAN/) JIANG C.
 PA (SAMA/) SAMARA R S.
 PA (PILG/) PILGRIM M L.
 PA (CREE/) CREELMAN R A.

PA (DUBE/) DUBELL A N.
 PA (RATC/) RATCLIFFE O.
 PA (KIMI/) KIMIMOTO R.
 PA (SHER/) SHERMAN B K.
 Query Match
 Best Local Similarity 2.3%; Score 33.8; DB 12; Length 820;
 48.2%; Pred. No. 1.4e+02;
 RESULT 1481
 ID ADO62434 standard; DNA; 820 BP.
 DE Transcription factor G961 orthologous sequence, SEQ ID 901.
 PN WO2004031349-A2.
 PD 15-APR-2004.
 PA (MENB-) MENDEL BIOTECHNOLOGY INC.
 Query Match
 Best Local Similarity 2.3%; Score 33.8; DB 12; Length 820;
 48.2%; Pred. No. 1.4e+02;
 RESULT 1482
 ID ABR34722 standard; cDNA; 882 BP.
 DE Coding sequence SEQ ID 80, upregulated in osteogenesis.
 PN WO200281745-A2.
 PD 17-OCT-2002.
 PA (AVET-) AVENTIS PHARMA SA.
 Query Match
 Best Local Similarity 2.3%; Score 33.8; DB 8; Length 882;
 49.2%; Pred. No. 1.5e+02;
 RESULT 1483
 ID ABX75345 standard; cDNA; 882 BP.
 DE Human cDNA encoding secreted frizzled related protein 1.
 PN WO200277204-A2.
 PD 03-OCT-2002.
 PA (AXOR-) AXORDIA LTD.
 Query Match
 Best Local Similarity 2.3%; Score 33.8; DB 8; Length 882;
 49.2%; Pred. No. 1.5e+02;
 RESULT 1484
 ID AAD52559 standard; DNA; 882 BP.
 DE SARP 1 DNA.
 PN WO200290992-A2.
 PD 14-NOV-2002.
 PA (AXOR-) AXORDIA LTD.
 Query Match
 Best Local Similarity 2.3%; Score 33.8; DB 8; Length 882;
 49.2%; Pred. No. 1.5e+02;
 RESULT 1485
 ID ABZ81831 standard; DNA; 882 BP.
 DE FRP nucleic acid sequence.
 PN WO2003012082-A2.
 PD 13-FEB-2003.
 PA (AXOR-) AXORDIA LTD.
 Query Match
 Best Local Similarity 2.3%; Score 33.8; DB 8; Length 882;
 49.2%; Pred. No. 1.5e+02;
 RESULT 1486
 ID ADK65947 standard; DNA; 882 BP.
 DE Gene #37 for inhibitory RNA to manipulate stem cell phenotype.
 PN WO2003069861-A2.
 PD 21-AUG-2003.
 PA (AXOR-) AXORDIA LTD.
 Query Match
 Best Local Similarity 2.3%; Score 33.8; DB 10; Length 882;
 49.2%; Pred. No. 1.5e+02;
 RESULT 1487
 ID ADA69490 standard; DNA; 1002 BP.
 DE Rice gene, SEQ ID 2813.
 PN WO2003000898-A1.
 PD 03-JAN-2003.
 PA (SYGN-) SYNGENTA PARTICIPATIONS AG.
 Query Match
 Best Local Similarity 2.3%; Score 33.8; DB 8; Length 1002;
 53.4%; Pred. No. 1.6e+02;
 RESULT 1488
 ID ADL12563 standard; cDNA; 1004 BP.
 DE Human steroid-induced C3A liver cell cDNA #292.
 PN US6673549-B1.
 PD 06-JAN-2004.
 PA (INCY-) INCYTE CORP.
 Query Match
 Best Local Similarity 2.3%; Score 33.8; DB 12; Length 1004;
 50.3%; Pred. No. 1.6e+02;
 RESULT 1489
 ID AAV60339 standard; cDNA; 1120 BP.
 DE cDNA sequence of fibroblast growth factor-2 (FGF-2).

PN WO9837880-A1.
PD 03-SEP-1998.
PA (CIBL-) CIBLEX CORP.
Query Match 2.3%; Score 33.8; DB 2; Length 1120;
Best Local Similarity 53.4%; Pred. No. 1.7e+02;
RESULT 1490
ID AAA53563 standard; cDNA; 1120 BP.
DE Human fibroblast growth factor 2 cDNA.
PN US6083706-A.
PD 04-JUL-2000.
PA (CIBL-) CIBLEX CORP.
Query Match 2.3%; Score 33.8; DB 3; Length 1120;
Best Local Similarity 53.4%; Pred. No. 1.7e+02;
RESULT 1491
ID AAS17400 standard; cDNA; 1120 BP.
DE Full length cDNA for human fibroblast growth factor 2, FGF-2.
PN US6306613-B1.
PD 23-OCT-2001.
PA (CIBL-) CIBLEX CORP.
Query Match 2.3%; Score 33.8; DB 6; Length 1120;
Best Local Similarity 53.4%; Pred. No. 1.7e+02;
RESULT 1492
ID ADP28744 standard; DNA; 1227 BP.
DE Human secreted protein encoding sequence SEQ ID #742.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 2.3%; Score 33.8; DB 12; Length 1227;
Best Local Similarity 50.3%; Pred. No. 1.7e+02;
RESULT 1493
ID ADP28745 standard; DNA; 1344 BP.
DE Human secreted protein encoding sequence SEQ ID #743.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 2.3%; Score 33.8; DB 12; Length 1344;
Best Local Similarity 50.3%; Pred. No. 1.8e+02;
RESULT 1494
ID ABK89965 standard; DNA; 1569 BP.
DE DNA encoding human alanine aminotransferase #1.
PN WO200255712-A2.
PD 18-JUL-2002.
PA (FARB) BAYER AG.
Query Match 2.3%; Score 33.8; DB 6; Length 1569;
Best Local Similarity 53.4%; Pred. No. 2e+02;
RESULT 1495
ID AAH13860 standard; cDNA; 1809 BP.
DE Human cDNA sequence SEQ ID NO:10847.
PN EPI074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 2.3%; Score 33.8; DB 4; Length 1809;
Best Local Similarity 52.5%; Pred. No. 2.1e+02;
RESULT 1496
ID ADD18814 standard; DNA; 1809 BP.
DE Human disease related protein DNA sequence SegID246.
PN WO2003018621-A2.
PD 06-MAR-2003.
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
Query Match 2.3%; Score 33.8; DB 10; Length 1809;
Best Local Similarity 52.5%; Pred. No. 2.1e+02;
RESULT 1497
ID ADR25867 standard; DNA; 1809 BP.
DE Breast cancer prognosis marker #1728.
PN WO2004065545-A2.
PD 05-AUG-2004.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
Query Match 2.3%; Score 33.8; DB 13; Length 1809;
Best Local Similarity 52.5%; Pred. No. 2.1e+02;
RESULT 1498
ID ADA70200 standard; DNA; 1980 BP.
DE Rice gene, SEQ ID 3523.

PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.3%; Score 33.8; DB 8; Length 1980;
Best Local Similarity 54.4%; Pred. No. 2.2e+02;
RESULT 1499
ID ADA48189 standard; DNA; 1980 BP.
DE Rice gene conferring disease resistance in plants.
PN WO2003000906-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.3%; Score 33.8; DB 9; Length 1980;
Best Local Similarity 54.4%; Pred. No. 2.2e+02;
RESULT 1500
ID ACC61932 standard; DNA; 2000 BP.
DE Gene sequence #SEQ ID 2646.
PN EPI258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZONE AG.
Query Match 2.3%; Score 33.8; DB 10; Length 2000;
Best Local Similarity 58.4%; Pred. No. 2.2e+02;

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OM nucleic - nucleic search, using sw model

Run on: March 28, 2005, 20:14:09 / Search time 6688 Seconds
(without alignments)
10758.971 Million cell updates/sec

Title: US-10-015-610A-195
Perfect score: 1485
Sequence: 1 gcgcgcacacgcagcagcagc.....tgaaaaaaaaaaaaaaaaaa 1485

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1500 summaries

Database :

GenEmbl:*
1: gb_ha:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_str:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
7	1485	100.0	1485	6	AX358856 Sequence
8	1485	100.0	1485	6	AX362349 Sequence
9	1485	100.0	1485	6	AX454624 Sequence
10	1485	100.0	1485	6	AX491102 Sequence
11	1485	100.0	1485	6	AX697127 Sequence
12	1485	100.0	1485	6	AX359067 Sequence
13	1485	100.0	1485	6	BD159667 Primer fo
14	1485	100.0	1485	6	AX882339 Sequence
15	1485	100.0	1485	6	AK022845 Homo sapi
16	1485	100.0	1485	6	AK135358 Sequence
17	1485	100.0	1485	6	AK30949 Sequence
18	1485	100.0	1485	6	AK057789 Sequence
19	1485	100.0	1485	6	BC009826 Homo sapi
20	1485	100.0	1485	6	BC009826 Homo sapi
21	1485	100.0	1485	6	CO851292 Sequence
22	1485	100.0	1485	6	AK128526 Homo sapi
23	1485	100.0	1485	6	AK091912 Homo sapi
24	1485	100.0	1485	6	BC021253 Human DNA
25	1485	100.0	1485	6	BD020049 Novel gen

20:	658.2	44.3	777	6	BD099987	BD099987 Novel gen	
c	21	638.2	43.0	768	6	BD020050 Novel gen	
c	22	638.2	43.0	768	6	BD099988 Novel gen	
23	616	41.5	857	6	BD147900	BD147900 Primer fo	
24	616	41.5	857	6	AX867838	AX867838 Sequence	
25	602.8	40.6	632	6	AR432559	AR432559 Sequence	
26	602.8	40.6	632	6	BD078618	BD078618 Human pro	
27	453	30.5	453	6	CO724408	CO724408 Sequence	
28	451.4	30.4	453	6	BD141440	BD141440 Novel phy	
29	448.2	30.2	453	6	E29045	E29045 ATG-1117 (A	
30	437.4	29.5	2967	10	BC024599	BC024599 Mus muscu	
31	395.4	26.6	453	10	AB035322	AB035322 Mus muscu	
32	296.6	20.0	552	6	E29047	E29047 ATG-1117 (A	
33	278.4	18.7	393	6	AX430948	AX430948 Sequence	
34	271.8	18.3	666	5	CR523365	CR523365 Gallus ga	
35	253.4	17.1	1788	5	AB012309	AB012309 Cyprinus	
36	243.4	16.4	2263	5	BC059529	BC059529 Danio rer	
37	209	14.1	1174	5	BC074259	BC074259 Xenopus 1	
38	206.6	13.9	967	5	BC073304	BC073304 Xenopus 1	
c	39	199	201	11	BV192584	BV192584 sqm17502	
40	192.2	12.9	444	6	BD141439	BD141439 Novel phy	
41	192.2	12.9	471	9	D86438	D86438 Homo sapien	
42	192.2	12.9	491	6	AR099732	AR099732 Sequence	
43	192.2	12.9	491	6	HSU19713	HSU19713 Human allog	
44	192.2	12.9	635	6	E28711	E28711 Novel spllc	
45	192.2	12.9	635	6	E28719	E28719 Novel spllc	
46	192.2	12.9	635	6	E29046	E29046 ATG-1117 (A	
47	192.2	12.9	635	9	HUM2D18G05	HUM2D18G05	
48	192.2	12.9	658	6	AR142887	AR142887 Sequence	
49	192.2	12.9	687	9	BC009474	BC009474 Homo sapi	
50	191	12.9	639	6	CO861548	CO861548 Sequence	
51	191	12.9	639	6	AX770561	AX770561 Sequence	
52	191	12.9	639	9	HSU49392	HSU49392 Human allog	
53	189.2	12.7	441	6	E49633	E49633 Macrophage	
54	186	12.5	658	6	AX888043	AX888043 Sequence	
55	186	12.5	592	6	BD027653	BD027653 Sequence	
56	185.2	12.5	592	10	D86382	D86382 Mus musculu	
57	185.2	12.5	598	10	AB013745	AB013745 Mus muscu	
58	185.2	12.5	610	10	AF074959	AF074959 Mus muscu	
59	184.2	12.4	686	4	AF346450	AF346450 Bos tauru	
60	183.6	12.4	780	10	BC021539	BC021539 Mus muscu	
61	183.2	12.3	597	6	AX899116	AX899116 Sequence	
62	183.2	12.3	597	6	BD034649	BD034649 Sequence	
63	182.2	12.3	441	6	E49634	E49634 Macrophage	
64	182	12.3	627	10	RNU17919	RNU17919 Rattus norv	
65	182	12.3	653	10	AB000818	AB000818 Rattus no	
66	180.4	12.1	627	6	AR099695	AR099695 Sequence	
67	180.4	12.1	651	6	I22424	I22424 Sequence 4	
68	178.4	12.0	467	6	CO684414	CO684414 Sequence	
69	174.4	11.7	810	10	D82069	D82069 Rat mRNA fo	
70	173.8	11.7	414	4	AF299326	AF299326 Sus scrofa	
71	171.6	11.6	625	5	AB019540	AB019540 Chrysophr	
72	167.8	11.3	441	6	E49639	E49639 Macrophage	
73	166.8	11.2	360	6	E49640	E49640 Macrophage	
74	163.8	11.0	345	6	E49635	E49635 Macrophage	
75	159.8	10.8	441	6	E49638	E49638 Macrophage	
76	159	10.7	480	6	CO689922	CO689922 Sequence	
77	154	10.4	460	6	CO707654	CO707654 Sequence	
78	146	9.8	451	6	CO683721	CO683721 Sequence	
79	144.8	9.8	25031	10	AB094629	AB094629 Mus muscu	
80	144.8	9.8	203946	2	AC069465	AC069465 Mus muscu	
c	81	144.8	9.8	235241	10	AL928893	AL928893 Mouse DNA
82	144	9.7	372	6	CO687682	CO687682 Sequence	
83	143.2	9.6	354	6	E49636	E49636 Macrophage	
84	142.4	9.6	353	6	CO692811	CO692811 Sequence	
85	141.6	9.5	223577	2	AC135374	AC135374 Rattus no	
86	141.6	9.5	253631	2	AC126155	AC126155 Rattus no	
87	137.4	9.3	358	6	CO711565	CO711565 Sequence	
88	133.2	9.0	522	3	SD018439	SD018439 Suberites d	
89	131.4	8.8	507	6	AX894754	AX894754 Sequence	
90	131.4	8.8	507	6	BD030287	BD030287 Sequence	
91	131.4	8.8	579	6	E28710	E28710 Novel spllc	
92	128.2	8.6	340	6	CO708190	CO708190 Sequence	

93	127.8	8.6	273	6	E49637	E49637 Macropodae	165	60.6	4.1	172	9	AP299329	AP299329 Homo sapi
94	126.8	8.5	402	5	AF162475	AF162475 Macaca mu	167	60.4	4.1	1000	6	C614982	C614982 Sequence
95	124	8.4	1678	10	RNU33471	U33371 Rattus norv	168	60.4	4.1	1556	3	AB081653	AB081653 Drosophila
96	121.8	8.2	282	9	AP299327	AP299327 Homo sapi	169	60.4	4.1	1634	3	AY094963	AY094963 Drosophila
97	120.6	8.1	1533	10	BC081822	BC081822 Rattus no	170	60.2	4.1	203946	2	AC069465	AC069465 Mus muscu
98	118.8	8.0	279	9	CR542151	CR542151 Homo sapi	171	60	4.0	1978	5	BX934902	BX934902 Gallus ga
99	117.8	7.9	424	10	RNU10894	U10894 Rattus norv	172	60	4.0	125020	9	AP429315	AP429315 Homo sapi
100	117	7.9	117	6	BD141426	BD141426 Rattus norv	173	59.4	4.0	117	6	BD141424	BD141424 Homo sapi
101	115.4	7.8	282	4	AF299325	AF299325 Sus scrof	174	59.2	4.0	258901	2	BD131482	BD131482 Rattus no
102	114.2	7.7	631	6	E28718	E28718 Novel splic	175	57.8	3.9	117	6	BD141425	BD141425 Novel phy
103	112.2	7.6	282	10	AF299328	AF299328 Rattus no	176	57.4	3.9	151250	2	AC151944	AC151944 Dasytus n
104	106.6	7.2	160875	5	BX517730	BX517730 Zebrafish	177	57.4	3.9	221092	2	AC096618	AC096618 Rattus no
105	106.6	7.2	195644	2	CR762385	CR762385 Dario rer	178	57.4	3.9	261112	2	AC105669	AC105669 Rattus no
106	104.2	7.0	117	6	BD141427	BD141427 Novel phy	179	57.4	3.9	10902	6	C6614981	C6614981 Sequence
107	94.8	6.4	331	6	AR099692	AR099692 Sequence	180	56	3.8	166918	2	AC017363	AC017363 Drosophila
108	94.8	6.0	117	6	I22421	I22421 Sequence 1	181	56	3.8	166918	2	AC009205	AC009205 Drosophila
109	88.8	5.5	101248	4	BX548169	BD141428 Novel phy	182	56	3.8	167777	3	AC009204	AC009204 Drosophila
110	81	5.3	164	6	E28716	BX548169 Pig DNA s	183	56	3.8	170546	3	AC011756	AC011756 Drosophila
111	79.4	5.3	164	6	E28716	E28716 Novel splic	184	56	3.8	265558	2	AE003661	AE003661 Drosophila
112	79.4	5.3	1235	9	HSU95213	U95213 Human inter	185	55.8	3.8	257681	5	EX784025	EX784025 Sequence
113	79.4	5.3	1235	9	HSU95213	U95213 Human inter	186	55.8	3.8	257681	5	EX784025	EX784025 Sequence
114	79.4	5.3	1364	6	CQ730868	CQ730868 Sequence	187	55	3.7	233	6	CQ665525	CQ665525 Sequence
115	79.4	5.3	16685	9	BX248305	BX248305 Human DNA	188	54.6	3.7	7218	6	BD050516	BD050516 Sequence
116	79.4	5.3	38324	9	HXBAT2	Z15025 Homo sapien	189	54.6	3.7	55	6	CQ056639	CQ056639 Sequence
117	79.4	5.3	81800	9	HSY14768	Y14768 Homo sapien	190	54.6	3.7	186	6	CQ075916	CQ075916 Sequence
118	79.4	5.3	94667	2	CR759761	CR759761 Homo sapi	191	54.4	3.7	186	6	CQ075916	CQ075916 Sequence
119	79.4	5.3	99109	2	AL805934	AL805934 Human DNA	192	54.4	3.7	186	6	CQ075916	CQ075916 Sequence
120	79.4	5.3	100000	9	AP000505	AP000505 Homo sapi	193	54.4	3.7	186	6	CQ075916	CQ075916 Sequence
121	79.4	5.3	106171	2	CR753892	CR753892 Homo sapi	194	54.4	3.7	186	6	CQ145548	CQ145548 Sequence
122	79.4	5.3	111554	2	CR753882	CR753882 Homo sapi	195	54.4	3.7	186	6	CQ145548	CQ145548 Sequence
123	79.4	5.3	13230	9	AL662801	AL662801 Homo sapi	196	54.4	3.7	186	6	CQ020357	CQ020357 Sequence
124	79.4	5.3	135784	9	AL662847	AL662847 Human DNA	197	54.4	3.7	186	6	CQ028756	CQ028756 Sequence
125	79.4	5.3	182826	9	AC148688	AC148688 Macaca mu	198	54.4	3.7	186	6	CQ268898	CQ268898 Sequence
126	79.4	5.3	184666	9	DJ201024	AP129756 Homo sapi	199	54.4	3.7	186	6	CQ030871	CQ030871 Sequence
127	78	5.3	41602	5	TRU50686	TRU50686 Takifugu	200	54.4	3.7	186	6	CQ341187	CQ341187 Sequence
128	76.8	5.2	3091	10	NM082932	U82792 Mus musculu	201	54.4	3.7	346	6	CQ064365	CQ064365 Sequence
129	76.8	5.2	5549	10	AB036423	AB036423 Mus muscu	202	54.4	3.7	500	6	CQ051671	CQ051671 Sequence
130	76.8	5.2	120990	10	NMHC188A7	AF109719 Mus muscu	203	54.4	3.7	500	6	CQ066728	CQ066728 Sequence
131	75.4	5.1	1271	5	BC059547	BC059547 Dario rer	204	54.4	3.7	500	6	CQ063770	CQ063770 Sequence
132	75.2	5.1	203633	2	AC136959	AC136959 Rattus no	205	54.4	3.7	500	6	CQ132547	CQ132547 Sequence
133	75.2	5.1	228453	2	AC094348	AC094348 Rattus no	206	54.4	3.7	500	6	CQ171119	CQ171119 Sequence
134	75.2	5.1	241558	2	AC130591	AC130591 Rattus no	207	54.4	3.7	500	6	CQ0200254	CQ0200254 Sequence
135	75.2	5.1	349047	10	BX683046	BD150126 Rattus no	208	54.4	3.7	500	6	CQ215758	CQ215758 Sequence
136	71.2	4.8	501	10	NM056065	BD150126 Rattus no	209	54.4	3.7	500	6	CQ254336	CQ254336 Sequence
137	69.2	4.7	646	6	BD150126	AX870064 Primer fo	210	54.4	3.7	500	6	CQ281370	CQ281370 Sequence
138	69.2	4.7	646	6	BD150126	AX870064 Primer fo	211	54.4	3.7	500	6	CQ281370	CQ281370 Sequence
139	68.8	4.6	1876	6	BD160145	AX883133 Sequence	212	54.4	3.7	175964	9	HS467K16	HS467K16 Sequence
140	68.8	4.6	1876	6	BD160145	AX883133 Sequence	213	54.4	3.7	199763	2	AL589992	AL589992 Homo sapi
141	68.8	4.6	1876	6	BD160145	AX883133 Sequence	214	54.2	3.6	6907	6	AX345468	AX345468 Sequence
142	68.8	4.6	1877	9	BC004128	BC004128 Homo sapi	215	54.2	3.6	185038	10	AC104894	AC104894 Sequence
143	68.8	4.6	1889	9	BC002449	BC002449 Homo sapi	216	54.2	3.6	349980	6	AX344556	AX344556 Sequence
144	68.8	4.6	1923	9	AF218006	AF218006 Homo sapi	217	52.6	3.5	148213	10	AL645731	AL645731 Sequence
145	66.4	4.5	418	6	CQ725802	CQ725802 Sequence	218	50.8	3.4	158629	10	AL928591	AL928591 Sequence
146	66.4	4.5	1562	6	AF193044	AF193044 Homo sapi	219	50.4	3.4	8964	3	SD0410885	SD0410885 Sequence
147	66.4	4.5	2250	5	BX933977	BX933977 Gallus ga	220	50	3.4	114458	2	BX293986	BX293986 Mouse DNA
148	65.6	4.4	125020	9	AF429315	AF429315 Homo sapi	221	49.8	3.4	70714	10	AC101499	AC101499 Mus muscu
149	64.4	4.3	2813	5	BC073325	BC073325 Xenopus l	222	49.8	3.4	114815	2	BX004973	BX004973 Mouse DNA
150	64.4	4.3	582	6	BD078619	BD078619 Human pro	223	49.8	3.4	272031	2	AL772221	AL772221 Mus muscu
151	64.2	4.3	723	6	CO722230	CO722230 Sequence	224	49.6	3.3	671	8	AF042839	AF042839 Oryza sat
152	64.2	4.3	2264	9	BC068473	BC068473 Homo sapi	225	49.6	3.3	830	8	AK119167	AK119167 Oryza sat
153	64.2	4.3	2265	9	BC0014923	BC0014923 Homo sapi	226	49.6	3.3	876	8	AK121606	AK121606 Oryza sat
154	64.2	4.3	2382	9	BC007233	BC007233 Homo sapi	227	49.6	3.3	968	8	AK059534	AK059534 Oryza sat
155	64.2	4.3	2382	9	BC007233	BC007233 Homo sapi	228	49.2	3.3	213656	2	AC107371	AC107371 Mus muscu
156	64.2	4.3	2387	9	BC023611	BC023611 Homo sapi	229	49.2	3.3	599	10	RATCMB	RATCMB Sequence
157	64.2	4.3	2806	5	BC076710	BC076710 Xenopus t	230	49.2	3.3	676	3	AB063182	AB063182 Rattus no
158	63.6	4.3	1358	6	CR385997	CR385997 Gallus ga	231	49.2	3.3	691	10	RSPRCM4	RSPRCM4 Sequence
159	63.2	4.3	1358	6	AR379539	AR379539 Sequence	232	49.2	3.3	776	3	DB8976	DB8976 Rattus no
160	62.6	4.2	2754	5	BD141423	BD141423 Novel phy	233	49.2	3.3	1013	3	BC063184	BC063184 Halichond
161	62.6	4.2	2754	5	BD141423	BD141423 Novel phy	234	49.2	3.3	1145	10	BC063187	BC063187 Rattus no
162	62.4	4.2	1854	10	BC063917	BC063917 Xenopus t	235	49.2	3.3	2000	6	AX655393	AX655393 Sequence
163	62.4	4.2	152781	2	AC064852	AC064852 Homo sapi	236	49.2	3.3	2180	5	BC045298	BC045298 Dario rer
164	61.2	4.1	191988	2	CR388129	CR388129 Homo sapi	237	49	3.3	490	4	AY575058	AY575058 Sus scrof
165	61	4.1	7218	6	166494	166494 Sequence 14	238	49	3.3	218880	2	AC124750	AC124750 Mus muscu

C 239	49	3.3	237712	9	AC012634	312	44.8	3.0	409	5	AB055386
C 240	48.8	3.3	174095	10	AC115863	313	44.8	3.0	453	8	OSCALM
C 241	48.8	3.3	220247	10	AC131660	314	44.8	3.0	712	8	BT014541
C 242	48.4	3.3	123678	10	AC122044	315	44.8	3.0	2260	10	AB050199
C 243	48.2	3.2	295500	1	AP005954	316	44.8	3.0	186125	10	AC132918
C 244	48	3.2	633	8	AF441190	317	44.8	3.0	203490	10	AC122851
C 245	48	3.2	148352	2	AC025309	318	44.6	3.0	643	5	AY190728
C 246	47.6	3.2	722	10	MUSCALMDA	319	44.6	3.0	720	11	BV177505
C 247	47.6	3.2	787	2	BC071404	320	44.6	3.0	785	9	HSR13727
C 248	47.6	3.2	964	3	D88977	321	44.6	3.0	835	5	AB110087
C 249	47.6	3.2	2155	10	BC050926	322	44.6	3.0	3372	6	AX211346
C 250	47.4	3.2	848	5	AB110086	323	44.6	3.0	3372	6	AF065164
C 251	47.4	3.2	181380	10	AC115123	324	44.6	3.0	3459	6	AX348086
C 252	47.2	3.2	208443	10	AC112791	325	44.6	3.0	3459	6	HSR102582
C 253	47.2	3.2	244722	2	AC11488	326	44.6	3.0	3891	9	AC005559
C 254	47	3.2	161092	2	AC102715	327	44.6	3.0	172171	10	AL670305
C 255	46.8	3.2	78373	10	AC098641	328	44.6	3.0	185620	10	AC127567
C 256	46.8	3.2	160207	2	AC130700	329	44.6	3.0	203422	10	AL773863
C 257	46.8	3.2	170340	10	AC122433	330	44.6	3.0	207701	2	BX545856
C 258	46.8	3.2	226502	2	AC139867	331	44.6	3.0	208399	2	AC140054
C 259	46.8	3.2	319614	2	AC126905	332	44.6	3.0	217225	2	AC137155
C 260	46.6	3.1	220976	10	AC132474	333	44.6	3.0	218826	2	AC118183
C 261	46.4	3.1	409	5	AB055385	334	44.6	3.0	228976	2	AC135869
C 262	46.4	3.1	179862	9	CNS057E	335	44.6	3.0	236342	10	AC129190
C 263	46.4	3.1	214267	9	AC008571	336	44.6	3.0	253693	2	AC093997
C 264	46.4	3.1	218171	2	AC123689	337	44.6	3.0	264062	10	AC099589
C 265	46.4	3.1	344321	1	BX640429	338	44.6	3.0	337486	2	AC114544
C 266	46.4	3.1	346274	1	BX640443	339	44.6	3.0	447	6	AX660867
C 267	46.4	3.1	349354	1	BX640416	340	44.4	3.0	787	6	AX660739
C 268	46.2	3.1	174030	2	AC133936	341	44.4	3.0	1519	8	MPCAM
C 269	46.2	3.1	244203	2	AC096313	342	44.4	3.0	116022	10	AC034254
C 270	46	3.1	924	3	AB175946	343	44.4	3.0	149237	2	AC139916
C 271	46	3.1	1111	3	TCCALB2	344	44.4	3.0	176602	9	AC116665
C 272	46	3.1	143226	9	AL353802	345	44.4	3.0	177085	10	AC142110
C 273	46	3.1	146005	10	AL845290	346	44.4	3.0	191255	10	AL671672
C 274	46	3.1	173929	2	AC112985	347	44.4	3.0	202533	10	AC099605
C 275	46	3.1	177882	9	AC013402	348	44.4	3.0	236635	2	AC126737
C 276	46	3.1	203921	2	AC119460	349	44.2	3.0	450	8	STU20294
C 277	46	3.1	207812	2	AC140280	350	44.2	3.0	144906	10	BX682542
C 278	46	3.1	244972	2	AC106489	351	44.2	3.0	153422	9	AC148715
C 279	45.8	3.1	776	5	CHK1NC	352	44.2	3.0	156052	10	AC104930
C 280	45.8	3.1	1350	6	BC071886	353	44.2	3.0	170101	10	AC140244
C 281	45.8	3.1	147896	10	AL607145	354	44.2	3.0	177018	2	AC099716
C 282	45.8	3.1	157891	10	AC133161	355	44.2	3.0	179050	2	AC131108
C 283	45.8	3.1	196150	10	AC147250	356	44.2	3.0	185378	10	AL772367
C 284	45.8	3.1	21979	2	AC109739	357	44.2	3.0	232502	2	AC110194
C 285	45.8	3.1	252384	10	AC123071	358	44	3.0	483	9	CR541864
C 286	45.6	3.1	452	6	AX885282	359	44	3.0	1251	6	BD160958
C 287	45.6	3.1	287	6	BD024892	360	44	3.0	1251	6	AX441273
C 288	45.6	3.1	480	9	CR541884	361	44	3.0	1290	12	RN055075
C 289	45.6	3.1	483	12	BT008003	362	44	3.0	1322	3	LR0291615
C 290	45.6	3.1	547	6	AX888042	363	44	3.0	2128	9	BC006182
C 291	45.6	3.1	547	6	BD027652	364	44	3.0	2175	9	HUMCMA
C 292	45.6	3.1	663	9	HUMTRC	365	44	3.0	2181	9	BC005137
C 293	45.6	3.1	677	6	C0727377	366	44	3.0	126106	10	AC125051
C 294	45.6	3.1	677	9	HSTRC2	367	44	3.0	144000	2	AC123764
C 295	45.6	3.1	706	9	BC005323	368	44	3.0	165718	2	AC127508
C 296	45.6	3.1	138179	9	AC145217	369	44	3.0	168263	2	AC148668
C 297	45.6	3.1	164485	2	AC026106	370	44	3.0	186596	2	AC141432
C 298	45.6	3.1	173370	10	AC144629	371	44	3.0	197999	2	AC134688
C 299	45.4	3.1	892	5	AB008555	372	44	3.0	207065	2	AC140324
C 300	45.4	3.1	2000	6	AX655393	373	44	3.0	207822	2	AC109321
C 301	45.4	3.1	178935	2	AC147339	374	44	3.0	213771	2	AC109215
C 302	45.4	3.1	202540	2	AC120854	375	44	3.0	214285	2	AC113532
C 303	45.4	3.1	239297	10	AC119848	376	44	3.0	221055	2	AC097131
C 304	45.4	3.0	121619	5	CR354385	377	44	3.0	226167	2	AC119258
C 305	45.2	3.0	168056	2	AC004458	378	44	3.0	239275	2	AC113512
C 306	45.2	3.0	184127	2	AC125846	379	44	3.0	262978	2	AC136272
C 307	45	3.0	1112	10	RATCMA	380	43.8	2.9	486	5	AY281129
C 308	45	3.0	136088	10	EX530092	381	43.8	2.9	1644	5	AF085250
C 309	45	3.0	178027	2	AC132041	382	43.8	2.9	100381	5	AL672097
C 310	45	3.0	182162	2	AC102917	383	43.8	2.9	138699	10	AC139157
C 311	45	3.0	226637	2	AC095337	384	43.8	2.9	177962	10	AC147251

C 385	43.8	2.9	180267	10	AC139324	AC139324 Mus muscu	C 458	43	2.9	172344	2	AC126228	AC126228 Mus muscu
C 386	43.8	2.9	183285	10	AC128655	AC128655 Mus muscu	C 459	43	2.9	184357	2	AC073728	AC073728 Mus muscu
C 387	43.8	2.9	205642	2	AC140691	AC140691 Rattus no	C 460	43	2.9	205623	10	AC123555	AC123555 Mus muscu
C 388	43.8	2.9	217775	10	AL5592224	AL5592224 Mouse DNA	C 461	43	2.9	214060	2	AC121522	AC121522 Mus muscu
C 389	43.8	2.9	243733	2	AC116381	AC116381 Mus muscu	C 462	43	2.9	245032	2	AC109749	AC109749 Rattus no
C 390	43.8	2.9	267434	2	AC128998	AC128998 Rattus no	C 463	43	2.9	256154	2	AC119386	AC119386 Rattus no
C 391	43.6	2.9	883	5	ELCCAMERL	J00931 E.lectricu	C 464	43	2.9	268984	3	AB001274	AB001274 Leishmani
C 392	43.6	2.9	1159	6	C0727058	C0727058 Sequence	C 465	43	2.9	450	5	ELCCALMA	ELCCALMA
C 393	43.6	2.9	1161	6	AX331133	AX331133 Sequence	C 466	42.8	2.9	595	12	SYNARBCAL	J04729 A.puncinulat
C 394	43.6	2.9	1161	9	HSU03270	HSU03270 Sequence	C 467	42.8	2.9	743	8	ZMRNCAL	X74490 Z.mays mRNA
C 395	43.6	2.9	1285	9	BC029515	BC029515 Homo sapi	C 468	42.8	2.9	103244	2	AC103394	AC103394 Rattus no
C 396	43.6	2.9	68456	10	BX324191	BX324191 Mouse DNA	C 469	42.8	2.9	110000	1	AP006840	AP006840 Rattus no
C 397	43.6	2.9	74301	2	AC137736	AC137736 Homo sapi	C 470	42.8	2.9	110000	2	AC116271	AC116271 Rattus no
C 398	43.6	2.9	110000	2	AC108345	AC108345 Rattus no	C 471	42.8	2.9	110000	2	AC116271	AC116271 Rattus no
C 399	43.6	2.9	127252	9	BS000559	BS000559 Pan trogl	C 472	42.8	2.9	150659	10	AC147159	AC147159 Mus muscu
C 400	43.6	2.9	150649	10	AC102918	AC102918 Mus muscu	C 473	42.8	2.9	153258	2	AC026206	AC026206 Homo sapi
C 401	43.6	2.9	152711	9	AP001178	AP001178 Homo sapi	C 474	42.8	2.9	167296	2	AC141904	AC141904 Rattus no
C 402	43.6	2.9	156080	2	CR759833	CR759833 Dario rer	C 475	42.8	2.9	169896	2	AC101922	AC101922 Mus muscu
C 403	43.6	2.9	165742	2	AC020697	AC020697 Homo sapi	C 476	42.8	2.9	170609	10	AC133992	AC133992 Mus muscu
C 404	43.6	2.9	174469	9	AC022882	AC022882 Homo sapi	C 477	42.8	2.9	176223	9	AC034192	AC034192 Homo sapi
C 405	43.6	2.9	178227	10	AL831766	AL831766 Mouse DNA	C 478	42.8	2.9	177176	2	AC130718	AC130718 Mus muscu
C 406	43.6	2.9	178668	10	AC131596	AC131596 Mus muscu	C 479	42.8	2.9	178023	10	AC130718	AC130718 Mus muscu
C 407	43.6	2.9	178779	2	AC117442	AC117442 Homo sapi	C 480	42.8	2.9	184836	2	AC139877	AC139877 Rattus no
C 408	43.6	2.9	228405	2	AC096406	AC096406 Rattus no	C 481	42.8	2.9	185277	10	AC098567	AC098567 Genomic s
C 409	43.6	2.9	230799	2	AC098397	AC098397 Rattus no	C 482	42.8	2.9	187083	10	AC117223	AC117223 Mus muscu
C 410	43.6	2.9	235924	10	AC112938	AC112938 Mus muscu	C 483	42.8	2.9	188351	10	AC141874	AC141874 Mus muscu
C 411	43.6	2.9	271915	2	AC096838	AC096838 Rattus no	C 484	42.8	2.9	190554	10	AC131726	AC131726 Mus muscu
C 412	43.6	2.9	298982	2	AC111908	AC111908 Rattus no	C 485	42.8	2.9	193624	10	AC107868	AC107868 Mus muscu
C 413	43.6	2.9	344682	2	AC096282	AC096282 Rattus no	C 486	42.8	2.9	201413	2	AC129583	AC129583 Mus muscu
C 414	43.4	2.9	650	8	AB050840	AB050840 Nicotiana	C 487	42.8	2.9	203839	10	AC021642	AC021642 Mus muscu
C 415	43.4	2.9	1084	6	C0858783	C0858783 Sequence	C 488	42.8	2.9	205206	2	AC135913	AC135913 Mus muscu
C 416	43.4	2.9	1084	6	RATCAM	M13312 Rat calmodu	C 489	42.8	2.9	215104	2	AC130218	AC130218 Mus muscu
C 417	43.4	2.9	1145	10	BC058485	BC058485 Rattus no	C 490	42.8	2.9	215104	2	AC107639	AC107639 Mus muscu
C 418	43.4	2.9	2466	6	BD269452	BD269452 Mitomycin	C 491	42.8	2.9	217293	10	AC099584	AC099584 Mus muscu
C 419	43.4	2.9	18034	6	BD269446	BD269446 Mitomycin	C 492	42.8	2.9	226769	10	AC113038	AC113038 Mus muscu
C 420	43.4	2.9	18034	6	AR266932	AR266932 Sequence	C 493	42.8	2.9	283323	2	AC101871	AC101871 Mus muscu
C 421	43.4	2.9	197761	2	AL807800	AL807800 Mouse DNA	C 494	42.6	2.9	523	5	AF187305	AF187305 Mus muscu
C 422	43.4	2.9	204317	2	AC105321	AC105321 Mus muscu	C 495	42.6	2.9	650	4	OCTROPC	AC125913 Mus muscu
C 423	43.4	2.9	214377	10	AC133511	AC133511 Mus muscu	C 496	42.6	2.9	3672	1	AF210634	AF210634 Mus muscu
C 424	43.4	2.9	227967	2	AC094951	AC094951 Mus muscu	C 497	42.6	2.9	10167	1	SFD08223	SFD08223 Mus muscu
C 425	43.4	2.9	239847	2	AC128434	AC128434 Rattus no	C 498	42.6	2.9	57881	10	BX682229	BX682229 Mouse DNA
C 426	43.4	2.9	2447	6	BD160956	BD160956 Method fo	C 499	42.6	2.9	130345	2	AC116710	AC116710 Mus muscu
C 427	43.4	2.9	239847	2	AC128434	AC128434 Rattus no	C 500	42.6	2.9	143926	10	AC123031	AC123031 Mus muscu
C 428	43.2	2.9	447	6	AX441271	AX441271 Sequence	C 501	42.6	2.9	150118	2	AC101293	AC101293 Mus muscu
C 429	43.2	2.9	447	6	AX441271	AX441271 Sequence	C 502	42.6	2.9	158958	2	AC007611	AC007611 Homo sapi
C 430	43.2	2.9	450	5	CHKCALMA	M36167 Chicken cal	C 503	42.6	2.9	161946	9	AC094014	AC094014 Papio anu
C 431	43.2	2.9	450	5	BT006855	BT006855 Homo sapi	C 504	42.6	2.9	177771	2	AC119903	AC119903 Mus muscu
C 432	43.2	2.9	450	12	BT007567	BT007567 Synthetic	C 505	42.6	2.9	182400	2	AC124010	AC124010 Mus muscu
C 433	43.2	2.9	564	6	AX887973	AX887973 Sequence	C 506	42.6	2.9	191067	2	AC107708	AC107708 Mus muscu
C 434	43.2	2.9	564	6	BD027583	BD027583 Sequence	C 507	42.6	2.9	192919	10	AL732464	AL732464 Mouse DNA
C 435	43.2	2.9	726	5	AB003083	AB003083 Halocynth	C 508	42.6	2.9	196102	2	AC149216	AC149216 Mus muscu
C 436	43.2	2.9	1100	5	AB003083	AB003083 Halocynth	C 509	42.6	2.9	196806	10	AC027184	AC027184 Mus muscu
C 437	43.2	2.9	1123	5	AB081672	AB081672 Gallus ga	C 510	42.6	2.9	200426	2	AC125948	AC125948 Rattus no
C 438	43.2	2.9	2908	8	MZESUS1A	L22226 Zea mays su	C 511	42.6	2.9	209428	10	AC139759	AC139759 Mus muscu
C 439	43.2	2.9	7341	8	MZESUS1C	L33244 Zea mays (c	C 512	42.6	2.9	242649	2	AC108648	AC108648 Rattus no
C 440	43.2	2.9	8648	8	MZESUS1C	L33244 Zea mays (c	C 513	42.6	2.9	251079	2	AC099134	AC099134 Mus muscu
C 441	43.2	2.9	75021	2	AC040889	AC040889 Homo sapi	C 514	42.4	2.9	354	8	LEH14764	LEH14764 Mus muscu
C 442	43.2	2.9	96360	10	BX294441	BX294441 Mouse DNA	C 515	42.4	2.9	450	5	CHKCM11	CHKCM11
C 443	43.2	2.9	121869	10	AL813739	AL813739 Mouse DNA	C 516	42.4	2.9	633	8	AF085344	AF085344 Pythium s
C 444	43.2	2.9	157092	10	AL805911	AL805911 Mouse DNA	C 517	42.4	2.9	13513	1	AY423269	AY423269 Streptomy
C 445	43.2	2.9	195294	9	AC132248	AC132248 Mus muscu	C 518	42.4	2.9	62074	2	AC101270	AC101270 Mus muscu
C 446	43.2	2.9	197310	9	AC099754	AC099754 Homo sapi	C 519	42.4	2.9	80682	10	AL953839	AL953839 Mouse DNA
C 447	43.2	2.9	198320	10	AL669814	AL669814 Mouse DNA	C 520	42.4	2.9	110000	2	AC151715	AC151715 Mus muscu
C 448	43.2	2.9	238830	2	AC102034	AC102034 Mus muscu	C 521	42.4	2.9	114337	10	AC122019	AC122019 Mus muscu
C 449	43.2	2.9	239908	2	AC131583	AC131583 Mus muscu	C 522	42.4	2.9	132761	10	AL772225	AL772225 Mouse DNA
C 450	43.2	2.9	262547	2	AC123999	AC123999 Mus muscu	C 523	42.4	2.9	133621	10	AC133585	AC133585 Mus muscu
C 451	43.2	2.9	296820	10	AF312033	AF312033 Mus muscu	C 524	42.4	2.9	142903	2	AC117253	AC117253 Mus muscu
C 452	43	2.9	5116	10	MMU66858	MMU66858 Mus muscu	C 525	42.4	2.9	145150	10	AC119980	AC119980 Mus muscu
C 453	43	2.9	603772	2	AC110005	AC110005 Mus muscu	C 526	42.4	2.9	152620	10	AC13081	AC13081 Mus muscu
C 454	43	2.9	142133	2	AC135014	AC135014 Felis cat	C 527	42.4	2.9	153994	2	AC136514	AC136514 Mus muscu
C 455	43	2.9	143681	2	AC115934	AC115934 Mus muscu	C 528	42.4	2.9	155130	2	AC147779	AC147779 Mus muscu
C 456	43	2.9	160269	9	AC024230	AC024230 Homo sapi	C 529	42.4	2.9	161408	5	BX511269	BX511269 Zebrafish
C 457	43	2.9	169004	2	AC121682	AC121682 Rattus no	C 530	42.4	2.9	184279	10	AC140393	AC140393 Mus muscu

531	42.4	2.9	187432	10	AC117750	AC117750 Mus muscu	604	41.8	2.8	1505	8	AB041712	AB041712 Chara cor
532	42.4	2.9	190733	10	AC117784	AC117784 Mus muscu	605	41.8	2.8	1862	3	AB044286	AB044286 Chara cor
533	42.4	2.9	191863	9	AC010888	AC010888 Homo sapi	606	41.8	2.8	2359	8	AF406767	AF406767 Leishmani
534	42.4	2.9	195273	10	AC113548	AC113548 Mus muscu	607	41.8	2.8	2537	9	AK094964	AK094964 Homo sapi
535	42.4	2.9	196468	10	AC111065	AC111065 Mus muscu	608	41.8	2.8	74530	9	AL606517	AL606517 Human DNA
536	42.4	2.9	201248	2	AC116494	AC116494 Mus muscu	609	41.8	2.8	87684	4	AY152828	AY152828 Fells cat
537	42.4	2.9	206358	2	AC139238	AC139238 Mus muscu	610	41.8	2.8	105208	4	AL671897	AL671897 Mouse DNA
538	42.4	2.9	220472	2	AC147511	AC147511 Mus muscu	611	41.8	2.8	145837	10	AL732527	AL732527 Mouse DNA
539	42.4	2.9	230629	2	AC127332	AC127332 Mus muscu	612	41.8	2.8	145837	10	AL732527	AL732527 Mouse DNA
540	42.4	2.8	779	8	TAU48689	U48689 Trilicium ae	613	41.8	2.8	154472	10	AC122412	AC122412 Mouse DNA
541	42.2	2.8	118080	2	AL844550	AL844550 Mouse DNA	614	41.8	2.8	165229	10	AC109302	AC109302 Mus muscu
542	42.2	2.8	140917	10	AL929380	AL929380 Mouse DNA	615	41.8	2.8	169150	10	AL732519	AL732519 Mouse DNA
543	42.2	2.8	157264	10	AC132914	AC132914 Mus muscu	616	41.8	2.8	178754	2	AC139446	AC139446 Ratius no
544	42.2	2.8	158921	8	AP003626	AP003626 Oryza sat	617	41.8	2.8	183795	2	AC116481	AC116481 Mus muscu
545	42.2	2.8	162556	10	AL672228	AL672228 Mouse DNA	618	41.8	2.8	190390	2	AC134400	AC134400 Mus muscu
546	42.2	2.8	163138	2	AC135081	AC135081 Mus muscu	619	41.8	2.8	190996	2	AC138084	AC138084 Mus muscu
547	42.2	2.8	163568	8	AP003711	AP003711 Oryza sat	620	41.8	2.8	203794	2	AC140930	AC140930 Mus muscu
548	42.2	2.8	174124	2	AC102872	AC102872 Mus muscu	621	41.8	2.8	204165	10	AC124717	AC124717 Mus muscu
549	42.2	2.8	181412	2	AC120001	AC120001 Mus muscu	622	41.8	2.8	205030	9	AL669911	AL669911 Mouse DNA
550	42.2	2.8	184677	10	AC140257	AC140257 Mus muscu	623	41.8	2.8	206482	9	AC091230	AC091230 Homo sapi
551	42.2	2.8	195978	10	AC111099	AC111099 Mus muscu	624	41.8	2.8	211034	10	AL731709	AL731709 Mouse DNA
552	42.2	2.8	202305	9	AC114291	AC114291 Homo sapi	625	41.8	2.8	212365	2	AC013350	AC013350 Mus muscu
553	42.2	2.8	213348	10	AC098883	AC098883 Mus muscu	626	41.8	2.8	218817	2	AC114704	AC114704 Ratius no
554	42.2	2.8	213848	2	AC139346	AC139346 Mus muscu	627	41.8	2.8	221399	10	AL604045	AL604045 Mouse DNA
555	42.2	2.8	227182	2	AC112692	AC112692 Mus muscu	628	41.8	2.8	221642	2	AC115978	AC115978 Mus muscu
556	42.2	2.8	232460	2	AC103188	AC103188 Ratius no	629	41.8	2.8	236031	2	AC105606	AC105606 Ratius no
557	42.2	2.8	243763	2	AC126724	AC126724 Ratius no	630	41.8	2.8	238341	2	AL773599	AL773599 Mus muscu
558	42.2	2.8	246940	2	AC106561	AC106561 Ratius no	631	41.8	2.8	242619	2	AC115464	AC115464 Ratius no
559	42.2	2.8	272459	2	AC109059	AC109059 Ratius no	632	41.8	2.8	247196	2	AC073822	AC073822 Mus muscu
560	42	2.8	556	11	AF096544	AF096544 Ratius no	633	41.8	2.8	251966	2	AC095883	AC095883 Ratius no
561	42	2.8	1110	9	AF490905	AF490905 Homo sapi	634	41.8	2.8	255347	2	AC112116	AC112116 Ratius no
562	42	2.8	75405	10	AL645746	AL645746 Mouse DNA	635	41.8	2.8	255447	2	AC096032	AC096032 Ratius no
563	42	2.8	110000	2	AC110363	Continuation (4 of	636	41.8	2.8	270435	2	AC096252	AC096252 Ratius no
564	42	2.8	110000	2	AC110363	Continuation (2 of	637	41.8	2.8	309266	2	AC106972	AC106972 Ratius no
565	42	2.8	110000	2	AC110363	Continuation (6 of	638	41.6	2.8	568	11	HUMUT5050	L17672 Human STS U
566	42	2.8	110000	2	AC110363	Continuation (6 of	639	41.6	2.8	581	11	BV048811	BV048811 S212P6010
567	42	2.8	120868	2	AC139379	AC139379 Mus muscu	640	41.6	2.8	748	8	AB050839	AB050839 Nicotiana
568	42	2.8	136064	10	AL928992	AL928992 Mouse DNA	641	41.6	2.8	807	2	SC0318521	SC0318521 Solanum c
569	42	2.8	142665	10	AL592545	AL592545 Mouse DNA	642	41.6	2.8	98392	8	AL590620	AL590620 Homo sapi
570	42	2.8	153994	2	AC136914	AC136914 Mus muscu	643	41.6	2.8	110000	2	AC107636	AC107636
571	42	2.8	155366	10	AC102012	AC102012 Mus muscu	644	41.6	2.8	114007	9	HS01185K9	HS01185K9 Human DNA
572	42	2.8	162282	2	AC132879	AC132879 Mus muscu	645	41.6	2.8	114007	9	HS01185K9	HS01185K9 Human DNA
573	42	2.8	182672	10	AC131332	AC131332 Homo sapi	646	41.6	2.8	152316	10	AC007844	AC007844 Mus muscu
574	42	2.8	183179	2	AL133212	AL133212 Homo sapi	647	41.6	2.8	157101	2	AC102892	AC102892 Mus muscu
575	42	2.8	183414	8	CNS0809CF	AL732640 Oryza sat	648	41.6	2.8	164277	10	AL840625	AL840625 Mouse DNA
576	42	2.8	184037	10	AC147369	AC147369 Mus muscu	649	41.6	2.8	170221	10	AC127421	AC127421 Mus muscu
577	42	2.8	186486	10	AC134259	AC134259 Mus muscu	650	41.6	2.8	171110	2	AC119699	AC119699 Ratius no
578	42	2.8	186505	10	AL772150	AL772150 Mouse DNA	651	41.6	2.8	172980	10	AC126671	AC126671 Mus muscu
579	42	2.8	190119	10	AC124441	AC124441 Mus muscu	652	41.6	2.8	173146	2	AC112522	AC112522 Mus muscu
580	42	2.8	191301	2	AC127820	AC127820 Ratius no	653	41.6	2.8	173643	10	AC122782	AC122782 Mus muscu
581	42	2.8	191669	10	AC118020	AC118020 Mus muscu	654	41.6	2.8	178135	2	AC101738	AC101738 Mus muscu
582	42	2.8	191692	2	AC023834	AC023834 Mus muscu	655	41.6	2.8	179481	2	AC034100	AC034100 Mus muscu
583	42	2.8	199341	2	AC113903	AC113903 Ratius no	656	41.6	2.8	187523	2	AC102882	AC102882 Mus muscu
584	42	2.8	211743	2	AC136147	AC136147 Mus muscu	657	41.6	2.8	188463	2	AC101787	AC101787 Mus muscu
585	42	2.8	213462	2	AC119365	AC119365 Ratius no	658	41.6	2.8	190519	2	AC119186	AC119186 Mus muscu
586	42	2.8	217397	10	AC123705	AC123705 Mus muscu	659	41.6	2.8	190679	2	AC147747	AC147747 Homo sapi
587	42	2.8	219293	2	AC141471	AC141471 Mus muscu	660	41.6	2.8	192561	10	AL805943	AL805943 Mouse DNA
588	42	2.8	219331	2	AC134216	AC134216 Ratius no	661	41.6	2.8	196274	2	AC106841	AC106841 Mus muscu
589	42	2.8	226724	10	AC125199	AC125199 Mus muscu	662	41.6	2.8	201114	10	AL808132	AL808132 Mouse DNA
590	42	2.8	235956	2	AC098638	AC098638 Ratius no	663	41.6	2.8	207182	2	AC115795	AC115795 Mus muscu
591	42	2.8	247575	2	AC133047	AC133047 Ratius no	664	41.6	2.8	210257	2	AC135865	AC135865 Ratius no
592	42	2.8	248124	2	AC096607	AC096607 Ratius no	665	41.6	2.8	21657	9	AC123605	AC123605 Mus muscu
593	42	2.8	248124	2	AC096927	AC096927 Ratius no	666	41.6	2.8	214702	9	AC020689	AC020689 Homo sapi
594	42	2.8	255446	2	AC095420	AC095420 Ratius no	667	41.6	2.8	216959	10	AC116998	AC116998 Homo sapi
595	42	2.8	256476	10	AC126940	AC126940 Mus muscu	668	41.6	2.8	231485	2	AC098427	AC098427 Mus muscu
596	42	2.8	258798	2	AC097761	AC097761 Ratius no	669	41.6	2.8	231485	2	AC098427	AC098427 Mus muscu
597	42	2.8	295760	2	AC125718	AC125718 Ratius no	670	41.6	2.8	239114	2	AC129936	AC129936 Mus muscu
598	42	2.8	325656	2	AC120265	AC120265 Ratius no	671	41.6	2.8	264155	2	AC111266	AC111266 Ratius no
599	41.8	2.8	580	5	AF469957	AF469957 Onchorhynch	672	41.6	2.8	271418	2	AC099434	AC099434 Ratius no
600	41.8	2.8	1361	6	CO858785	CO858785 Sequence	673	41.6	2.8	316435	2	AC113678	AC113678 Ratius no
601	41.8	2.8	1361	6	AX305360	AX305360 Sequence	674	41.6	2.8	316435	2	AC118697	AC118697 Mus muscu
602	41.8	2.8	1361	10	MMCALMOD	X61432 M.musculus	675	41.4	2.8	468	6	CO721078	CO721078 Sequence
603	41.8	2.8	1430	8	AB041711	AB041711 Chara cor	676	41.4	2.8	627	11	HUMUT290	L36211 Human STS U

677	41.4	2.8	2452	3	TRBMRSG	K02944 Trypanosoma	750	41.2	2.8	194401	2	AC139951	AC139951 Rattus no
678	41.4	2.8	42053	10	CR626863	CR626863 Mouse DNA	751	41.2	2.8	197700	2	AC102812	AC102812 Mus muscu
679	41.4	2.8	54708	2	AC132904	AC132904 Homo sapi	752	41.2	2.8	197934	2	AC117676	AC117676 Mus muscu
680	41.4	2.8	68951	2	AC100065	AC100065 Mus muscu	753	41.2	2.8	200746	10	AC117232	AC117232 Mus muscu
681	41.4	2.8	99670	8	AC123709	AC123709 Mus muscu	754	41.2	2.8	204037	10	AL566207	AL566207 Mouse DNA
682	41.4	2.8	110000	10	CR382133_11	Continuaction (12 o	755	41.2	2.8	205819	10	AC115954	AC115954 Mus muscu
683	41.4	2.8	132878	9	AC007972	AC007972 Homo sapi	756	41.2	2.8	205924	2	AC132143	AC132143 Mus muscu
684	41.4	2.8	133780	2	AL356293	AL356293 Homo sapi	757	41.2	2.8	206739	2	AC113846	AC113846 Rattus no
685	41.4	2.8	136268	10	AC068496	AC068496 Mus muscu	758	41.2	2.8	216337	10	AL831741	AL831741 Mouse DNA
686	41.4	2.8	139891	2	AC090647	AC090647 Genomic B	759	41.2	2.8	217223	2	AC093472	AC093472 Mus muscu
687	41.4	2.8	140098	2	AC024510	AC024510 Homo sapi	760	41.2	2.8	218226	2	AC126634	AC126634 Rattus no
688	41.4	2.8	142204	2	BX327383	BX327383 Mus muscu	761	41.2	2.8	221782	2	AC115156	AC115156 Rattus no
689	41.4	2.8	150645	10	AC131774	AC131774 Mus muscu	762	41.2	2.8	222259	2	AC110858	AC110858 Rattus no
690	41.4	2.8	165852	10	AC147262	AC147262 Mus muscu	763	41.2	2.8	226637	2	AC124813	AC124813 Mus muscu
691	41.4	2.8	166883	2	AC112923	AC112923 Mus muscu	764	41.2	2.8	227759	2	AC107446	AC107446 Rattus no
692	41.4	2.8	171820	10	AC128550	AC128550 Mus muscu	765	41.2	2.8	235070	10	AL808103	AL808103 Mouse DNA
693	41.4	2.8	183378	2	AL607151	AL607151 Mus muscu	766	41.2	2.8	235874	10	AC130831	AC130831 Mus muscu
694	41.4	2.8	183518	10	AC097366	AC097366 Genomic B	767	41.2	2.8	238800	2	AC111768	AC111768 Rattus no
695	41.4	2.8	184383	2	AC097632	AC097632 Mus muscu	768	41.2	2.8	242744	2	AC110204	AC110204 Mus muscu
696	41.4	2.8	187197	2	AC117766	AC117766 Mus muscu	769	41.2	2.8	245937	2	AC133984	AC133984 Rattus no
697	41.4	2.8	189115	10	AL1772346	AL1772346 Mouse DNA	770	41.2	2.8	247187	2	AC094928	AC094928 Rattus no
698	41.4	2.8	191132	2	AC126895	AC126895 Rattus no	771	41.2	2.8	248294	2	AC097690	AC097690 Rattus no
699	41.4	2.8	191132	2	AC126895	AC126895 Rattus no	772	41.2	2.8	249086	2	AC131856	AC131856 Rattus no
700	41.4	2.8	202763	10	AC121279	AC121279 Mus muscu	773	41.2	2.8	251158	2	AC117023	AC117023 Rattus no
701	41.4	2.8	209227	2	AC140380	AC140380 Mus muscu	774	41.2	2.8	251173	2	AC095202	AC095202 Rattus no
702	41.4	2.8	212472	2	AC121077	AC121077 Mus muscu	775	41.2	2.8	2556597	2	AC095202	AC095202 Rattus no
703	41.4	2.8	212472	10	AC125079	AC125079 Mus muscu	776	41.2	2.8	256597	2	AC109662	AC109662 Rattus no
704	41.4	2.8	213482	10	AC073883	AC073883 Mus muscu	777	41.2	2.8	262608	2	AC092362	AC092362 Homo sapi
705	41.4	2.8	215528	2	AC095866	AC095866 Mus muscu	778	41.2	2.8	262608	2	AC092362	AC092362 Homo sapi
706	41.4	2.8	220758	10	AC117200	AC117200 Mus muscu	779	41.2	2.8	271135	2	AC105492	AC105492 Rattus no
707	41.4	2.8	224056	2	AC122832	AC122832 Mus muscu	780	41.2	2.8	272030	2	AC105482	AC105482 Rattus no
708	41.4	2.8	225880	2	AC131693	AC131693 Mus muscu	781	41.2	2.8	291544	2	AC128496	AC128496 Rattus no
709	41.4	2.8	235918	2	AC129279	AC129279 Rattus no	782	41.2	2.8	297149	2	AC097944	AC097944 Rattus no
710	41.4	2.8	239423	2	AC096602	AC096602 Rattus no	783	41.2	2.8	309050	1	SC0939117	SC0939117 Streptomy
711	41.4	2.8	244529	2	AC121112	AC121112 Mus muscu	784	41.2	2.8	6222	8	BSU90351	BSU90351 Arabidops
712	41.4	2.8	248760	2	AC137456	AC137456 Rattus no	785	41.2	2.8	749	6	BSU070036	BSU070036 Arabidops
713	41.4	2.8	253139	2	AC094876	AC094876 Rattus no	786	41.2	2.8	975	6	AX507498	AX507498 Sequence
714	41.4	2.8	254578	10	AC109253	AC109253 Mus muscu	787	41.2	2.8	975	6	AX589929	AX589929 Sequence
715	41.4	2.8	255871	2	AC095418	AC095418 Rattus no	788	41.2	2.8	1152	6	AX651961	AX651961 Sequence
716	41.4	2.8	255871	2	AC095418	AC095418 Rattus no	789	41.2	2.8	1152	8	AF424577	AF424577 Arabidops
717	41.4	2.8	255946	2	AC091514	AC091514 Rattus no	790	41.2	2.8	1183	8	AY120719	AY120719 Arabidops
718	41.4	2.8	262917	2	AC097239	AC097239 Rattus no	791	41.2	2.8	1183	8	AY120719	AY120719 Arabidops
719	41.4	2.8	266099	2	AC094795	AC094795 Rattus no	792	41.2	2.8	13756	14	AY318876	AY318876 Pseudorab
720	41.4	2.8	284127	2	AC128719	AC128719 Rattus no	793	41.2	2.8	51743	2	AC100147	AC100147 Mus muscu
721	41.4	2.8	285425	2	AC131435	AC131435 Rattus no	794	41.2	2.8	78291	2	AC023216	AC023216 Homo sapi
722	41.2	2.8	447	6	AX660884	AX660884 Sequence	795	41.2	2.8	110000	2	AC151831_0	AC151831_0 Mus muscu
723	41.2	2.8	450	3	BLRNAC	Y09880 B.lanceolat	796	41.2	2.8	129653	2	AC027081	AC027081 Homo sapi
724	41.2	2.8	480	8	AF031482	AF031482 Zea mays	797	41.2	2.8	132457	2	AC102180	AC102180 Mus muscu
725	41.2	2.8	616	3	LTCAMA	X80231 L.carentolia	798	41.2	2.8	134805	10	AC099998	AC099998 Mus muscu
726	41.2	2.8	819	8	PPCAMPROT	X90560 Physcomitre	799	41.2	2.8	135967	10	AL638934	AL638934 Mouse DNA
727	41.2	2.8	942	8	ZMCAM1	X77396 Z.mays Cam1	800	41.2	2.8	136809	10	AL638934	AL638934 Mouse DNA
728	41.2	2.8	1353	3	AB003081	AB003081 Branchios	801	41.2	2.8	149871	9	AL928991	AL928991 Mouse DNA
729	41.2	2.8	1375	3	AB003082	AB003082 Branchios	802	41.2	2.8	166977	9	AC007198	AC007198 Homo sapi
730	41.2	2.8	1405	3	BFBNAC	Y09863 B.floridiae	803	41.2	2.8	167994	10	AC134569	AC134569 Mus muscu
731	41.2	2.8	42262	9	AL662837	AL662837 Human DNA	804	41.2	2.8	169687	9	AC103871	AC103871 Homo sapi
732	41.2	2.8	113421	5	BX284637	BX284637 Zebrafish	805	41.2	2.8	174533	2	AC073718	AC073718 Mus muscu
733	41.2	2.8	149727	10	AL929901	AL929901 Mouse DNA	806	41.2	2.8	181088	2	AC102356	AC102356 Mus muscu
734	41.2	2.8	149407	10	AL671984	AL671984 Mouse DNA	807	41.2	2.8	181467	10	AL844586	AL844586 Mouse DNA
735	41.2	2.8	150222	10	AL845319	AL845319 Mouse DNA	808	41.2	2.8	187930	2	AC127555	AC127555 Mus muscu
736	41.2	2.8	152462	10	AC131998	AC131998 Mus muscu	809	41.2	2.8	191020	2	AC090758	AC090758 Homo sapi
737	41.2	2.8	159330	10	AC118047	AC118047 Mus muscu	810	41.2	2.8	193105	10	AC107236	AC107236 Mus muscu
738	41.2	2.8	163300	2	AC132363	AC132363 Mus muscu	811	41.2	2.8	195294	2	AC051623	AC051623 Mus muscu
739	41.2	2.8	163379	2	AC140394	AC140394 Mus muscu	812	41.2	2.8	196557	10	AC131742	AC131742 Mus muscu
740	41.2	2.8	164223	2	AC127176	AC127176 Rattus no	813	41.2	2.8	196736	2	AC102262	AC102262 Mus muscu
741	41.2	2.8	164885	2	AC132365	AC132365 Mus muscu	814	41.2	2.8	197909	10	AL928719	AL928719 Mouse DNA
742	41.2	2.8	168786	9	AC104864	AC104864 Homo sapi	815	41.2	2.8	200824	2	AC015825	AC015825 Mus muscu
743	41.2	2.8	172837	9	AL450304	AL450304 Human DNA	816	41.2	2.8	201367	2	AC073786	AC073786 Mus muscu
744	41.2	2.8	179333	2	AC117658	AC117658 Mus muscu	817	41.2	2.8	202804	10	AC021630	AC021630 Mus muscu
745	41.2	2.8	182061	10	AC107869	AC107869 Mus muscu	818	41.2	2.8	202807	2	AC021063	AC021063 Mus muscu
746	41.2	2.8	187977	10	AL672229	AL672229 Mouse DNA	819	41.2	2.8	204935	2	AC123793	AC123793 Mus muscu
747	41.2	2.8	188255	2	AC124990	AC124990 Mus muscu	820	41.2	2.8	207949	2	AC131720	AC131720 Mus muscu
748	41.2	2.8	188853	10	AC102105	AC102105 Mus muscu	821	41.2	2.8	208738	10	AC130528	AC130528 Mus muscu
749	41.2	2.8	191721	10	AC101883	AC101883 Mus muscu	822	41.2	2.8	208738	10	AC130528	AC130528 Mus muscu

823	41	2.8	209523	10	AC084386	AC084386 Mus muscu	896	40.8	2.7	234448	10	AC122202	AC122202 Mus muscu
824	41	2.8	210688	10	AC127371	AC127371 Mus muscu	897	40.8	2.7	235509	10	AC091523	AC091523 Mus muscu
825	41	2.8	216860	10	AC134793	AC134793 Mus muscu	898	40.8	2.7	244042	2	AC103004	AC103004 Rattus no
826	41	2.8	218815	2	AL807384	AL807384 Mouse DNA	899	40.8	2.7	244759	2	AC098158	AC098158 Rattus no
827	41	2.8	226196	2	AC138621	AC138621 Mus muscu	900	40.8	2.7	246557	2	AC106539	AC106539 Rattus no
828	41	2.8	228400	10	AC131711	AC131711 Mus muscu	901	40.8	2.7	251814	10	AL591882	AL591882 Mouse DNA
829	41	2.8	229494	10	AL627328	AL627328 Mouse DNA	902	40.8	2.7	252645	2	AC130522	AC130522 Rattus no
830	41	2.8	235915	10	AC129606	AC129606 Mus muscu	903	40.8	2.7	253645	2	AC137382	AC137382 Rattus no
831	41	2.8	240534	2	AC102528	AC102528 Mus muscu	904	40.8	2.7	253945	2	AC119776	AC119776 Rattus no
832	41	2.8	251814	10	AL591882	AL591882 Mouse DNA	905	40.8	2.7	258088	2	AC073766	AC073766 Mus muscu
833	41	2.8	272588	2	AC109673	AC109673 Rattus no	906	40.8	2.7	259834	2	AC128503	AC128503 Rattus no
834	41	2.8	278111	2	AC148992	AC148992 Mus muscu	907	40.8	2.7	264127	2	AC102974	AC102974 Rattus no
835	41	2.8	286588	2	AC106454	AC106454 Rattus no	908	40.8	2.7	268510	2	AC095840	AC095840 Rattus no
836	41	2.8	289531	2	AC113695	AC113695 Rattus no	909	40.8	2.7	272147	2	AC095648	AC095648 Rattus no
837	41	2.8	300574	2	AC097618	AC097618 Rattus no	910	40.6	2.7	447	6	BD2314	BD2314 DNA encodin
838	41	2.8	314521	2	AC126972	AC126972 Rattus no	911	40.6	2.7	796	8	TMU4688	TMU4688 Triticum ae
839	40.8	2.7	7405	8	BP0ALMGEN	X89890 B.pilosa mr	912	40.6	2.7	816	8	TAU48242	TAU48242 Triticum ae
840	40.8	2.7	7608	5	AK062496	AK062496 Oryza sat	913	40.6	2.7	1358	8	PHTCALP1A	PH3535 P.infestans
841	40.8	2.7	839	5	BC041530	BC041530 Xenopus 1	914	40.6	2.7	1362	12	AB178711	AB178711 Synthetic
842	40.8	2.7	1090	5	AB003078	AB003078 Xenopus 1	915	40.6	2.7	1962	12	AB178712	AB178712 Synthetic
843	40.8	2.7	1378	5	AY235104	AY235104 Melaleucis	916	40.6	2.7	1962	12	AB178713	AB178713 Synthetic
844	40.8	2.7	42204	2	AC099977	AC099977 Mus muscu	917	40.6	2.7	2076	12	AB178714	AB178714 Synthetic
845	40.8	2.7	54536	8	AH151534	AH151534 Antitritin	918	40.6	2.7	61310	10	AL691462	AL691462 Mouse DNA
846	40.8	2.7	61518	2	AC133877	AC133877 Mus muscu	919	40.6	2.7	77710	10	AL844552	AL844552 Mouse DNA
847	40.8	2.7	79284	2	BX927314	BX927314 Dantio rer	920	40.6	2.7	81270	10	BX679673	BX679673 Mouse DNA
848	40.8	2.7	84664	10	BX005298	BX005298 Mouse DNA	921	40.6	2.7	101335	10	AL928822	AL928822 Mouse DNA
849	40.8	2.7	87478	2	AC139860	AC139860 Mus muscu	922	40.6	2.7	110000	2	AC103072_0	AC103072 Rattus no
850	40.8	2.7	110000	2	AC098192_0	AC098192 Rattus no	923	40.6	2.7	115932	9	AC011446	AC011446 Homo sapi
851	40.8	2.7	118604	10	AL774010	AL774010 Mouse DNA	924	40.6	2.7	133633	10	AL928857	AL928857 Mouse DNA
852	40.8	2.7	134073	10	AC110734	AC110734 Mus muscu	925	40.6	2.7	149358	10	AC087251	AC087251 Rattus no
853	40.8	2.7	143702	9	AC091940	AC091940 Homo sapi	926	40.6	2.7	152651	2	AC015556	AC015556 Homo sapi
854	40.8	2.7	151259	2	AP002019	AP002019 Homo sapi	927	40.6	2.7	153520	8	AP005727	AP005727 Oryza sat
855	40.8	2.7	151702	10	AC141876	AC141876 Mus muscu	928	40.6	2.7	154002	10	AL662902	AL662902 Mouse DNA
856	40.8	2.7	153791	2	AC119629	AC119629 Rattus no	929	40.6	2.7	162394	10	AC114555	AC114555 Mus muscu
857	40.8	2.7	154245	10	AL805895	AL805895 Mouse DNA	930	40.6	2.7	165818	10	AC121941	AC121941 Mus muscu
858	40.8	2.7	154573	2	BX001062	BX001062 Mouse DNA	931	40.6	2.7	168030	2	AC091462	AC091462 Mus muscu
859	40.8	2.7	159605	10	AC120405	AC120405 Mus muscu	932	40.6	2.7	171142	10	AC011378	AC011378 Rattus no
860	40.8	2.7	161858	2	AC110909	AC110909 Mus muscu	933	40.6	2.7	175948	10	AC109307	AC109307 Mus muscu
861	40.8	2.7	162375	10	AL808124	AL808124 Mouse DNA	934	40.6	2.7	176916	10	AC084387	AC084387 Mus muscu
862	40.8	2.7	169256	10	AC127264	AC127264 Mus muscu	935	40.6	2.7	176191	2	AC113321	AC113321 Mus muscu
863	40.8	2.7	172299	10	AC126679	AC126679 Mus muscu	936	40.6	2.7	178988	2	AC107687	AC107687 Mus muscu
864	40.8	2.7	173460	10	AC137154	AC137154 Mus muscu	937	40.6	2.7	183877	10	BX649561	BX649561 Mouse DNA
865	40.8	2.7	180668	2	AC020857	AC020857 Mus muscu	938	40.6	2.7	195082	10	AC140245	AC140245 Mus muscu
866	40.8	2.7	181029	10	AC140183	AC140183 Mus muscu	939	40.6	2.7	195555	10	AC121603	AC121603 Mus muscu
867	40.8	2.7	184106	2	AC116277	AC116277 Rattus no	940	40.6	2.7	198030	10	AC124585	AC124585 Mus muscu
868	40.8	2.7	184607	10	BX465196	BX465196 Mouse DNA	941	40.6	2.7	199872	2	AC121012	AC121012 Rattus no
869	40.8	2.7	187880	2	AC114669	AC114669 Mus muscu	942	40.6	2.7	200102	5	AC145955	AC145955 Gallus ga
870	40.8	2.7	188575	10	AC107758	AC107758 Mus muscu	943	40.6	2.7	202788	2	AC136457	AC136457 Mus muscu
871	40.8	2.7	192550	2	AC025584	AC025584 Mus muscu	944	40.6	2.7	205925	9	AC009711	AC009711 Homo sapi
872	40.8	2.7	193004	10	AL591177	AL591177 Mouse DNA	945	40.6	2.7	206182	10	AC107720	AC107720 Mus muscu
873	40.8	2.7	194194	2	AC103378	AC103378 Mus muscu	946	40.6	2.7	218291	10	AC146610	AC146610 Mus muscu
874	40.8	2.7	197132	2	AC144519	AC144519 Mus muscu	947	40.6	2.7	221455	10	AL606831	AL606831 Mouse DNA
875	40.8	2.7	198784	10	AC091521	AC091521 Mus muscu	948	40.6	2.7	225159	10	AC135086	AC135086 Mus muscu
876	40.8	2.7	200923	9	AC091928	AC091928 Homo sapi	949	40.6	2.7	231530	2	AC120878	AC120878 Mus muscu
877	40.8	2.7	201275	10	AC102613	AC102613 Mus muscu	950	40.6	2.7	236969	10	AC093467	AC093467 Mus muscu
878	40.8	2.7	202444	10	AC098705	AC098705 Mus muscu	951	40.6	2.7	237284	2	AC097207	AC097207 Rattus no
879	40.8	2.7	203805	10	AC055817	AC055817 Mus muscu	952	40.6	2.7	245617	2	AC095526	AC095526 Rattus no
880	40.8	2.7	205508	10	AC079243	AC079243 Mus muscu	953	40.6	2.7	248140	2	BX901898	BX901898 Dantio rer
881	40.8	2.7	208503	2	AC128820	AC128820 Rattus no	954	40.6	2.7	250759	2	AC115228	AC115228 Rattus no
882	40.8	2.7	212974	10	AC118630	AC118630 Mus muscu	955	40.4	2.7	2240	6	AKX83471	AKX83471 Sequence
883	40.8	2.7	214035	2	AC148503	AC148503 Callithr	956	40.4	2.7	2240	6	AKX96294	AKX96294 Homo sapi
884	40.8	2.7	214062	2	AC123354	AC123354 Rattus no	957	40.4	2.7	2284	6	COB42342	COB42342 Sequence
885	40.8	2.7	215819	2	AC099288	AC099288 Rattus no	958	40.4	2.7	2284	3	AK128821	AK128821 Homo sapi
886	40.8	2.7	216882	2	AC132716	AC132716 Rattus no	959	40.4	2.7	2632	3	AY568293	AY568293 Cithidia
887	40.8	2.7	218468	2	AC123108	AC123108 Rattus no	960	40.4	2.7	7722	1	AE013394	AE013394 Homo sapi
888	40.8	2.7	220848	10	AC091579	AC091579 Homo sapi	961	40.4	2.7	11677	1	AE013391	AE013391 Xanthomon
889	40.8	2.7	222845	10	AC100491	AC100491 Mus muscu	962	40.4	2.7	110000	2	AC097101_4	AC097101_4 Continuation (5 of
890	40.8	2.7	223845	2	AC132661	AC132661 Rattus no	963	40.4	2.7	110000	2	AC108688	AC108688 Rattus no
891	40.8	2.7	224735	2	AC112971	AC112971 Rattus no	964	40.4	2.7	110000	8	CR382130_28	CR382130_28 Continuation (5 of
892	40.8	2.7	226642	2	AC122971	AC122971 Rattus no	965	40.4	2.7	110000	8	CR382130_28	CR382130_28 Continuation (29 of
893	40.8	2.7	229220	10	AC091519	AC091519 Mus muscu	966	40.4	2.7	137571	2	AC118969	AC118969 Rattus no
894	40.8	2.7	233132	2	AC118308	AC118308 Rattus no	967	40.4	2.7	145678	2	AC118969	AC118969 Rattus no
895	40.8	2.7	233519	2	AC098446	AC098446 Rattus no	968	40.4	2.7	154608	10	BX664619	BX664619 Mouse DNA

969	40.4	2.7	157159	2	AC026279	AC026279 Homo sapi
970	40.4	2.7	161461	10	AC124355	AC124355 Mus muscu
971	40.4	2.7	163773	10	AC125402	AC125402 Mus muscu
972	40.4	2.7	169834	10	AC124430	AC124430 Mus muscu
973	40.4	2.7	169865	2	AC125341	AC125341 Mus muscu
974	40.4	2.7	174025	9	AC073288	AC073288 Homo sapi
975	40.4	2.7	175583	9	AL590502	AL590502 Human DNA
976	40.4	2.7	177779	2	AC116870	AC116870 Mus muscu
977	40.4	2.7	183797	2	AC022400	AC022400 Homo sapi
978	40.4	2.7	185867	10	AL606744	AL606744 Mouse DNA
979	40.4	2.7	186589	2	AC023000	AC023000 Homo sapi
980	40.4	2.7	188201	10	AC122303	AC122303 Mus muscu
981	40.4	2.7	190462	9	AC092535	AC092535 Homo sapi
982	40.4	2.7	192717	10	AC121291	AC121291 Mus muscu
983	40.4	2.7	194715	9	AC078898	AC078898 Homo sapi
984	40.4	2.7	197176	2	AC022763	AC022763 Homo sapi
985	40.4	2.7	198218	2	AC037447	AC037447 Homo sapi
986	40.4	2.7	200858	10	AC118255	AC118255 Mus muscu
987	40.4	2.7	203180	10	AC145307	AC145307 Mus muscu
988	40.4	2.7	203669	2	AC113929	AC113929 Homo sapi
989	40.4	2.7	203720	2	AC093861	AC093861 Homo sapi
990	40.4	2.7	207120	2	AL844520	AL844520 Homo sapi
991	40.4	2.7	208432	10	AC114411	AC114411 Mus muscu
992	40.4	2.7	209336	10	AC108840	AC108840 Mus muscu
993	40.4	2.7	210188	2	AC124611	AC124611 Mus muscu
994	40.4	2.7	213660	2	AC073699	AC073699 Mus muscu
995	40.4	2.7	215660	2	AC115801	AC115801 Mus muscu
996	40.4	2.7	216800	10	AL589744	AL589744 Mouse DNA
997	40.4	2.7	220638	10	AL645723	AL645723 Mouse DNA
998	40.4	2.7	221526	10	AC117668	AC117668 Mus muscu
999	40.4	2.7	223366	10	AC023174	AC023174 Mus muscu
1000	40.4	2.7	226373	2	AC119821	AC119821 Mus muscu
1001	40.4	2.7	229658	2	AC096408	AC096408 Rattus no
1002	40.4	2.7	237875	2	AC117027	AC117027 Rattus no
1003	40.4	2.7	240822	2	AC095369	AC095369 Rattus no
1004	40.4	2.7	243589	2	AC114132	AC114132 Rattus no
1005	40.4	2.7	248550	1	SC093120	SC093120 Streptomy
1006	40.4	2.7	249638	2	AC107177	AC107177 Rattus no
1007	40.4	2.7	263668	2	AC126697	AC126697 Rattus no
1008	40.4	2.7	272384	2	AC125722	AC125722 Rattus no
1009	40.4	2.7	277285	2	AC110434	AC110434 Rattus no
1010	40.4	2.7	301833	2	AC112629	AC112629 Rattus no
1011	40.4	2.7	315176	2	AC078956	AC078956 Homo sapi
1012	40.4	2.7	320381	2	AC126143	AC126143 Rattus no
1013	40.4	2.7	331543	2	AC111236	AC111236 Rattus no
1014	40.2	2.7	654	6	E02315	E02315 DNA encodin
1015	40.2	2.7	654	6	AX401676	AX401676 Sequence
1016	40.2	2.7	1246	6	AX164174	AX164174 Sequence
1017	40.2	2.7	1446	10	RNRCM1	RNRCM1
1018	40.2	2.7	3513	10	AF178845	AF178845 Rattus no
1019	40.2	2.7	4021	10	BC054805	BC054805 Mus muscu
1020	40.2	2.7	4229	8	AK120277	AK120277 Oryza sat
1021	40.2	2.7	104563	2	AL442065	AL442065 Human DNA
1022	40.2	2.7	105608	2	AC116396	AC116396 Mus muscu
1023	40.2	2.7	110000	10	AF162137-1	AF162137-1
1024	40.2	2.7	112171	8	AL837506	AL837506 Mouse DNA
1025	40.2	2.7	125217	8	AP003930	AP003930 Oryza sat
1026	40.2	2.7	130604	9	HS1007616	HS1007616 Human DNA
1027	40.2	2.7	137127	2	AC113343	AC113343 Homo sapi
1028	40.2	2.7	144131	10	AC110822	AC110822 Mus muscu
1029	40.2	2.7	152876	2	AC099488	AC099488 Homo sapi
1030	40.2	2.7	153754	2	BS000598	BS000598 Pan trogl
1031	40.2	2.7	153867	2	AC132224	AC132224 Mus muscu
1032	40.2	2.7	158009	10	AL837508	AL837508 Mouse DNA
1033	40.2	2.7	163444	2	AC025866	AC025866 Homo sapi
1034	40.2	2.7	163780	2	AC146215	AC146215 Pan trogl
1035	40.2	2.7	163914	9	AC098487	AC098487 Homo sapi
1036	40.2	2.7	168027	9	AC147337	AC147337 Pan trogl
1037	40.2	2.7	168364	10	AC116507	AC116507 Mus muscu
1038	40.2	2.7	168605	2	AC022477	AC022477 Homo sapi
1039	40.2	2.7	169342	2	AL136991	AL136991 Human DNA
1040	40.2	2.7	172116	2	AC087100	AC087100 Mus muscu
1041	40.2	2.7	173169	9	AC068538	AC068538 Homo sapi
1042	40.2	2.7	176104	2	AC143751	AC143751 Macaca mu
1043	40.2	2.7	176184	2	AC119918	AC119918 Mus muscu
1044	40.2	2.7	177152	2	AC012115	AC012115 Homo sapi
1045	40.2	2.7	177770	9	AC110027	AC110027 Homo sapi
1046	40.2	2.7	178137	9	AC011302	AC011302 Homo sapi
1047	40.2	2.7	179254	2	AC134306	AC134306 Homo sapi
1048	40.2	2.7	181413	9	AC080032	AC080032 Homo sapi
1049	40.2	2.7	181851	10	AC102413	AC102413 Mus muscu
1050	40.2	2.7	185121	2	AC149619	AC149619 Papio anu
1051	40.2	2.7	189782	2	AC117808	AC117808 Mus muscu
1052	40.2	2.7	190904	2	AC138081	AC138081 Homo sapi
1053	40.2	2.7	194176	2	AC132155	AC132155 Homo sapi
1054	40.2	2.7	199227	2	AC110876	AC110876 Mus muscu
1055	40.2	2.7	201126	10	AC138318	AC138318 Mus muscu
1056	40.2	2.7	203668	2	AC084411	AC084411 Mus muscu
1057	40.2	2.7	204205	10	AL669929	AL669929 Mouse DNA
1058	40.2	2.7	204533	9	AC116994	AC116994 Mus muscu
1059	40.2	2.7	207366	2	AC090001	AC090001 Homo sapi
1060	40.2	2.7	210291	10	AC129533	AC129533 Mus muscu
1061	40.2	2.7	210849	9	AC104209	AC104209 Homo sapi
1062	40.2	2.7	212373	10	AL606927	AL606927 Mouse DNA
1063	40.2	2.7	215129	2	AC131861	AC131861 Rattus no
1064	40.2	2.7	215390	10	AL672089	AL672089 Mouse DNA
1065	40.2	2.7	215676	2	AC131299	AC131299 Mus muscu
1066	40.2	2.7	221792	2	AC112344	AC112344 Rattus no
1067	40.2	2.7	225600	10	AC115936	AC115936 Mus muscu
1068	40.2	2.7	227696	2	AC112936	AC112936 Mus muscu
1069	40.2	2.7	232409	10	AL772187	AL772187 Mouse DNA
1070	40.2	2.7	235732	2	AC098491	AC098491 Rattus no
1071	40.2	2.7	237732	2	AC111246	AC111246 Rattus no
1072	40.2	2.7	240692	2	AC096178	AC096178 Rattus no
1073	40.2	2.7	252366	2	AC132869	AC132869 Mus muscu
1074	40.2	2.7	266770	2	AC130136	AC130136 Rattus no
1075	40.2	2.7	267438	2	AC101942	AC101942 Mus muscu
1076	40.2	2.7	276248	2	AC087561	AC087561 Mus muscu
1077	40.2	2.7	282163	2	AC113669	AC113669 Rattus no
1078	40.2	2.7	285591	2	AC123095	AC123095 Rattus no
1079	40.2	2.7	290433	2	AC111255	AC111255 Rattus no
1080	40.2	2.7	300620	1	AE016782	AE016782 Pseudomon
1081	40.2	2.7	300800	2	SC0939112	SC0939112 Streptomy
1082	40.2	2.7	314959	2	AC106099	AC106099 Rattus no
1083	40.2	2.7	314959	2	AC106099	AC106099 Rattus no
1084	40.2	2.7	340972	2	AC109045	AC109045 Rattus no
1085	40.2	2.7	303	6	CQ727832	CQ727832 Sequence
1086	40.2	2.7	334	8	LEY14765	LEY14765 Lycopodium
1087	40.2	2.7	447	8	BD174656	BD174656 Fluoresce
1088	40.2	2.7	1278	6	AX534969	AX534969 Sequence
1089	40.2	2.7	1278	6	AX534969	AX534969 Sequence
1090	40.2	2.7	3144	14	SHDNARPOLA	SHDNARPOLA
1091	40.2	2.7	4732	9	HSMB04662	HSMB04662
1092	40.2	2.7	47198	2	AC090252	AC090252 Homo sapi
1093	40.2	2.7	79560	9	AL591471	AL591471 Human DNA
1094	40.2	2.7	87140	9	AL669942	AL669942 Human DNA
1095	40.2	2.7	105298	9	BX664727	BX664727 Human DNA
1096	40.2	2.7	107879	2	AC114962	AC114962 Homo sapi
1097	40.2	2.7	110000	2	AC094437-2	AC094437-2
1098	40.2	2.7	110000	2	AL360016-2	AL360016-2
1099	40.2	2.7	111183	9	AC008950	AC008950 Homo sapi
1100	40.2	2.7	127405	10	AL645599	AL645599 Mouse DNA
1101	40.2	2.7	133753	9	AC131180	AC131180 Homo sapi
1102	40.2	2.7	133910	10	AL929253	AL929253 Mouse DNA
1103	40.2	2.7	134736	2	AC151293	AC151293 Sorex ara
1104	40.2	2.7	140817	10	AC127231	AC127231 Mus muscu
1105	40.2	2.7	142178	10	AL603705	AL603705 Mouse DNA
1106	40.2	2.7	143650	10	AL928862	AL928862 Mouse DNA
1107	40.2	2.7	148251	9	AC083867	AC083867 Homo sapi
1108	40.2	2.7	148996	9	AC102953	AC102953 Homo sapi
1109	40.2	2.7	151087	10	BX649549	BX649549 Mouse DNA
1110	40.2	2.7	151398	2	AC102324	AC102324 Mus muscu
1111	40.2	2.7	158419	10	AC137901	AC137901 Mus muscu
1112	40.2	2.7	161940	10	AL929117	AL929117 Mouse DNA
1113	40.2	2.7	163776	2	AC109289	AC109289 Mus muscu
1114	40.2	2.7	164256	2	AC134725	AC134725 Rattus no

1115	40	2.7	164795	9	AP002518	Homo sapi	1188	39.8	2.7	634	8	AK104031	AK104031 Oryza sat
1116	40	2.7	166743	2	AC140242	Mus muscu	1189	39.8	2.7	681	6	AX899104	AX899104 Sequence
1117	40	2.7	168026	3	AL445670	Human DNA	1190	39.8	2.7	681	6	BD034637	BD034637 Sequence
1118	40	2.7	168976	8	AP001539	Oryza sat	1191	39.8	2.7	731	8	AK071852	AK071852 Oryza sat
1119	40	2.7	169442	10	AC124545	Mus muscu	1192	39.8	2.7	798	8	AX652177	AX652177 Sequence
1120	40	2.7	170540	2	AC133333	Mus muscu	1193	39.8	2.7	813	6	AF441191	AF441191 Oryza sat
1121	40	2.7	172539	10	AC110523	Mus muscu	1194	39.8	2.7	970	5	AF180890	AF180890 Dantio rer
1122	40	2.7	173136	9	AC103380	Mus muscu	1195	39.8	2.7	1139	10	RNMRBCB	X52840 Rat mRNA fo
1123	40	2.7	174241	2	AC018634	Human Chr	1196	39.8	2.7	1248	6	AX653136	AX653136 Sequence
1124	40	2.7	174613	2	AC012522	Homo sapi	1197	39.8	2.7	1491	5	BC064284	BC064284 Dantio rer
1125	40	2.7	176001	2	AC118688	Mus muscu	1198	39.8	2.7	1635	3	AK112671	AK112671 Clona Int
1126	40	2.7	176616	2	AC150016	AC150016 Papio anu	1199	39.8	2.7	2022	9	AF105372	AF105372 Homo sapi
1127	40	2.7	177191	2	AC145146	Homo sapi	1200	39.8	2.7	2312	9	AB047906	AB047906 Macaca fa
1128	40	2.7	177630	2	AC087156	Mus muscu	1201	39.8	2.7	3612	10	MMCOLA4	X067777 Mouse mRNA
1129	40	2.7	177830	2	AC123821	Mus muscu	1202	39.8	2.7	6512	6	AX306181	AX306181 Sequence
1130	40	2.7	179299	10	AC132295	Mus muscu	1203	39.8	2.7	6512	10	MUSCOL144	U04694 Mus musculu
1131	40	2.7	182517	2	AC149571	AC149571 Rhinoloph	1204	39.8	2.7	6522	10	BC072650	BC072650 Mus muscu
1132	40	2.7	184536	2	AC068682	Homo sapi	1205	39.8	2.7	13697	9	AP001475	AP001475 Homo sapi
1133	40	2.7	186265	2	AC016602	Homo sapi	1206	39.8	2.7	79560	9	AL591471	AL591471 Human DNA
1134	40	2.7	186713	2	AC123644	Mus muscu	1207	39.8	2.7	105929	9	BX664727	BX664727 Human DNA
1135	40	2.7	188616	10	AC123795	Mus muscu	1208	39.8	2.7	106214	8	AP003818	AP003818 Oryza sat
1136	40	2.7	188889	10	AC122381	AC122381 Mus muscu	1209	39.8	2.7	110000	1	BX571966_30	Continuation (31 o
1137	40	2.7	190557	2	AC130064	Rattus no	1210	39.8	2.7	110000	2	CP000011_22	Continuation (23 o
1138	40	2.7	190654	2	AC018949	Homo sapi	1211	39.8	2.7	110000	2	AC094428	Continuation (2 of
1139	40	2.7	190680	2	AC147575	AC147575 Homo sapi	1212	39.8	2.7	112597	9	HS8210_1	Continuation (2 of
1140	40	2.7	191965	9	CNS05TDG	AC140122 Homo sapi	1213	39.8	2.7	130805	9	AC118283	AC118283 Homo sapi
1141	40	2.7	191965	9	CNS05TDG	AC156756 Human chr	1214	39.8	2.7	130973	8	AP003813	AP003813 Oryza sat
1142	40	2.7	192135	10	AC122274	Mus muscu	1215	39.8	2.7	133289	9	AC012317	AC012317 Homo sapi
1143	40	2.7	194209	2	AC119581	Rattus no	1216	39.8	2.7	140367	10	AL7732439	AL7732439 Mouse DNA
1144	40	2.7	194476	2	AC147745	AC147745 Homo sapi	1217	39.8	2.7	145972	10	AC145608	AC145608 Mus muscu
1145	40	2.7	195226	2	AC141305	AC141305 Homo sapi	1218	39.8	2.7	149791	2	CR848007	CR848007 Homo sapi
1146	40	2.7	195226	2	AC141305	AC139199 Mus muscu	1219	39.8	2.7	152564	10	AC127549	AC127549 Mus muscu
1147	40	2.7	195650	2	AC139199	AC124730 Mus muscu	1220	39.8	2.7	155416	10	AL160286	AL160286 Human DNA
1148	40	2.7	198026	2	AL928812	AL928812 Mouse DNA	1221	39.8	2.7	158398	9	AL929020	AL929020 Mouse DNA
1149	40	2.7	199019	10	AC078911	AC078911 Mus muscu	1222	39.8	2.7	160321	10	AL772321	AL772321 Mouse DNA
1150	40	2.7	200329	2	AC116611	AC116611 Rattus no	1223	39.8	2.7	163641	9	AL591441	AL591441 Human DNA
1151	40	2.7	200329	2	AC116611	AC139809 Homo sapi	1224	39.8	2.7	164926	4	AC095021	AC095021 Sus scrof
1152	40	2.7	203786	2	AC139809	AC139809 Homo sapi	1225	39.8	2.7	165932	10	AC132948	AC132948 Mus muscu
1153	40	2.7	203865	10	EX088573	EX088573 Mouse DNA	1226	39.8	2.7	167861	10	AC126059	AC126059 Mus muscu
1154	40	2.7	206973	10	AC149059	AC149059 Mus muscu	1227	39.8	2.7	169726	2	AC1120421	AC1120421 Mus muscu
1155	40	2.7	208885	2	AC101703	AC101703 Homo sapi	1228	39.8	2.7	171267	2	AC124922	AC124922 Rattus no
1156	40	2.7	209885	2	AC139829	AC139829 Homo sapi	1229	39.8	2.7	171749	9	AC145538	AC145538 Dideiphis
1157	40	2.7	211763	2	AC123558	AC123558 Mus muscu	1230	39.8	2.7	175334	9	AC007920	AC007920 Homo sapi
1158	40	2.7	215524	10	AL603913	AL603913 Mouse DNA	1231	39.8	2.7	176681	10	AC1326437	AC1326437 Mus muscu
1159	40	2.7	221389	2	AC112122	Rattus no	1232	39.8	2.7	178786	10	AC126437	AC126437 Mus muscu
1160	40	2.7	221803	2	AC106977	AC106977 Rattus no	1233	39.8	2.7	178786	2	AC119920	AC119920 Mus muscu
1161	40	2.7	222825	2	AC094945	AC094945 Rattus no	1234	39.8	2.7	178786	2	AC145538	AC145538 Dideiphis
1162	40	2.7	224522	2	AC129172	AC129172 Rattus no	1235	39.8	2.7	178786	2	AC110195	AC110195 Mus muscu
1163	40	2.7	224760	10	AC124543	AC124543 Mus muscu	1236	39.8	2.7	178786	2	AC110195	AC110195 Mus muscu
1164	40	2.7	231371	2	AC118527	AC118527 Rattus no	1237	39.8	2.7	178786	2	AC133515	AC133515 Mus muscu
1165	40	2.7	231530	2	AC120878	AC120878 Mus muscu	1238	39.8	2.7	178786	2	AC026402	AC026402 Homo sapi
1166	40	2.7	231593	10	AC140433	AC140433 Mus muscu	1239	39.8	2.7	178786	10	AL645471	AL645471 Mouse DNA
1167	40	2.7	232410	2	AC094535	AC094535 Rattus no	1240	39.8	2.7	178786	2	AC006115	AC006115 Homo sapi
1168	40	2.7	234139	2	AC094725	AC094725 Rattus no	1241	39.8	2.7	178786	2	AC145190	AC145190 Sus scrof
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1171	40	2.7	241781	2	AC122087	Rattus no	1244	39.8	2.7	182366	9	AC017014	AC017014 Homo sapi
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1182	40	2.7	286117	2	AC115390	AC115390 Rattus no	1255	39.8	2.7	199215	10	AC146609	AC146609 Mus muscu
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1184	40	2.7	302564	2	AC105608	Rattus no	1257	39.8	2.7	203301	2	AC147067	AC147067 Homo sapi
1185	40	2.7	303091	2	AC084799	Mus muscu	1258	39.8	2.7	205129	2	AC148031	AC148031 Homo sapi
1186	40	2.7	450	8	OSCALMOD1	Z18827 O. sativa ge	1259	39.8	2.7	206377	10	AC126689	AC126689 Mus muscu
1187	40	2.7	450	8	RICALMODU	L18913 Oryza sativ	1260	39.8	2.7	207841	2	AC072019	AC072019 Homo sapi

1261	39.8	2.7	209178	10	AC120425	AC120425 Mus muscu	1334	39.6	2.7	161274	2	AC139613	AC139613 Rattus no
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ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
REFERENCE	1 Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A., Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P., Watanabe, C.K. and Wood, W.I. Secreted and transmembrane polypeptides and nucleic acids encoding the same Patent: WO 0193983-A 109 13-DEC-2001; Genentech INC. (US)					
JOURNAL	Location/Qualifiers					
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LOCUS Sequence 109 from Patent WO0208288.
ACCESSION AX362349
VERSION AX362349.1 GI:18694632
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1
Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,
Waranabe, C.K. and Wood, W.I.
Secreted and transmembrane polypeptides and nucleic acids encoding
the same
Patent: WO 0208288-A 109 31-JAN-2002;
Genentech, Inc. (US)
FEATURES
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Db 421 CGAGACTTTGTGAACATGATGCTGAGGAAACGATGCTGCTCAAGTTAGTATGATG 480

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pd- 20 July 2002

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LOCUS AX697127
DEFINITION Sequence 195 from Patent WO078961.
ACCESSION AX697127
VERSION AX697127.1 GI:29498088
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE
AUTHORS 1
Ferrara, N., Stewart, T.A., Williams, P.M., Baker, K.P., Desnoyers, L.,
Bacon, D.L., Gao, W.O., Pan, J., Borstein, D., Fong, S., Goddard, A.,
Gidycz, P.J., Guirney, A.L., Smith, V., Tuma, D., Wood, W.I.,
Grimaldi, C.J., Hillan, K.J., Paoni, N.F., Roy, M.A. and Watanabe, C.K.
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Patent: WO 0078961-A 195 28-DEC-2000; pub
Genentech Inc. (US)
JOURNAL location/Qualifiers
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ORIGIN

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Qy	1141	AAGGAAAGACCTTGGGCACTTGGGAGCCCTTCAAGAAGTA	CCAGAAGAACCTTCAGTC	1200	
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 VERSION AY359067.1 GI:37183251
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 SOURCE
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 AUTHORS Clark,H.F., Garney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J., Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Denel,B., Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E., Helens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S., Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C., Schenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V., Stimson,J., Vagts,A., Vandalen,R., Watanabe,C., Wiend,D., Woods,K., Xie,M.H., Yanusura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z., Goddard,A., Wood,W.I. and Godowski,P.
 TITLE The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins
 JOURNAL A Bioinformatics Assessment
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 2 (bases 1 to 1485)
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 AUTHORS Clark,H.F.
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 JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA
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ORIGIN

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QY	61	GCCGCTTCGGGAAGCTTGAGCCGGCGGGAGCCCGCGCTCGCATGTCCGGGCGAGCTC	120						
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ACCESSION AX882339
VERSION AX882339.1 GI:40037187
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
Primer for synthesising full-length cDNA and their use
Patent: EP 1074617-A 17244 07-FEB-2001;
Research Association for Biotechnology (JP)
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ORIGIN
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LOCUS
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Homo sapiens cDNA FLJ12783 fig. clone NT2RP2001876, moderately
similar to ALLOGRAFT INFLAMMATORY FACTOR-1.

ACCSSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AK022845 GI:10434474
oligo capping; fis (full insert sequence) .
Homo sapiens (human)
Homo sapiens

REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1
Oca,T., Suzuki,Y., Nishikawa,T., Otsuki,T., Sugiyama,T., Irie,R.,
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Nagase,T., Nomura,N., Kikuchi,H., Masuho,Y., Yamashita,R.,

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Complete sequencing and characterization of 21,243 full-length
human cDNAs
Nat. Genet. 36 (1), 40-45 (2004)
14702039
2
Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
Nishikawa,T., Nagai,K., Sugano,S., Takahashi-Fujii,A., Hara,H.,
Tanase,T., Nomura,Y., Togiya,S., Komai,F., Hara,R., Takeuchi,K.,
Arita,M., Nabekura,T., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J.,
Wakamatsu,A., Nakamura,Y., Nagahara,K., Masuho,Y. and Oshima,A.
NEDO human cDNA sequencing project
Unpublished
3 (bases 1 to 3375)
Isogai,T. and Otsuki,T.
Direct Submission
Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel.81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing; Research Association for Biotechnology; cDNA library
construction, 5'- & 3'-end one pass sequencing and clone selection;
Helix Research Institute (supported by Japan Key Technology Center
etc.) and Department of Virology, Institute of Medical Science,
University of Tokyo.
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VERSION AR135358.1 GI:14476030
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ORGANISM Unknown.
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AUTHORS 1 (bases 1 to 3449)
Hillman,J.L., Lal,P., Tang,Y.Tom., Yue,H., Au-Young,J.,
Corley,N.C., Guegler,K.J. and Baughn,M.R.
TITLE Human immune system associated molecules
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ORIGIN

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Job time : 6885 secs